Preface

Drosophila melanogaster is a species of Diptera, or the order of flies, in the family Drosophilidae. This species is one of the most commonly used model organisms in biology, including studies in genetics, physiology, microbial pathogenesis and life history evolution because they are easy to take care of, breed quickly and lay many eggs. In this book, the authors present current research in the study of drosophila melanogaster including: the gametogenesis, embryonic and post-embryonic development of drosophila melanogaster; the significance of stellate genes in drosophila melanogaster; the evolution of drosophila melanogaster retroviruses and the morphogenesis of drosophila melanogaster macrochaetes.

Chapter 1 - Gametogenesis in all animals, seems to be a much more sensitive developmental stage than later stages of their lives. In *Drosophila melanogaster*, gametogenesis -especially oogenesis - is shown to be a very sensitive biological phase, in response to exogenous stress factors like radiation - including electromagnetic fields (EMFs) - chemicals, elevated or low temperature, food deprivation, etc. Stress-induced cell death during oogenesis is already studied for a variety of stress factors. The high sensitivity of oogenesis, in combination with the fact that particularly in *Drosophila* it is very well studied, makes this animal a valuable tool for the study of the biological activity of different environmental agents. The developmental stages of oogenesis, embryonic, and post-embryonic development in *Drosophila* exhibit a good timing under certain environmental conditions, and this has led us to the design of experimental protocols based on the assessment of the reproductive capacity, by the number of the first filial generation (F_1) pupae, reflecting the effect of the different exogenous factors on gametogenesis and, in turn, on oviposition. Due to the existence of special

checkpoints during oogenesis (most sensitive developmental stages), all the abnormally developing eggs are properly eliminated by stress-induced cell death on the nurse and follicle cells during early and mid-oogenesis leading to the destruction of the whole egg-chamber. Thus, usually, environmental factors do not have an effect on the offspring's genome and morphology but rather on the number of laid eggs (oviposition) and, consequently, on the number of developing post-embryos (larvae and pupae). For this, the number of F_1 pupae, under certain conditions, may reflect biological changes due to exogenous factors. The situation may be more complicated when the exogenous stress factor is microwave radiation. This kind of man-made radiation is found to damage DNA not only in the nurse and follicle cells during oogenesis as by other previously known stress factors, but also in the oocyte from which the progeny organism will be developed after fertilization. DNA damage in the oocyte may result in inherited mutations transferred to the next generations and for this reason the biological changes due to microwave radiation may not be restricted only to changes in the reproductive capacity. In this chapter, *Drosophila* gametogenesis, embryonic, post-embryonic development and life-cycle are briefly described. The chapter then focuses on stress-induced cell death during oogenesis, and discusses a basic experimental protocol regarding the effect of environmental stress factors on reproductive capacity, based on the increased sensitivity of *Drosophila* gametogenesis and the good timing of the embryonic and post-embryonic developmental phases.

Chapter 2 - Regulation of the testis-specific *crystal-Stellate* genetic system in *Drosophila melanogaster* is a subject of intensive investigation. The X-linked tandem testis-specific clusters of *Stellate* genes encode proteins homologous to the regulatory β-subunit of CK2 protein kinase, CK2β, and are not expressed in wild-type flies. Repression of *Stellate* genes is carried out with the assistance of the Y-linked *crystal* locus (also known as *Su(Ste)*, *Supressor of Stellate*). The *Su(Ste)* repeats are highly homologous to *Stellate* genes, and normally, the expression of *Stellate* is repressed by short RNAs provided by anti-sense transcription of *Su(Ste)*, via piRNA silencing. Derepression of *Stellate* genes in the absence of the *crystal* locus (*crystal* line) leads to the accumulation of Stellate protein crystals in spermatocytes, defects in condensation and segregation of meiotic chromosomes and also partial or complete male sterility. Functions of these genes are unclear, whereas CK2 plays an important role in the regulation of transcription and cell division in *D.melanogaster* and other eukaryotes. Why the *crystal-Stellate* system had appeared and for what function, as well as the exact mechanism of the Stellate pathogenesis, have not yet been revealed. *Stellate* genes are found only in

D.melanogaster and are believed to originate due to the amplification of the *CK2βtes* autosomal gene encoding another regulatory β-subunit of CK2. The soluble Stellate protein exists in the nuclei of the spermatocytes of the *crystal* line flies, where it interacts with the catalytic α-subunit of CK2 (CK2α), causing a modulation of phosphorylation of some nuclear proteins. Stellate also undergoes lysine methylation and mimics the trimethyl-H3K9 epigenetic modification of the histone H3 tail. In this chapter, the authors summarize the current conceptions of the origin and organization of the *crystal-Stellate* system, and transcriptional and post-transcriptional regulation of *Stellate* expression. They also discuss presumable mechanisms of pathogenesis caused by the hyper-expression of Stellate protein.

Chapter 3 - The evolutionarily conserved family of *nxf* genes is found in most eukaryotic organisms. *Drosophila melanogaster* and *Mus musculus* have four genes belonging to this family (FlyBase, 2010; Sasaki et al., 2005); *Homo sapiens* has five genes (Herold et al., 2000). The main gene that gave the family its name is the *nxf1* (Nuclear eXport Factor) gene. In *D. melanogaster* the *Dm nxf1* gene was primarily named the *small bristles* (*sbr*) gene (Herold et al., 2000; Tretyakova et al., 2001; Wilkie et al., 2001). Orthologs of the *nxf1* gene in different organisms facilitate the transport of most, if not all, mRNAs from the nucleus to the cytoplasm (Kang, Cullen, 1999; Conti, Izaurralde, 2001; Herold et al., 2003; Sasaki et al., 2005). The appearance of paralogous genes belonging to the *nxf* family has been probably due to the specialization of NXF in term of transport of certain types of mRNA (Jun et al., 2001). Herein the authors discuss their own data and the results accumulated by other groups in an attempt to shed light on the evolution of *nxf* family in different organisms and its functional specialization.

Chapter 4 - Over the past hundred years *Drosophila melanogaster* is being used as a genetic model to study gene interactions, genetic mechanisms of development and molecular processes. The *D. melanogaster* genome was one of the first sequenced genomes. Then Drosophila was chosen as a model of comparative (evolutionary) genomics: the genomes of 11 more different Drosophila species were also sequenced.

Chapter 5 - Formation of specialized spatial structures comprising various cell types is most important in the ontogenesis of multicellular organisms. An example is the D. melanogaster bristle organs. Bristles (micro- and macrochaetes) are external sensory organs, elements of the peripheral nervous system, playing the role of mechanoreceptors. Their comparatively simple organization comprising only four specialized cells and a common origin of these cells make macrochaetes a convenient model for studying cell

differentiation. The four cells forming bristle organ result from two successive divisions of a single cell, sensory organ precursor (SOP) cell. The number of macrochaetes on drosophila body corresponds to the number of SOP cells. The morphogenesis of macrochaetes comprises three stages, the first two determining a neural fate of the cells. The third stage is cell specialization into components of the bristle organ—neuron, thecogen, tormogen, and trichogen. Development of each bristle commences from segregation of proneural clusters, of 20–30 cells, from the massif of undifferentiated cells of the wing imaginal disc. At this stage, each cluster cell can potentially become a SOP cell. At the second stage, the only SOP cell and its position are determined within each cluster. Finally, two asymmetric divisions of the SOP cell with subsequent differentiation of the daughter cells gives the bristle organ. Several dozens genes are involved in the control of macrochaete morphogenesis. The main component of this system is the proneural genes of achaete-scute complex (AS-C). An increased content of proneural proteins fundamentally distinguished the cells that will follow the neural developmental pathway from the disc epidermal cells. A local AS-C expression, initiated at specified disc sites by specific transcription factors, determines the number and topology of proneural clusters. The expression of AS-C genes, continuing in the cells of the cluster, increases the difference in proneural protein content, first, between the cluster cells and then, between the cluster cells and the single SOP cell, where it reaches the maximum level. This process is provided by both the intracellular regulation of AS-C gene activity and intercellular events mediated via the EGFR and Notch signaling pathways. The third stage in macrochaete morphogenesis comprises two successive asymmetric SOP cell divisions, determining the final specialization. The selector genes, in particular, numb, neuralized, tramtrack, and musashi, play the key role in cell type specification. This review systematizes the data on molecular genetic system controlling drosophila bristle morphogenesis and proposes an integral scheme of its functioning.

Chapter 6 - Although sleep has been studied in humans and rodents for several decades, it has become clear more recently that sleep is an evolutionarily conserved process that is present in several arthropods including cockroaches [1] and bees [2] as well as in the nematode C. elegans [see chapter 5]. Drosophila is a genetic model system that has been used extensively to successfully elucidate the mechanisms underlying numerous developmental, neurobiological, and behavioral phenomena. Over the past decade, data have shown that quiescence in Drosophila meets the same behavioral criteria that have been used to characterize sleep in other

arthropods [3, 4]. More recently, studies have indicated that sleep alters the transcription of similar genes in flies and rodents [5, 6]. Additional experiments using Drosophila have identified several genetic pathways that influence sleep and have suggested that sleep may play an evolutionarily conserved function in learning and memory.