

Preface

Human life expectancy has nearly doubled over the last 100 years due, in part, to a wide range of novel medical technologies and treatments. The trend toward increased life expectancy in the developed countries is accompanied by the increased number of people surviving to an advanced age and having different chronic age-associated pathologies. This trend leads to the need to understand the genetic and physiological mechanisms underlying aging processes and particularly those that promote healthy aging. Moreover, in recent years, substantial evidence has emerged supporting the possibility of the radical human life extension, primarily due to the rapid development of genetic and stem cell-based technologies.

In the development of such technologies, several insect models may provide useful starting points prior to animal and human studies. The use of insect models seems particularly reasonable since, despite the large phylogenetic distance between insects and mammals, some metabolic processes and signaling pathways were shown to play an evolutionarily conserved role in aging across various insect and mammal species. Among them, the insulin/insulin growth factor signaling pathway, histone deacetylases, and genes involved in oxidative stress all exert evolutionarily conserved effects on aging and life span in a wide range of model organisms. These data suggest that aging itself is an evolutionarily conserved process and not simply an inevitable deterioration of biological systems. The high degree of conservation between diverse species in the genetic pathways that regulate longevity suggests that work in model organisms can expand the theoretical knowledge of aging, yield valuable insight into the molecular and cellular processes that underlie aging process, and perhaps provide new therapeutic targets for the treatment of age-related disorders.

Among the widespread model organisms, the fruit fly, *Drosophila melanogaster*, is likely one of the most appropriate model organisms to study biological mechanisms of aging due to its relatively short life span (60–80 days), convenient husbandry, and well-studied genetics. The *Drosophila* genome was one of the first to be sequenced. It has powerful systems for gene knockout and targeted mutagenesis. The large brood sizes also make it possible to measure survival in large numbers of individuals within each experimental cohort in controlled environments and to test

the functional consequences of senescence either longitudinally in individuals or as sampled from the aging population. Furthermore, almost all cells in adult insects are postmitotic except a few cells in the malpighian tubules, gut, and gonads. Therefore, the age-related decline in cellular functions may be examined without interference from newly dividing cells. Certainly, not all senescent physiological changes revealed in flies can be simply translated to humans. However, flies and humans often show very similar age-related physiological phenotypes, suggesting that at least some of the basic biological properties and mechanisms that regulate longevity are conserved between flies and humans. In the last years, *Drosophila* models have been developed for a large variety of aging-related processes and diseases.

The goal of this book is to provide the reader with an overview of current research concerned with the use of the *Drosophila* experimental model as a tool for unraveling the genetic, molecular, and physiological mechanisms underlying the aging process and to search for life-extending remedies. This research field is currently a hot topic in biomedicine. Thereby, the present book, which is a collective work of the world's leading researchers in the field of biogerontology, may be of interest to a wide audience, ranging from academic researchers to the general public.

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