Book Review

Author: Zima, Jan

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Macholán M., Baird S.J.E., Munclinger P. & Piálek J. (eds.) 2012: Evolution of the house mouse. *Cambridge Studies in Morphology and Molecules: New Paradigms in Evolutionary Biology. Cambridge University Press. xx + 526 pp. ISBN 978-0-521-76066-9.*

The Cambridge book series devoted to evolutionary problems addresses the interface between morphological and molecular research in living and extinct organisms. This topic is almost ideally reflected in studies of evolution of the house mouse. The house mouse is the most successful and ubiquitous invasive mammal after man and this success is due to its commensal interactions with humans. This species has become the most important model and tool for explorations in a wide spectrum of questions of contemporary biology. The free-living mouse populations are the source of the genetic variation in laboratory mice, an indispensable experimental animal in biological and biomedical laboratories all over the world. Laboratory mice have contributed enormously to our knowledge of the genetics and evolutionary biology.

The nearly complete genome sequences of the house mouse have been available since 2002 and this achievement extended considerably the general knowledge of mouse genetics and biology and enhanced the importance of this model in evolutionary studies. The rapidly growing genome resources derived from the special status of the house mouse as a model laboratory organism make them an ideal subject for comparative and synthetic studies of gene evolution across a wide range of evolutionary scales. The house mouse is a model organism that also provides an exciting natural setting to study different mechanisms and steps in the process of speciation. Its research offers an exceptional playground for evolutionary biologists with a multidisciplinary approach.

This book provides the review of progress achieved in various fields of mouse research with special attention to phylogeny, phylogeography, origin of commensalism, behaviour and adaptations, and evolutionary relationships between populations and subspecies. The chapters included in the book are authored by 44 contributors from 14 countries and about 40 different labs. Featuring a number of high-profile researchers, this book introduces and summarizes our current understanding of individual topics related to the systematics, phylogeny, and biogeography of the genus *Mus* and the house mouse, the mouse mandible as a model system for complex morphological structures, speciation studies, research of hybrid zones, hybrid sterility, and the role of the X chromosome, behaviour and social environment, chemical communication and vocalization, t-haplotype as a selfish hereditary element, and chromosomal versus molecular evolution. The collection of articles releases many original and concise ideas that can influence biological thinking of readers and help them to perceive the significant aspects. The book is a fitting successor to a number of publications which have integrated mice into evolutionary disciplines with varying but growing success. It is a mature fruit of the recognition that geneticists and ecologists need each other to fully understand evolutionary situations and to cooperate closely.

The volume is aimed to offer resources for students entering the field but it also highlights the cooperative nature of research across countries, laboratories and generations. The book is targeted primarily at professional researchers working in mouse-related research but will be attractive to scholars of evolutionary biology. As Professor R. J. Berry says in the Foreword, this volume is “an indispensable milestone for those taking the mouse route to understand evolutionary processes.“ It is obvious that the work will go on and the present book is an important landmark on the way. In their conclusions the authors and the editors indicate also possible perspectives in this research field. New high-throughput tools are now becoming available in molecular studies with much higher resolution than former markers. Expanding genomic technology has given us a unique and novel view of genome dynamics in particular neutral and adaptive variants. The overall perspective provided by the classical markers will be apparently retained, but genome-wide studies will be rich in complementary information.

In this view, the book is a highly useful and amusing piece of reading and can be recommended both to professional scientists and all the students interested in biological ideas and the current ways of thinking about biology.

Jan Zima