

help of a selection committee of six animal behaviorists of different backgrounds. With few exceptions their choices seem convincing. Sadly, some of the major figures—among them Karl von Frisch and David Lack—had already passed away. Others who were asked declined for various reasons. Altogether 19 autobiographies have been assembled, in alphabetical order: Baerends, Dethier, Eibl-Eibesfeld, Fuller, Griffin, Hediger, Hess, Hinde, King, Leyhausen, Lorenz, Manning, Marler, Maynard Smith, Richter, Scott, Tinbergen, Wilson, and Wynne-Edwards. I found the chapters by Baerends, Eibl-Eibesfeld, Lorenz, Marler, Maynard Smith, Tinbergen, and Wilson particularly illuminating and stimulating. Of course, everyone will miss some favorites in an assembly like this. This reviewer, for instance, would have expected to find Martin Lindauer and Thomas Eisner included. (I refrain from suggesting who could have been deleted.) Overall the vertebrate bias is fairly strong. I also missed at least some of the founding fathers of neuroethology or more generally of the study of the physiological mechanisms of animal behavior. These points of criticism cannot, however, detract from the fact that overall this book is very successful in meeting its goals. Exactly because it is so it makes one ask for more. One last quibble: it is nice to find portraits accompanying all the contributions; it would have been easy to give dates of birth of the contributors in the legends. A fair number of the authors take the fact of their birth so much for granted that they do not bother to mention when the event occurred.

HUBERT MARKL  
Fakultät für Biologie,  
Universität Konstanz, D-7750 Konstanz,  
Federal Republic of Germany

## Molecular Evolution

**Molecular Evolutionary Genetics.** Ross J. MACINTYRE, Ed. Plenum, New York, 1985. xxii, 610 pp., illus. \$79.50. Monographs in Evolutionary Biology.

Molecular evolution is a synthetic field that brings together population genetics and molecular genetics in a novel and fruitful alliance. Its aims are to understand the processes that govern the evolution of genes, gene families, and entire genomes and to use molecular data to make inferences about phylogenetic history. The enterprise encompasses a wide diversity of research methods ranging from the mathematical analysis of models of molecular change, originating in

formal population genetic theory, to the molecular dissection of gene structure and function, originating in the rich experimental traditions of molecular biology.

One of the great attractions of the study of molecular evolution is that a wealth of evolutionary phenomena have come to light that were unknown or only vaguely suspected by earlier generations of evolutionary geneticists. Some of the recent discoveries that shatter earlier notions about the processes of genetic change are the concerted evolution of multigene families, the ubiquitous nature of transposable elements, the horizontal transfer of retroviral sequences, and the ability of the plant mitochondrial genome to assimilate foreign DNA. The present book explores many of these issues in detail and also explores many of the less revolutionary aspects of molecular change.

Three chapters are concerned with the evolution of repeated gene families where there is a wealth of descriptive information on structural organization and comparative evolution. In the case of satellite DNAs, we still know little about function or about the processes responsible for the generation of these highly repetitive sequence arrays. Dispersed repeat families, such as the *Alu* family, which makes up 5 percent of the human genome, are particularly enigmatic. They are transcribed and exhibit transposon-like characteristics, but nothing is known of their biological function, if any. The best understood multigene family codes for the ribosomal RNA subunits, and in this case it is possible to analyze evolutionary change in the context of gene function. Thus compensatory mutations, which reestablish base pairing in putative stem structures, are found to be common. The phenomenon of concerted evolution, whereby mutations in particular gene copies are laterally propagated to other members of the gene family, is also best documented in the ribosomal RNA gene family.

There are two excellent chapters on organelle genome structure and evolution. It is now well established that the vertebrate mitochondrial genome (mtDNA) evolves at an exceptionally rapid pace, possibly owing to the absence of repair mechanisms. The situation in plants, where chloroplast and plant mitochondrial protein coding genes appear to evolve conservatively, stands in sharp contrast. The plant mtDNA varies greatly in size among related taxa and is promiscuous in the sense that it has been shown to incorporate foreign DNA sequences. Moreover, the plant mtDNA has associated plasmid-like DNAs that may be implicated in the uptake of foreign sequences. Owing to a conservative rate of evolution, the chloroplast genome has been

very successfully exploited for the study of plant phylogeny.

The time clock hypothesis was the first major idea to arise from the union of population genetic theory and molecular genetics. According to this hypothesis neutral mutation should be substituted in evolution at a rate proportional to the mutation rate. A long debate has ensued over the constancy of nucleotide and amino acid substitution rates in evolution. One major problem has appeared to be a substitution rate determined by celestial time and not generation time. That problem is resolved in a detailed chapter on the estimation of substitution rates through the analysis of a much larger data base. This analysis reveals that synonymous substitutions are functions of generation time, whereas missense substitutions appear to depend on calendar time, as might be expected if they were subject to selection.

A chapter on retroviral evolution in mammals documents at least five cases of interspecies transmissions of retroviral sequences. The evolution of oncogenes and their association with retroviral sequences represents yet another intriguing aspect of genomic evolution still in very early stages of investigation. Interesting data are also presented on the evolution of mammalian linkage groups. Primates generally show highly conserved chromosomal homologies, while some other mammalian lineages (for example the rodents) exhibit much greater chromosomal shuffling in evolution.

The present book is largely restricted to the processes that govern the evolution of gene families and genomes. It is also heavily weighted toward vertebrate and particularly mammalian evolution. The individual chapters present long, detailed and comprehensive reviews of the subjects they cover. Most of the eight chapters exceed 60 pages, and there is an extensive index that makes the book exceptionally valuable as a reference work. There is some variation in style and quality among the chapters, but the general level of scholarship is far above that of the typical compilation. Moreover, there is a serious, and on the whole successful, effort to make the presentation accessible to a general reader. One may question the choice of topics, and particularly the failure to include chapters dealing with transposable element evolution or with the use of molecular data to infer phylogenetic history. But the book abounds in provocative observations that reveal how far we must go to gain anything like a complete picture of the processes that govern molecular change.

MICHAEL T. CLEGG  
Department of Botany and Plant Sciences,  
University of California,  
Riverside, CA 92521