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Even Part 5 of the book, titled "Paleobiology and Macroevolution" (only 15% of the book), did not relate what happened during this process of evolution. The closest the book gets to relating evolutionary history is a good, if abbreviated, discussion of the mammal-like reptiles. Not even in an appendix titled "The Fossil Record" (containing information about geology, radiometric dating, and so forth) was there any information about current thought on the outline of the history of life or the relationships among major branches of life.

This omission may not matter to many potential users of this book, which, as I have pointed out, is excellent in presenting the mechanisms and processes of evolutionary biology. But I missed the historical context usually associated with a course on "evolution."

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EVOLUTIONARY BIOLOGY, *Volume 28.*

Edited by Max K. Hecht, Ross J. MacIntyre, and Michael T. Clegg. Plenum Press, New York. \$75.00. xiv + 274 p.; ill.; index. ISBN: 0-306-44927-7. 1995.

This is the latest volume in this highly regarded series. Throughout its long (almost 30 years) and successful history, *Evolutionary Biology* has published one of the most often cited classics in evolutionary biology. There are only a handful of outlets (e.g., *The Quarterly Review of Biology*, *Annual Reviews in Ecology and Evolution*, and *Oxford Surveys in Evolutionary Biology*) that continue to publish thorough reviews on a wide range of topics in evolutionary biology. *Evolutionary Biology* maintains very high standards, is always current and manages to invite the most highly regarded researchers to contribute.

These are exciting times for evolutionary research. The lines between traditionally separate subdisciplines in biology are becoming more blurred. This new interdisciplinary approach has already led to fruitful reciprocal illumination and has advanced our understanding of evolutionary processes at both the organismal and molecular levels. This volume provides current examples of this trend in evolutionary biology. One of the new hybrid areas is the connection of development and evolution. Every broadly interested evolutionary biologist will find this volume to be a "must read."

The first chapter by Brian K. Hall on "Homology and embryonic development" is testimony to how illuminating an evolutionary view of development can be. Hall is a leader in the field of evolutionary developmental biology, a new discipline that combines development and evolution—two biological disciplines, that after a long lapse, are again regarded as intricately interwoven. [Hall recently

edited a book on the old question "what if anything is homology" (*Homology: The Hierarchical Basis of Comparative Biology*, Academic Press, San Diego, 1994)]. In this chapter he summarizes his view of this still unsolved, but highly significant (both for evolutionary biology and yes, also for developmental biology) issue.

In the second chapter, Neil Shubin presents his latest ideas on the developmental and evolutionary origin of the tetrapod limb. Shubin and Alberch provided new ideas on the evolution of tetrapod limbs about eight years ago. Since then the "homeobox revolution" hit the developmental-evolutionary biology community. Homeobox genes (particularly *Abdominal-B*-related homeobox genes) are expressed in developing limbs, and might hence provide proximal (developmental) and ultimate (evolutionary) explanations for the origin and subsequent diversification of tetrapod limbs. This is a very attractive scenario that, at least at the evolutionary level, is still highly speculative—its testing hindered by the fact that most sarcopterygian groups of fishes that are at the base of tetrapods are either extinct or not easily amenable to developmental work. Nonetheless, this is one of the hottest and most exciting areas in the new field of evolutionary developmental biology, and an area that is worth following.

Jeffrey R. Powell and Rob DeSalle beautifully summarize current knowledge and the history of approaches on "*Drosophila* molecular phylogenies and their uses" in Chapter Three. They go the step beyond the phylogeny to provide examples of how a molecular phylogeny can provide hypotheses and answers, or at least a framework, in which to study a variety of biological questions. In *Drosophila*, in particular, an historic perspective might be very illuminating, even mandatory, for the understanding of development—an area where *Drosophila* is still the model organism in invertebrates. This chapter is a treasure chest of ideas and research hypotheses for future work based on the phylogeny of *Drosophila*. Since *Drosophila* has been a model not only in developmental biology but also in population genetics and evolution, the connection between development and evolution promises to be particularly interesting within a phylogenetic framework.

Pamela S. Soltis and Douglas E. Soltis summarize the current state of knowledge in "Plant molecular systematics" in Chapter Four. Since the Soltis laboratory is among the major contributors to plant molecular systematics, they are uniquely qualified to provide their view of the field. What is the large ribosomal RNA for phylogenetic questions among animals, is in plants the *rbcL* gene from the chloroplast genome (although there is some work on rRNA of plants). This gene, which encodes the

main carbon-fixing enzyme, has already provided a wealth of information during the last five years, and continues to surprise in cases where molecular phylogenies differ from classic ones, thus pinpointing where further study is required. In contrast to the animal molecular world, some 38 contributors coauthored key papers on plants. Much progress already has been made both at the organismal and the molecular phylogenetic levels for understanding plant systematics and evolution. Many examples, from plant chemistry, to chloroplast capture, to speciation are presented. The authors point out, however, that not all problems have been solved at either level and much more work lies ahead as well, in the development-evolution connection.

In Chapter Five, Richard B. Meagher discusses the impact of historical contingency on gene phylogeny based on the example of diversity in the plant actin gene. Meagher develops an interesting theory that links contingency, phylogeny, and macroevolution. Three categories of historical contingencies are postulated to link them to macroevolution: functional, developmental, and phylogenetic.

A. Brosset and D. Lachaise provide, in Chapter Six, an overview of their work on the biology and evolution of killifishes. Killifishes are small annual fishes with interesting biological features, and are among the most colorful and beautiful fishes (color illustrations would have been a real advantage for this paper). This chapter touches on many different issues from behavior, ecology, and karyology to the evolution and genetics of these fishes. Several competing hypotheses from historical biogeography, catastrophes, lotteries and karyotype-driven speciation are discussed.

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EVOLUTION IN AGE-STRUCTURED POPULATIONS. *Second Edition. Cambridge Studies in Mathematical Biology. By Brian Charlesworth. Cambridge University Press, Cambridge and New York. \$29.95 (paper). xiii + 306 p.; ill.; author and subject indexes. ISBN: 0-521-45967-2. 1994.*

This a new, improved version of an influential and useful book. Life history evolution is one arena in which population genetics and population ecology have a chance of consummating their long-awaited fusion, and the second edition of this book, like the first, is the only reasonably comprehensive, clear, concise, and (usually) balanced guide to the subject. When I reviewed the first edition in this journal (*Q. Rev. Biol.*, 56:334-335, 1981), I felt that Charlesworth's precision and clarity would be valuable. My view is borne out by the book's obvious influence on the field in the last decade.

What is new here? Several chapters (especially Chapter 5) have been rewritten or extended to include newer work, or to provide a fuller account of a subject. Examples of new topics: Selection on quantitative life history characters; demography and life histories in randomly varying environments; kin selection; density-dependent dynamics; sex differences and selection; and, the experimental evidence bearing on theories of life history evolution. These are the ones that stood out; there are smaller changes elsewhere and some updating of citations in places where the discussion has not changed.

What did I dislike? The study of structured population models that use stage, size and similar variables instead of (or in addition to) age, is brushed aside with the curious remark that they ignore changes in vital rates with age. In contrast, I think that such models provide much closer contact with experiments, and may well be more useful in studying evolution than simple age-structured models. The theory of selection on quantitative characters described here relies on weak selection and little linkage; there is little attention to the possible limits on this theory. Surely evolution cares about more than r in a life history, unless much of the variation we see is really irrelevant to evolution.

One book can't do everything, of course, but this one is valuable regardless. I strongly recommend it to anyone, theorist or experimentalist, working on life history evolution.

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REPRODUCTION & DEVELOPMENT

UNDERSTANDING AGEING. *Developmental and Cell Biology Series.*

By Robin Holliday; Series Editors: P. W. Barlow et al. Cambridge University Press, Cambridge and New York. \$24.95 (paper). xiv + 207 p.; ill.; author and subject indexes. ISBN: 0-521-41788-0 (hc); 0-521-47802-2 (pb). 1995.

Four major books on the biology of aging appeared in the early 1990s (Finch, 1990; Bernstein and Bernstein, 1991; Rose, 1991; Gavrilov and Gavrilova, 1991). Taken together, these books illustrate two distinct approaches in the biology of aging. Most biogerontologists work on proximate, physiological mechanisms, the "how" of aging, while a smaller group studies ultimate, evolutionary explanations, the "why" of aging. Robin Holliday's book attempts to integrate these two approaches.