

## **Molecular Approaches in Natural Resource Conservation and Management**

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as inherently discontinuous, complex systems with perhaps an array of cascading interactions will greatly benefit from this book. Additionally, the even more complicated socioecological relations are neither theorized nor included in the volume. Instead, a sort of eco-totalitarian “measurement regime” (p. 436) is proposed to address the human-environmental condition, framed predominantly as an issue of carrying capacity. There seems to be agreement across most chapters that this is best achieved in combination with global, investor-driven management solutions such as virtual water trade, carbon finance markets, and “ecosystem services markets” (p. 436). In the editors’ concluding remarks, however, two different views are expressed, proposing a co-adaptive rather than a geoengineering approach. *BioScience* readers should perhaps start with this contradiction (p. 470), read the respective background information (chapter 3), turn to pages 462–463 (where the editors wrap up the synthesis chapters, also drawing conclusions for their own industrial ecology agenda), and then decide whether to dive into the details of the full volume.

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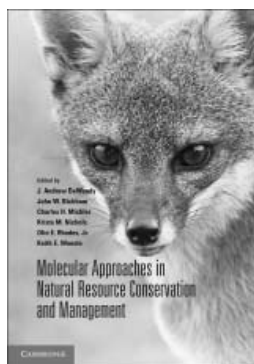
## CONSERVATION GENETICS FOR NATURAL RESOURCES

**Molecular Approaches in Natural Resource Conservation and Management.** J. Andrew DeWoody, John W. Bickham, Charles H. Michler, Krista M. Nichols, Olin E. Rhodes Jr., and Keith E. Woeste, eds. Cambridge University Press, 2010, 392 pp., illus. \$55.00 (ISBN 9780521731348 paper).

The use of molecular genetic markers is now widespread in aspects of endangered species conservation,

and some geneticists suggest that we are entering the era of conservation genomics (Allendorf et al. 2010, Ooborg et al. 2010). *Molecular Approaches in Natural Resource Conservation and Management*, a compilation of 13 articles with example boxes by other authors in each chapter, attempts to link molecular conservation genetics to species generally associated with natural resource management—that is, species important in forestry, fisheries, and wildlife. In many ways, those species involved in conservation genetics investigations and those in natural resources are at opposite ends of a spectrum. Endangered species are generally rare, not harvested, and not directly selected by humans, whereas natural resource species are common, harvested, and sometimes undergoing direct human-caused selection (think Monterey pines, Pacific salmon, and white-tailed deer).

The 91 contributors to this volume are mostly researchers involved in basic science investigations in molecular ecology, evolution, popula-



tion genetics, and related topics rather than the applied management orientation traditionally found in the natural resource research community. Their research contributions, first presented at a Purdue University conference in 2008, are spread over a variety of organisms and include chapters with animals, plants, or both as examples. The meeting and this book were supported financially (and logistically) by the Department of Forestry and Natural Resources at Purdue.

Natural resource scientists in fisheries and wildlife often focus on management;

those in forestry focus on both management and artificial selection for production. Wildlife biologists have generally been slow to integrate modern techniques into their research and are often resistant to conservation efforts by scientists in molecular ecology and evolution; they may claim to be conservation biologists, but their conservation efforts primarily are directed toward hunted game species. This perspective was dramatically illustrated to me when I attended a bighorn sheep meeting and was surprised to find that I was nearly the only academic scientist present among the many state wildlife managers and trophy hunters. I discovered that the motto of the group was “keeping sheep on the mountain,” mainly so they would be there for hunting—hardly “conservation,” in my view.

As in all compilations, the articles in this book vary in their level of research sophistication. Here, they also vary in the extent of their focus on current molecular approaches. I highlight five contributions that, in my opinion, provide excellent introductions to their topics in keeping with the theme of the book.

The first article in *Molecular Approaches in Natural Resource Conservation and Management*, by Honeycut, Hillis, and Bickham, discusses biodiversity (the number of species) found in different groups of organisms and shows how molecular genetics and phylogenetics have contributed to our understanding of biodiversity. Their discussion of evolutionary distinctiveness, barcoding, and cryptic species is particularly worthwhile. The only European contribution among the articles is by Kremer, Le Corre, Petit, and Ducouso, on the adaptive differentiation in oak trees. It provides an example of what molecular genetics in an evolutionary context can contribute to the understanding of adaptation in natural resource species. They use Europe-wide pollen data from the past 15,000 years to present an historical perspective, molecular genetics to describe evolutionary and

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contemporary genetic differentiation, common garden data to estimate adaptive differences, and theoretical simulations to investigate the impact of evolutionary factors influencing adaptive differentiation ( $Q_{ST}$ ). Nichols and Neale give a general introduction to the molecular genetic approaches used to map genes of adaptive significance (QTL or quantitative trait loci), and then summarize all the known studies that have identified these genes in relevant animals and plants. In a similar vein, Zamudio and Harrison discuss the evolutionary consequences of hybridization in endangered species, summarize all the studies of hybridization in endangered and nonendangered species, and then discuss the implications. Finally, Ivy and Lacy provide a useful introduction to the genetic management of captive breeding programs and then demonstrate how molecular data can be incorporated into them.

Several of the examples deserve mention. In particular, Schall and her coauthors present research on the origin of weedy rice in Thailand; Devlin and Sundström discuss the impact of transgenes on growth in Pacific salmon; Ritland discusses the “Spirit bear,” a rare white black bear; and Busch, McCreight, and Waser discuss their long-term studies on the banner-tailed kangaroo rat.

*Molecular Approaches in Natural Resource Conservation and Management* should provide readers with a good introduction to a number of topics in conservation genetics. As the editors suggest, this volume could be useful to “academics interested in conservation genetics, molecular ecology, and the quantitative genetics of wild organisms.” The editors also state that the book could serve as a “text for graduate ecology/genetics courses but also, perhaps, in advanced undergraduate courses.” In my opinion, however, a more thorough introduction to conservation genetics can be found in the coordinated and comprehensive treatments of the field from several textbooks now available, namely *Conservation*

*and the Genetics of Populations* (Allendorf and Luikart 2007) and *Introduction to Conservation Genetics, 2nd ed.* (Frankham et al. 2010). On the other hand, some of the chapters present detailed information and examples that would not be found in a textbook and provide more advanced coverage of specific topics. In other words, I generally liked the book and the diversity of topics, but it is not a textbook and it is also not largely composed of “original” articles. Only in specific reviews that bring together summaries of research does it provide articles that are likely to be cited and later used.

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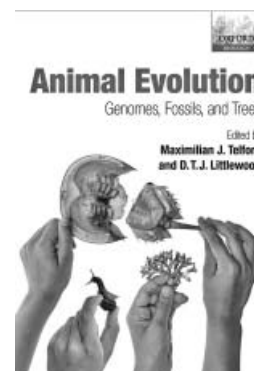
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### A BIRDS-EYE VIEW OF ANIMAL EVOLUTION

**Animal Evolution: Genomes, Fossils, and Trees.** Maximilian J. Telford and D. T. J. Littlewood, eds. Oxford University Press, 2009. 264 pp., illus. \$80.00 (ISBN 9780199570300 paper).

**A**nimal *Evolution: Genomes, Fossils, and Trees* is the latest synthesis of data assembled from paleontology, molecular systematics, and developmental biology to help readers answer the big questions of metazoan

evolution. The book falls into a long and distinguished line of past volumes emphasizing one or another aspect of the big picture of animal evolution and development: books such as *Genome Evolution* (edited by Gaby Dover and Richard Flavell, 1980), Stephen Jay Gould’s *Wonderful Life* (1989), Claus Nielsen’s *Animal Evolution* (1995), and Sean Carroll’s *From DNA to Diversity* (2001). In a very real sense, Maximilian J. Telford and D. T. J. Littlewood’s *Animal Evolution* is a mix of all of these. In 18 chapters the book surveys the latest discoveries and controversies surrounding the relationships among metazoan lineages, when they diversified, and what this can tell us about the evolution of morphology and development. Or, as the summary more succinctly states, “Arguably, there is one underlying common quest that unites the goals of individual researchers [of animal evolution]: the search for homology—recognizing it, defining it, and using it.”



*Animal Evolution* is one of the best recent examples of integrative biology I’ve read. The book’s major methodological approaches—paleontology, phylogenomics, and morphogenetic studies of animal development—emerge not only from the diversity of individual chapters and researchers but often as a dialogue within individual chapters. A high degree of collaboration is evident: 13 of 18 chapters are multiauthored and the chapters often include researchers from departments of molecular

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