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BOOK REVIEW

Molecular approaches in natural resource conservation and management

J. A. DeWoody, J. W. Bickham, C. H. Michler, K. M. Nichols, O. E. Rhodes, Jr. and K. E. Woeste (eds.): Cambridge University Press, Cambridge and New York, 2010, 374 pp, illus (some col.), maps (some col.), 26 cm, Hardback, ISBN 978-0-521-51564-1, US$130; Paper, ISBN 978-0-521-73134-8, US$55

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The first rule of intelligent tinkering, Aldo Leopold famously noted, is to keep all the wheels and cogs. Rodney Honeycutt, David Hillis, and John Bickham take the analogy a step further: Not only are conservation biologists like car mechanics trying to keep an engine running, but they are aware of the existence—let alone the function—of only a small percentage of the engine components. “The other 90% of the parts are falling off the engine faster than they can be discovered,” they write, “and it is unclear how much longer the car will keep running.”

Honeycutt and colleagues contribute a chapter about the discovery and importance of biodiversity in *Molecular Approaches in Natural Resource Conservation and Management*. This text, edited by J. Andrew DeWoody and five of his colleagues at Purdue University, provides scientists and managers interesting and relevant examples of how molecular genetic techniques can be employed to better understand the composition and function of genetic variation within species and of species diversity existing within ecosystems. More than 80 geneticists and molecular ecologists contributed to the 13 chapters in the book; many of these authors are prominent international experts in their fields.

Molecular genetic approaches, from microsatellites to micro-arrays to whole genome sequencing, have advanced by leaps and bounds in the last decade, just as the cost of these methods have declined. While field work is, and will remain, critical to making management and conservation decisions, molecular data generated in the lab can add new and more precise data to the mix. The case studies presented in *Molecular Approaches in Natural Resource Conservation and Management* span a wide variety of applications, from assessing the impacts on biodiversity caused by gene flow from genetically modified crops (Chapter 2), to identifying genes associated with adaptive divergence among individuals and populations (Chapter 6), to guiding the management of genetic diversity in captive breeding programs (Chapter 11).

Only a handful of chapters directly address relationships between spatial patterns and evolutionary processes. Landscape ecologists, however, are likely to find much to pique their interest throughout the book since (1) many of the tools and methods described are, or could be, employed in landscape genetics studies, and (2) evolutionary processes in wild organisms nearly always have strong spatial and temporal components.

Consider, for example, the theme of gene dispersal that occurs repeatedly throughout the book. The

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movement of genes between wild and cultivated rice in Thailand has resulted in an invasive weedy intermediate that reduces agricultural yield and might displace native species, suggesting the potential for significant impacts if rice with genetically introduced herbicide resistance were to escape cultivation (Chapter 2). Increasing evidence exists that transgenic organisms can move beyond their intended destinations, with the potential to cause unintended ecological consequences for communities and ecosystems (Chapter 3). The existing genetic architecture of European white oaks was determined by the separation of the species into three refugia during the Pleistocene, followed by northward advancement disrupted by local founder effects associated with long-distance dispersal events; pollen migration between stands from the three origins increased over time, gradually reducing trait differentiation (Chapter 5). The persistence of a reintroduced wildlife species may be dependent in part on the connectivity among a network of spatially proximate populations, as well as on the size of the populations (Chapter 12).

Meanwhile, two other chapters are likely to be of specific interest to landscape geneticists, with each focusing on the genetic impacts of human-caused habitat fragmentation. In Chapter 8, “Pollen and seed movement in disturbed tropical landscapes,” J. L. Hamrick describes the immediate, short-term, and long-term genetic effects of landscape fragmentation. He then explains how to test whether these effects have occurred, outlines five case studies from tropical tree species, and recommends that disturbed landscapes be managed to maximize species diversity and genetic diversity within species. “An understanding of the genetic connectivity occurring within fragmented landscapes can be used to identify remnant populations and isolated individuals who are essential to the maintenance of genetic diversity within the landscape,” he notes.

In Chapter 9, “Implications of landscape alternation for the conservation of genetic diversity of endangered species,” Paul Leberg and his colleagues underscore the importance of understanding the relationship between species rarity and the genetic effects of fragmentation, and present results from their studies of two endangered bird species, the black-capped vireo and the golden-cheeked warbler. The authors also discuss findings from a meta-analysis of more than 100 fragmentation studies. Some were expected, including increased levels of genetic differentiation among fragmented populations, and, to a lesser degree, lessened genetic diversity in fragmented populations. Other results were unexpected: Rare species were not more likely than common species to experience genetic effects from fragmentation, and species with lower dispersal abilities were not more likely than long-distance dispersers to have undergone such an effect. “Given the large number of apparently highly vagile species that exhibit at least some of the genetic consequences of fragmentation,” they write, “we suggest the need for additional investigations into how factors such as interfragment land cover and social behavior might limit dispersal among fragments.”

Note that while Chapter 13 (“Evolutionary Toxicology”) provides descriptions of commonly used molecular markers, this book does not explain the nuts and bolts of collecting, processing and analyzing molecular genetic data to answer natural resource management questions. Managers and scientists who need a comprehensive explanation of the methods mentioned in this book will need to look elsewhere. *Molecular Markers, Natural History and Evolution* (Avise 2004) is a good starting point. Other texts provide solid overviews of the conservation genetics concepts and approaches that underlie much of this book, such as *Introduction to Conservation Genetics* (Frankham et al. 2010) and *Forest Conservation Genetics: Principles and Practice* (Young et al. 2000).

At the same time, the cutting-edge research described in *Molecular Approaches in Natural Resource Conservation and Management* demonstrates that quantifying genetic patterns and processes, particularly within a spatial context, is essential for understanding the ecosystem wheels and cogs that Aldo Leopold urged us keep.

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