BOOK REVIEWS

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EVOLUTIONARY QUESTIONS IN AN ECOLOGICALLY RELEVANT CONTEXT[1]

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The fields of evolution, ecology, and conservation biology have long confronted questions concerning the origin and maintenance of variation in nature. In this recently edited volume, Mousseau et al. assert that the study of adaptive genetic variation in natural populations is necessary to build a relevant and predictive framework for these disciplines. This multiauthored collection, drawn from a symposium of the 1998 Ecological Society of America, highlights many possibilities for integrating these diverse fields through the study of adaptive genetic variation. As biologists with diverse interests in ecology, evolution, behavior, and conservation, we were particularly interested in the editors' suggestion that studying adaptive genetic variation in the wild is critical to predict population responses to environmental change. Our impression is that this volume does not provide a direct answer to this contention, but does present an intriguing collection of tools and examples to guide those asking such questions.

At the heart of this book is the assertion that studies of adaptive genetic variation must be conducted in a population's natural environment. Natural populations are often genetically structured across time (Grant and Grant) and space (Mopper) and subject to unpredictable episodes of gene flow and drift. Species interactions (Mazer and Meade) and polymorphisms within a species (Smith and Girman, Robinson and Schluter) introduce additional complexity that cannot easily be replicated in the lab. Differences in environmental context and individual condition can often result in marked differences between laboratory and field measures of heritability (Hoffman), thereby questioning the potential of ecologically relevant predictions based solely on laboratory measures.

Recognizing the value and inherent difficulties of measuring genetic variation in a natural context, the authors of this volume provide an array of techniques to answer specific questions in the field. These methods include common garden experiments (Mazer and Meade, Mousseau), long-term studies of marked individuals (Grant and Grant, Sinervo), reciprocal transplants (Mousseau), and the establishment of artificial populations in the wild (Mopper et al.). Although some chapters (e.g., Mousseau, Ritland) promote the use of molecular techniques, the focus of this volume is almost exclusively limited to classical quantitative genetic approaches, and it overlooks the potential of quantitative trait locus (QTL) mapping for investigating the genetic architecture of quantitative traits (e.g., Bradshaw et al. 1995). Nonetheless, the practical description of methods and the assemblage of studies presented are strengths of this volume, and it will serve as a valuable resource for biologists interested in measuring genetic variation in the wild.

Adaptive genetic variation is broadly defined within this volume, with multiple interpretations by its authors. The lack of a single, clear definition can lead to some confusion. At times, adaptive genetic variation is interpreted as variation in genetic traits that have adaptive value for individuals. In other cases, it is the population's genetic variation itself that appears adaptive. This is best illustrated by several authors' discussions of gene flow. Mousseau suggests that, as a result of disparate evolutionary and ecological histories, gene flow between ''adjacent but ecologically different'' populations may be maladaptive for individuals. However, Grant and Grant show that gene flow can sustain population viability in fluctuating environments. Both interpretations, adaptive genes and adaptive variation, are valid. However, it is clear from the diversity of opinions in these chapters that a consensus concerning the definition of adaptive genetic variation is still forthcoming.

In the preface, Mousseau contends that a fundamental objective of studying natural adaptive variation is to predict populations' responses to future conditions and anthropogenic change. If so, evolutionary biologists' predictions concerning responses to selection will be strengthened by an informed measure of heritability (Barton and Turelli 1989). From an applied perspective, better predictive power would facilitate the conservation of evolving organisms in changing environments. Unfortunately, authors rarely explicitly address the implications of their studies for conservation. A notable exception is by Robinson and Schluter, who argue that global warming may endanger feeding polymorphisms in Nearctic fish species by allowing a host of competing invaders to enter the food web. Other potential applications are much more implied. For example, Grant and Grant show that the actual genetic variation in finch populations was significantly higher than predicted population models using effective population size. This finding suggests that effective population size calculations used by conservation biologists may be excessively conservative. Reviews of theoretical models of evolutionary change (e.g., Lynch and Lande 1993) and comparisons of heritability, ''evolvability'' (Houle 1992), and phenotypic plasticity as indices of environmental

[1] *Adaptive Genetic Variation in the Wild.* T. A. Mousseau, B. Sinervo, and J. Endler, eds. 2000. Oxford University Press, Oxford, U.K. 274 pp. HB $60.00; ISBN 0-19-512183-X. The quote is by T. Mousseau, p. 242.

flexibility also could have provided insight for conservation biologists.

Adaptive Genetic Variation in the Wild highlights successful applications of quantitative genetic techniques to discern adaptive genetic variation in the wild. These case studies demonstrate the ubiquity of genetic variation for ecologically important traits in diverse organisms. As such, the book lays the groundwork for future research on questions that are outlined in a final chapter by Endler. A number of these questions are longstanding, such as how within-population genetic variation is translated into variation among populations and variation among species, what mechanisms maintain genetic variation in the face of selection, and to what extent changing environments and genotype × environment interactions influence and maintain variation. These and other research questions clearly require careful measurement of genetic variation in the field, and this book provides some good examples that should serve as models for future work.

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