Post-modern synthesis

Evolutionary Genetics: Concepts and Case Studies edited by Charles W. Fox and Jason B. Wolf. Oxford University Press, 2006. £26.99 pbk (544 pages), ISBN-13 978 0 19 516817 4 ISBN-10 978 0 19 516818 1

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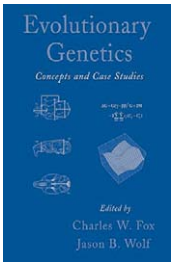

Providing a comprehensive and authoritative introduction to the diverse and dynamic field of evolutionary genetics is a tall order and there are few, if any, individuals with the breadth of knowledge to do so effectively. Therefore, a multi-author book is an attractive proposition. The format has been tried with *Evolutionary Ecology: Concepts and Case Studies* [1] and now Fox and Wolf have provided a sister volume, *Evolutionary Genetics: Concepts and Case Studies*.

This is an exciting time to be working at the interface between evolutionary biology and genetics but a difficult time to produce a book on the subject. Technological advances make it possible to study an increasing number of loci using larger and larger sample sizes, the types of genetic variation that can be accessed are many and varied, and we can measure gene expression as well as structural variation. Computing power and sophisticated analytical approaches, especially those based on coalescent theory, are making it possible to ask questions that could not have been addressed previously. Evolutionary genetics is also finding more applications: in conservation biology, in historical biogeography, in epidemiology and in our understanding of human genetic disorders. Long-recognised issues, such as the genetics of speciation or the genetic basis of morphological change, are yielding new insights in response to the application of the latest approaches.

Just within the past year, impressive advances have been made. One of the most fascinating was the fine-scale mapping of patterns of recombination throughout the human genome by Myers and colleagues [2]. This analysis utilised data on 1.6 million SNPs in 71 individuals from three ethnic groups, inferring recombination using Bayesian techniques to model the evolutionary history of the sample of haplotypes. The resolution achieved could not be matched by conventional nonevolutionary approaches. Not only does the pattern of highly localised recombination hotspots provide a novel insight into the evolution of recombination, but it is also crucial for association-mapping studies of human disease susceptibility loci.

Gene mapping in a non-model organism, the three-spine stickleback *Gasterosteus aculeatus*, provided another recent breakthrough. Sticklebacks have colonised low-predation pressure environments in many parts of the world and have evolved reduced 'armour', spines and bony plates, as a result. A single locus has been identified that is responsible for most of this morphological change, and the same locus is implicated in independent parallel evolutionary events in different geographical regions [3]. This study was based on QTL mapping using molecular markers in laboratory crosses, but it is now also possible to detect regions of the genome under selection using patterns of variation in natural populations. This 'population genomics' approach [4] typically uses microsatellite or amplified fragment length polymorphisms (AFLPs) but microarrays can be used to survey whole genomes. When applied to forms of the mosquito *Anopheles gambiae* that exhibit incomplete reproductive isolation, the microarray approach enabled Turner and colleagues [5] to detect three small regions, containing only 67 loci, that are strongly differentiated. This provides a powerful new tool to dissect the genetic basis of speciation. Studies such as these led to 2005 being dubbed a 'banner year' for the impact of genetics on understanding how evolution actually proceeds [6].

In *Evolutionary Genetics*, Fox and Wolf have assembled a stunning cast of authors, with the standing to give the book real influence. In 32 chapters, they have achieved an extraordinary breadth of coverage. The biggest challenge would have been to manage all of these contributors in a way that resulted in a coherent level and style of treatment. The intended approach is encapsulated in the subheading *Concepts and Case Studies* and this spirit is evident in most chapters. The intended level is said to be 'advanced undergraduates, graduate students, and established researchers in genetics or evolution'. This broad remit is reflected in some unevenness between contributions: all chapters are challenging, as they should be, often taking non-standard approaches to familiar issues, but a few are, frankly, inaccessible to all but the favoured few. So, although I will not be recommending this volume to my undergraduate classes, I will certainly encourage research students to use it and I expect my own copy to be very well thumbed over the next five years.

References

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