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## Dispersal: where, why and how?

Dispersal Ecology and Evolution. Jean Clobert, Michel Baguette, Tim G. Benton & James M. Bullock (editors), 2012, Oxford University Press, 498 pp. £80 (hardback) / £39.95 (paperback) ISBN 9780199608898 / 9780199608904; <http://ukcatalogue.oup.com/>

Can a unified, cross-species framework describe the causes and consequences of dispersal? Rockall winkles, water voles and 'ghost' plants are just some of the examples that are included in 'Dispersal Ecology and Evolution' by Clobert and colleagues, which provides a thoughtful synthesis of a broad range of literature, incorporating both empirical and theoretical studies. Perhaps the best answer to the question of whether a unified framework exists is summarised by Hanski (Chapter 23), who suggests that variation in species' biology means there is unlikely to be a single explanation for the origin and maintenance of dispersal strategies. What is apparent on reading the discrete but linked chapters of this book, however, is that parallels exist amongst disparate groups of organisms—both plant and animal.

'Dispersal Ecology and Evolution' deals carefully with both the causes and consequences of dispersal and places them in a historical context. Processes are the focus of each chapter, with exemplar studies such as lizards, spiders and weed plants, and arguments supported by evidence from a range of other taxa. Early on there is careful discussion and explanation of how the term 'dispersal' can be used differently among biological disciplines. Leptokurtic distribution of dispersal distances is a recurring theme, with examples such as the mahaleb cherry and cow wheat used to illustrate that this type of distribution can occur over very different geographic scales.

The theoretical framework within which each of the chapters of this book is placed is one of the strong points of the text. For example the section on dispersal kernels deals with theory and then presents empirical data that indicate the potentially confounding effects of temporal variation. The theory underlying the integration between dispersal and other factors is also considered, which may be of particular relevance for a broad readership. For example, the relationship between dispersal and environmental heteroge-

neity in a spatial and temporal context is explored, as is the relationship between dispersal and body condition. Rather interestingly, one of the models presented by Kisdi and colleagues (Chapter 11) makes the prediction that dispersal syndromes are independent of the spatio-temporal structure of the environment— in other words, that distributions of body condition are the same in all patches, regardless of natal patch quality, and regardless of whether patch quality is fluctuating or fixed. This prediction could be tested with empirical data.

A further strength of this text is that many of the described studies deal with broader concepts than dispersal *per se*. These include phylogeographic patterns, temporal range changes and ongoing metapopulation processes. Each of these is considered both from empirical and theoretical perspectives. Reviews of the studies of lizards highlight the likely importance of heterogeneity in dispersal syndromes or strategies, for example as driven by intraspecific variation in social attraction or repulsion, in influencing metapopulation processes. Indeed, there are data to indicate that, in some cases, behaviour not specifically for dispersal, such as searching for conspecifics by 'social' individuals, may in the long term contribute significantly to patterns of movement. The relationship between dispersal and population density also provides an interesting section, for example in pointing out that dispersal might in itself be an altruistic trait if it limits kin competition. (An explicit discussion of sex-linked dispersal in relation to fluctuations in sex ratio, and the consequences for processes such as sexual selection in this context, might have been beneficial here.)

Other topics considered include the concept of extinction and recolonisation at the edge of a species' range, with instances of historical range shifts including skipper butterflies and knapweed. Climate change is dealt with extensively from a

modelled perspective and with empirical exemplars from the literature. Phylogenetic inferences form another interesting section of the book, as applied to the study of plant dispersal and adaptation. The duplication and diversification of genes in both rice domestication and *Brassica* fruiting is one fascinating example where the underlying molecular pathways for the adaptations have been identified. Of particular interest in this case was that *Brassica* and rice were found to share the same nucleotide variant in a particular gene, but this variant produced different phenotypes in each species (evolution of the fruit *versus* traits selected for during the process of domestication respectively).

The book also looks to the future, and considers subjects such as ‘landscape genomics’, which it argues are likely to prove fruitful avenues of further work. Particular examples cited include the Natterjack toad, where a more detailed understanding of the genetic landscape will enable us to reconcile empirical data on observed dispersal patterns with patterns of genetic connectivity. In this regard, perhaps the book stops short of discussing the wider issues pertaining to landscape genetics and identifying the methods through which these advances are likely to be achieved (Manel & Holderegger 2013). Quantitative trait loci (QTLs) are covered in some detail and references are made to transcriptome profiling via microarrays. However both of these are likely to be superseded by the use of next generation sequencing (NGS), which is anticipated to become the mainstay of population genomic studies because it does not rely on knowledge of a reference

genome and therefore can be used on any species of choice (Flintoft 2013). Strong arguments are made for taking a ‘candidate gene’ approach in some instances and this may well be the most obvious choice for model organisms such as *Drosophila*. However, the NGS approach may be more beneficial even here, for example using the restriction site associated DNA sequencing (RAD) method (sequencing many fragments of DNA that lie close to restriction enzyme sites) to search for loci linked to genes of interest. This is likely to allow much more rapid identification of the precise molecular basis for particular phenotypic traits in the future.

Overall, ‘Dispersal Ecology and Evolution’ will be of interest to a broad readership, both as a reference text and as a source of stand-alone examples for biogeographers, ecologists, evolutionary biologists and geneticists alike, whether they be working on theory or generating empirical data—from winkle to water vole.

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