
Preface to the second edition

How fast ecological genomics has moved forward since the first edition of this book! The few years that have elapsed since then (2006–2011) have not only seen the rise of extremely fast, so-called ‘next-generation’ DNA sequencing technology, but also a host of excellent new studies in which genomics technology has been applied to address ecological questions. We are particularly impressed by the massive progress in comparative genomics, phylogenomics, population genomics, and metagenomics. We tried to pay particular attention to the new frontiers created by these fields as we prepared the second edition of this book.

In comparison to the previous edition, we skipped the ‘Genome analysis’ chapter, as the technology has moved forward to such an extent that a great deal of that chapter was considered outdated. Instead, we added a separate section on methodology and data analysis to Chapter 1, in which we also treat the new-generation sequencing technologies.

Furthermore, we have included a completely new chapter on variation and adaptation, in which we treat the various aspects of genome variability, and pay a good deal of attention to population genomics, a topic of increasing popularity among population-oriented ecological genomicists. In this chapter the reader may also find extensive reference to the issue of neutrality in molecular evolution. In addition we discuss the various aspects of genome archi-

tecture in relation to gene expression and epigenetic regulation of genes. Altogether we believe that this new chapter has expanded the scope of the book to include a wider variety of topics of interest to evolutionary ecologists.

We have retained our ‘problem-orientated’ approach to introduce each chapter, plus an appraisal section at the end. With this design we want to emphasize that, in the end, ecological genomics is just another branch of ecology and that it addresses questions that all ecologists ask, only with different technology. On the other hand, it is our opinion that ecological genomics also brings new questions to the discourse that were not raised before or could not be answered by more traditional ecological approaches.

What was marginally doable in 2005 has now become an impossibility: to summarize all publications of relevance to ecological genomics in a single book. We hope that the reader may find guidance and inspiration in this book to further study more specialized areas of their interest that we could not cover.

We hope this book will support graduate programmes of Ecology, Evolutionary Biology, or similar programmes, and stimulate students to proceed with their career in the exciting field of ecological genomics, while it is—still—relatively new.

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