

Preface

Speciation is a fundamental process responsible for creating the diversity of life on Earth through the origin of new species. Patterns and mechanisms of speciation have attracted researchers' attention since at least the time of the modern evolutionary synthesis and have already resulted in an impressive volume of scientific literature. Why then another book on speciation and biodiversity? In addition to a number of excellent books, there have been special issues of journals such as *Philosophical Transactions of the Royal Society B Biological Sciences* (vol. 367, 2012) and *International Journal of Ecology* (2012), to mention just the two most recent journals solely devoted to speciation. Despite very significant progress in the field, we are barely scratching the surface of the phenomenon. Many important questions still await answers and even more new questions are being asked – a clear indication of a vibrant and productive area of research. Speciation is critical not only for understanding biodiversity and our place amidst it, but also its protection, so “the greatest show on Earth” can go on and remain awe-inspiring for generations to come. This book offers new glimpses into the current state of the exciting field. I am in big debt to all my colleagues who enthusiastically agreed to share their views, as well as new results of their research presented on the pages of the book.

This collection is loosely organized around three major and interlocking themes of speciation, as defined by the Marie Curie Speciation Network (*Trends in Ecology and Evolution* 27: 27-39; 2012): (i) relationship between speciation and biodiversity patterns (chapters 1-3), (ii) mechanisms that drive the build-up of reproductive isolation and adaptation (chapters 4-8), and (iii) genetics and genomics of speciation (chapters 9-11). The convention for describing the origin of reproductive isolation is whether gene flow is prevented before (‘prezygotic’) or after (‘postzygotic’) hybrid zygote formation, and we follow the scheme. The biodiversity patterns can be informative of speciation mechanisms and, vice versa, speciation mechanisms can be used to explain the patterns of biodiversity. The significance of geographical isolation is reevaluated in the context of sympatric and parapatric speciation (see chapter 2), but geography is almost by definition omnipresent in biodiversity descriptions. This book will take readers on a journey to Lakes Baikal and Yellowstone, through a remote Lord Howe Island in the Pacific, African savannas and parts of Asia, to the deserts of western North America.

Despite striking biodiversity and ecological importance of microeukaryota, chapter 1 reminds us how little we actually know about the speciation of eukaryotic microorganisms. Therein, Cooper and Masly use a combination of taxonomy, paleontology, and genomics to

explore speciation patterns in diatoms, or microeukaryota that are responsible for 40-45% of oceanic production (more than all rainforests combined). In chapters 2 and 3, phylogenetic methods are employed to guide hypotheses about speciation scenarios in multicellular eukaryotic taxa as well: plants (Papadopoulos *et al.*) and gazelles (Lerp *et al.*). Sharakhov (chapter 4) discusses the role of chromatin plasticity and chromosomal inversions in diversification of the African malaria mosquito *Anopheles gambiae* species/population cluster.

Traditionally, research focused on the genetics of reproductive isolation has been heavily dependent on *Drosophila* fruit flies. Although no longer granted monopoly, as exemplified by our book, *Drosophila* species do remain a very attractive model system for speciation and other evolutionary studies. For example, Matzkin and Markow (chapter 5) show how four subspecies of cactophilic *Drosophila mojavensis* evolved in response to different cactus host species with distinct chemical profiles, and how this is reflected by gene expression changes at the genome-wide level of the flies. Courtship "love" songs have been shown to promote sexual isolation between *Drosophila* species, among other organisms. Oliveira and colleagues (chapter 6) describe how courtship songs evolved in another cluster of cactophilic fruit flies, *D. buzzatii*, within a rigorous phylogenetic context. In addition to acoustic signals, there are other important sensory cues used by insects during mating. Chapter 7 (Giesbers and colleagues) provides an overview of courtship characteristics implicated in prezygotic isolation between species of parasitic *Nasonia* wasps. By no means does prezygotic isolation end on courtship or even on copulation. For example, female sperm storage has been known to serve as an arena for cryptic female choice and sperm competition, thus providing a hidden substrate for postmating prezygotic isolation. Marshall (chapter 8) synthesizes what we know about interacting sex proteomes, cell structures, and reproductive physiologies, and hypothesizes that a particular set of genes and physiological pathways underlie much of the postmating prezygotic isolation seen in nature.

Genes underpinning postzygotic reproductive isolation, or hybrid defects, have been the Holy Grail of speciation studies for years. What emerges from the studies is a picture much more complex than predicted by the simple Dobzhansky-Muller model of genetic incompatibilities between alleles. Phadnis and Malik (chapter 9) review the molecular biology of *Odysseus* and *Overdrive*, two well established hybrid male sterility genes in *Drosophila*. Both gene products likely play roles in heterochromatin binding that leads to (at least in the case of *Overdrive*) genetic conflicts manifested as segregation distortion. In chapter 10, Watson and Demuth further explore the landscape of selfish genomic elements – namely mobile elements. By inserting themselves into coding or regulatory regions, mobile elements tend to have deleterious consequences, but they have recently contributed to novel coding and regulatory sequences during their proliferation. These functional and regulatory novelties along with element-mediated rearrangements are occasionally associated with speciation events, whereas remobilization of dormant elements in interspecific hybrids may result in a suite of maladaptive traits. Our book concludes (Johnson, chapter 11) with a call to better integration between cell biology, epigenetics, and evolutionary biology in the study of the evolutionary genetics of hybrid incompatibility.

It was not our intention to deliver a new theoretical framework or a comprehensive synthesis of ongoing research on speciation. Instead, we wanted to signalize encouraging developments in the field that result from the emergence of new technologies and ways of

thinking, such as high-throughput genomics and epigenetics, as well as integration between traditionally distinct disciplines.

Before I sign off, I would like to thank Maureen Lawrence-Kuether for assistance with editorial work, and Carra Feagaiga from Nova Science Publishers, Inc., for shepherding and patience of the matador throughout all stages of the book's development.

Chapter 1

Speciation in Cyanobacteria: Patterns and Processes

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Abstract

Cyanobacteria represent one of the most speciose groups of organisms within the prokaryotes—they occupy almost every aquatic niche worldwide, provide important functions within ecosystems as a major contributor of oxygen, divide fixation from the atmosphere, and also serve as a major contributor to the base of the aquatic food web. Despite this striking example of biodiversity, and their ecological importance, we know relatively little about the speciation processes at work in this group. In this chapter, we review the patterns of speciation in cyanobacteria and discuss the evidence with respect to their processes of speciation. We also discuss the evidence for the role of horizontal gene transfer in speciation. We summarize the evidence for the role of horizontal gene transfer in speciation and discuss recent work on understanding the mechanisms of speciation in cyanobacteria that point to the microtubule.

We also discuss aspects of the speciation process in cyanobacteria that point to the potential role of speciation in this group. Finally, we discuss the role of a natural model system that presents a unique opportunity to address some of the outstanding questions in speciation research.

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