

Preface

The past thirty years have witnessed remarkable advances in our ability to describe the structure and dynamics of genetic diversity in wild populations. Beginning with the classical applications of allozyme electrophoresis to populations of *Drosophila* and man, there has been an escalation of molecular methodologies which explore the genetic relationships among individuals, populations and species, a field that has become known as "molecular ecology". The ubiquity across taxa of molecular genetic markers provided by allozymes, restriction fragment length polymorphisms, DNA fingerprinting, microsatellites and DNA sequencing, has enabled wide-scale exploration of problems in ecology and evolution, yielding insights into the origin, maintenance and exploitation of biodiversity.

Much effort has been expended in the development of new molecular technologies, together with concerted attempts to describe the molecular basis and evolutionary dynamics of the various classes of molecular variants utilised. The development of novel methodologies, most notably the discovery of the polymerase chain reaction (PCR) and disclosure of highly repetitive DNA has revolutionised the breadth of tractable problems. Enhanced marker variability, coupled with the relative ease and speed afforded by PCR-based methods, has facilitated opportunities to explore new applications and perspectives. Noteworthy contributions include studies on direct estimates of fitness variation in the wild, the application of ancient DNA to historical population analysis, the mapping of quantitative genetic variation and its ecological significance, and the molecular analysis of microbial population structure and diversity. In view of the wide variety of molecular and analytical methodologies and contemporary applications, it is timely to consider some major contributions and future priorities of the molecular approach, and in particular to enhance our understanding of the markers employed.

It was against this background of escalating activities and outputs in molecular ecology, and a need for consolidation and synthesis, that the NATO Advanced Study Institute (ASI) on Advances in Molecular Ecology was held at the Ettore Majorana, International Centre for Scientific Culture in Erice, Italy, in March 1998. Fifteen lecturers and over seventy students spent ten days engaged in instruction and discussion. The ASI provided the first international opportunity for a comprehensive consideration of how recent advances, most notably, the PCR-based technology had impacted on concepts and applications in ecology and evolution. Researchers across the fields of animals, plants and microbial communities presented a thematic approach, with emphasis on the integration of concepts independently of taxon. A hierarchical structure to the ASI was adopted, starting out with an overview of the molecular methodologies available, including both protein and DNA-based techniques, and proceeding onto deliberations at the individual, population and higher taxonomic levels.

In this book, we present some of the contributions delivered by the NATO lecturers, encompassing aspects of approach and methodology, and illustrated by a diversity of applications. Each author was asked to examine how molecular genetic tools have contributed to their specific area of consideration, identifying novel insights, controversies and future priorities. The coverage is not intended to be comprehensive across all

contemporary fields in molecular ecology, but rather illustrative of the diversity of approach and application, and with emphasis on the genetic and evolutionary characteristics of the markers employed. It is only through the use of appropriate sampling design, choice of marker or marker combinations, and apposite statistical analysis of data that meaningful tests and interpretations can be attained. The examples presented here endorse such an approach by considering not only how molecular markers have impacted on concepts and theory, but also by demonstrating through recent developments how they can be employed with effect.

The book begins by placing the approach of molecular ecology into context (Gary Carvalho), pointing out the conceptual contributions of classical ecological genetics, and the impact of advances in DNA technology. Emphasis is placed on the need to consider more widely the genetic and evolutionary characteristics of marker variants as a basis for their effective use. There follows methodological considerations of how frequency data in molecular ecology can be analysed using a phylogenetic approach (David Hillis), and the relative merits of conventional and coalescent approaches to describing population structure and gene flow (Peter Beerli). Arnaud Estoup and Bernard Anders describe the use of variable number of tandem repeats (VNTR) as markers in ecology and evolution in relation to their molecular and evolutionary characteristics. Estoup and Anders conclude that microsatellites offer particularly powerful tools in molecular ecology, including a consideration of contributions at the individual, population and phylogenetic levels. Applications of molecular markers to describe microbial population and community structure are highlighted by Gerard Muyzer. Not only is the wealth of microbial diversity in the wild only now becoming evident, but molecular technology is providing a powerful approach for exploring linkages between bacterial diversity, environmental heterogeneity and bacterial function. Peter Young discusses various recombination mechanisms in bacteria as evidenced by recent applications of the molecular approach, and considers how the nature of bacterial species can offer a new perspective on the general issues surrounding the nature of species. Franco Rollo introduces the concept of ancient DNA, and explains how it can be applied with caution to reveal information on the structure and diversity of ancient bacterial communities, including their association with man. Bob Vrijenhoek reviews the theories to explain the evolution of sex by reference to molecular studies on clonal organisms, and concludes that although clonality is widespread, with few exceptions there is little evidence for the existence of ancient clonal lineages or diversified asexual taxa.

Andrew Schnabel deals with the reconstruction of mating and dispersal processes in natural and experimental plant populations, with emphasis on the methods for assessing parentage of individual progeny and the contribution of molecular markers, especially in relation to estimating relative fertilities of individual parents in populations. Lorenz Hauser and Bob Ward address the contribution that molecular tools have made in the analysis of highly mobile pelagic fishes. They emphasize not only differences in the ability of various markers to detect structuring, but also the influence of ecology and pelagic lifestyle on population structure. Jeffery Mitton reviews how molecular markers can be used to explore the operation of natural selection in the wild, with particular emphasis on some recent allozyme studies, as well as insights provided by mitochondrial and microsatellite markers. Loren Rieseberg describes the contributions of molecular markers to our understanding of hybrid zone structure and dynamics, and how such information has informed our perspectives on introgression, hybrid speciation, species extinction and phylogenetic incongruence. Paul Hebert considers patterns of species diversification in inland waters, and offers molecular evidence for the role that environmental stress may play in modulating

mutation and evolutionary rates. Contributions from two other lecturers at Erice, Ciro Rico (animal mating and social systems) and Søren Sørensen (experimental evolution of microbes and GMOs), and are not included in this book.

To increase the practical utility of the book, we conclude with a summary of current software that is available for the analysis of data in molecular ecology, detailing information on names of authors, date of latest update, compatible operating systems, types of data handled and analyses supported. A glossary of terms is provided to facilitate access to unfamiliar topics.

A major advantage of the NATO Advanced Study Institute scheme is the speed of publication of the associated book, allowing a synthesis of contemporary issues, together with an up to date coverage of literature. This is especially valuable in an approach such as molecular ecology, where methodological and analytical methods develop rapidly. The cost, however, has been the demanding schedule imposed on all those who have contributed to the book, either through general organisation of the ASI, those that acted as referees and, of course, those that contributed as authors. The NATO lecturers survived a punishing schedule, and I thank them sincerely for devoting so much time to the ASI, and in providing timely and lively reviews. Additionally, the content and stimulus for respective contributions owe much to the committed and imaginative discussions with the ASI students.

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Finally, but most importantly, this book is dedicated to the fond memory of the late Professor Goffredo Cognetti, the local organiser of the ASI, who first suggested the idea of an advanced meeting to consider recent advances in molecular ecology. His desire to bring together specialists and students in molecular ecology, and through discussion, explore controversies and future directions, was in keeping with the spirit of the venue and its history, some of which we hope is captured in this book.

Gary Carvalho, Hull, August, 1998