

Preface

Importance of the topic

One of the greatest unmet issues in conservation biology is the genetic management of fragmented animal and plant populations. Many species across the planet have fragmented distributions with some small isolated populations that are potentially suffering from inbreeding, loss of genetic diversity, and elevated extinction risk (genetic erosion). Fortunately, these effects can usually be remedied by augmenting gene flow (crossing populations within species), but this is rarely conducted. Disturbingly, evidence of any genetic differentiation among populations typically leads managers to conclude that the populations should be kept isolated, thereby dooming many to eventual extinction. We are particularly concerned with populations fragmented by human actions in the last 500 years, encompassing most of the impacts arising from a 13-fold increase in the human population.

A paradigm shift is urgently required where the existence of genetic differentiation among populations acts as a trigger to ask if any populations are suffering from genetic problems. If so, are there populations to which they can be crossed to reduce inbreeding and augment genetic diversity, and will this gene flow be beneficial or harmful?

Whether to maintain genetic isolation is a major issue for managers of wild animal and plant populations. It is critical that managers, and those who advise them, become aware of the issues relating to restoration of genetic diversity and contribute to the reversal of genetic deterioration associated with small population size.

Genesis of this book

The events that triggered this book began in February 2007 during a book writing session on the 2nd edition of *Introduction to Conservation Genetics* involving Jon Ballou and Dick Frankham. When revising material on population fragmentation, we were deeply concerned about over-emphasis in the literature on the risks of outbreeding depression (where crossing between populations is harmful), while the benefits of crossing between populations within species to rescue small inbred populations were largely neglected. We subsequently outlined means to predict the risk of outbreeding depression (thus allowing the benefits of genetic rescue to be utilized widely), recruited Mark Eldridge, Kathy Ralls, Bob Lacy, Michele Dudash, and Charlie Fenster as collaborators, and subsequently published the Frankham et al. (2011) paper on the topic. That work influenced a paper on the use of genetic translocations to cope with global climate change (Weeks et al. 2011) co-authored by Mark Eldridge, Dick Frankham, and Paul

Sunnucks among others. Our paper on implications of different species concepts for biodiversity conservation (Frankham et al. 2012) was provoked by practical concerns that Ingrid Porton of St Louis Zoo had about genetic management of ruffed lemurs in light of taxonomic revisions and competing taxonomies, and also drew upon our work on predicting outbreeding depression.

This book arose as an extension of the above studies and our previous work on inbreeding depression, evolutionary potential, outbreeding depression, genetic rescue, and genetic management of fragmented populations, plus our extensive involvement in threatened species recovery. While drafting Chapter 6 on genetic rescue, Dick Frankham identified the lack of a quantitative overview and this provoked him to complete two meta-analyses that inform the book chapter (Frankham 2015, 2016), as did the content of a symposium on the topic at the 2014 meeting of the Society for Conservation Biology in Missoula, Montana.

The material on managing gene flow among isolated population fragments (optimizing gene flow) was initiated largely as an extension of the seminal Ballou & Lacy (1995) work on genetic management by minimizing mean kinship—the recommended management strategy for threatened species in captivity. The content of this book was also informed by a symposium on genetic management of fragmented populations at the 2011 meeting of the Society for Conservation Biology in New Zealand, organized by authors of this book.

Purpose

This book provides the conceptual background for understanding genetic issues in the management of fragmented wild animal and plant populations, and offers means for making practical decisions on genetic management of population fragments. We focus particularly on the harmful consequences of mating among relatives on offspring fitness (inbreeding depression) that is universal among sexually reproducing non-haploid organisms. A second major focus is on the maintenance of genetic diversity, so that species and populations can continue to adapt to changing environments. We also define the criteria that must be satisfied by definitions of species for conservation purposes, and make recommendations regarding definitions that are appropriate and inappropriate. Our goal of preserving endangered species through genetic management can provide additional benefits beyond single species preservation, because species interact within communities that are subject to abiotic and biotic environments, contributing to ecosystem function and overall global biodiversity.

Intended audience

This book is designed for senior undergraduate and graduate students and professional scientists in conservation and wildlife biology, and evolutionary ecology, as well as for managers of wild animal and plant populations. We will subsequently write a shorter, simpler Practical Guide for managers who are less familiar with conservation genetics.

To make the book accessible to a wide audience, we have assumed knowledge only of introductory genetics and basic statistics. For the same reason, we have restricted use of mathematics to simple algebra, even though genetic management requires a quantitative approach. Readers wishing for a simple concise introduction to conservation genetics are referred to *A Primer of Conservation Genetics* by Frankham et al. (2004) or the Italian, Portuguese, or Korean translations of it.

Précis of contents

The first eight chapters of the book consist of background material and concepts, the subsequent six chapters are concerned with genetic management (including objectives, questions, and decision trees), and the final chapter summarizes the messages from the prior chapters. Genetic issues in single populations are addressed prior to the more complex issues of multiple populations.

Chapter 1 provides a general outline of the issues involved in genetic management of fragmented animal and plant populations and its importance.

Section I provides detailed background on genetic problems in fragmented populations. This begins with a brief introduction to the evolutionary genetics of small populations (Chapter 2) where the roles of mutation, migration, selection, and chance (genetic drift) are described, inbreeding and its measurement considered, and population size in the evolutionary genetics context (effective population size) defined.

Threats to small isolated populations from inbreeding depression and mutational accumulation are covered in Chapter 3, and those from reduced ability to adapt genetically in Chapter 4. We next address genetic problems caused by inadequate gene flow in fragmented populations (Chapter 5).

Section II addresses risk/benefit analyses of remedies for genetic problems in fragmented populations. Genetic rescue by augmenting gene flow is addressed in Chapter 6. Chapter 7 delineates the causes of outbreeding depression and considers the potential of populations to recover from outbreeding depression through natural selection. Chapter 8 evaluates how expectations for remedies and risk from crossing populations need to be modified for species with diverse mating systems and modes of inheritance (self-incompatible, self-fertilizing, asexual, polyploid, haploid, haplodiploid, etc.).

Section III of the book deals with genetic management of fragmented populations. Chapter 9 defines the criteria that must be satisfied by a species definition used for conservation purposes, provides recommendations on definitions that are and are not appropriate, identifies the many pitfalls in species delineation, and recommends remedies. Chapter 10 covers methods for delineating the number and locations of population fragments. Chapter 11 presents practical guidelines (including decision trees) for determining whether populations are suffering genetic erosion and whether they would benefit from augmented gene flow. Chapters 12 and 13 address management of gene flow among isolated population fragments, the former chapter based on limited information, and the latter on extensive genetic information (using mean kinship). Chapter 14 explores genetic management under the moving target created by global

climate change. Finally, Chapter 15 draws the prior threads together to present the **Take home messages** from the book.

Format

To make the books easy to read and follow, we use a textbook format similar to that of the Frankham, Ballou, and Briscoe textbooks *Introduction to Conservation Genetics* (2nd edn, 2010) and *A Primer of Conservation Genetics* (2004). In particular, we use:

- main messages boxes at the start of each chapter
- list of terms for each chapter
- frequent headings and sub-headings
- small main point boxes and dot point lists throughout chapters
- ample use of figures, maps, and tables
- boxes with case studies
- example boxes
- decision trees
- line drawings by Karina McInnes
- links to software for genetic analysis and management
- List of symbols
- Glossary
- Appendices
- References and Index.

We use questions for most of the major headings within chapters, as science seeks to answer questions. This approach was successfully trialed in undergraduate teaching, presentations to professional scientists, and for communicating genetic concepts to conservation practitioners.

References

Given length constraints and issues of readability, we restrict referencing to examples and a few recent or key citations (especially meta-analyses and reviews) to allow access to the relevant literature, except for contentious issues where we present more extensive referencing.