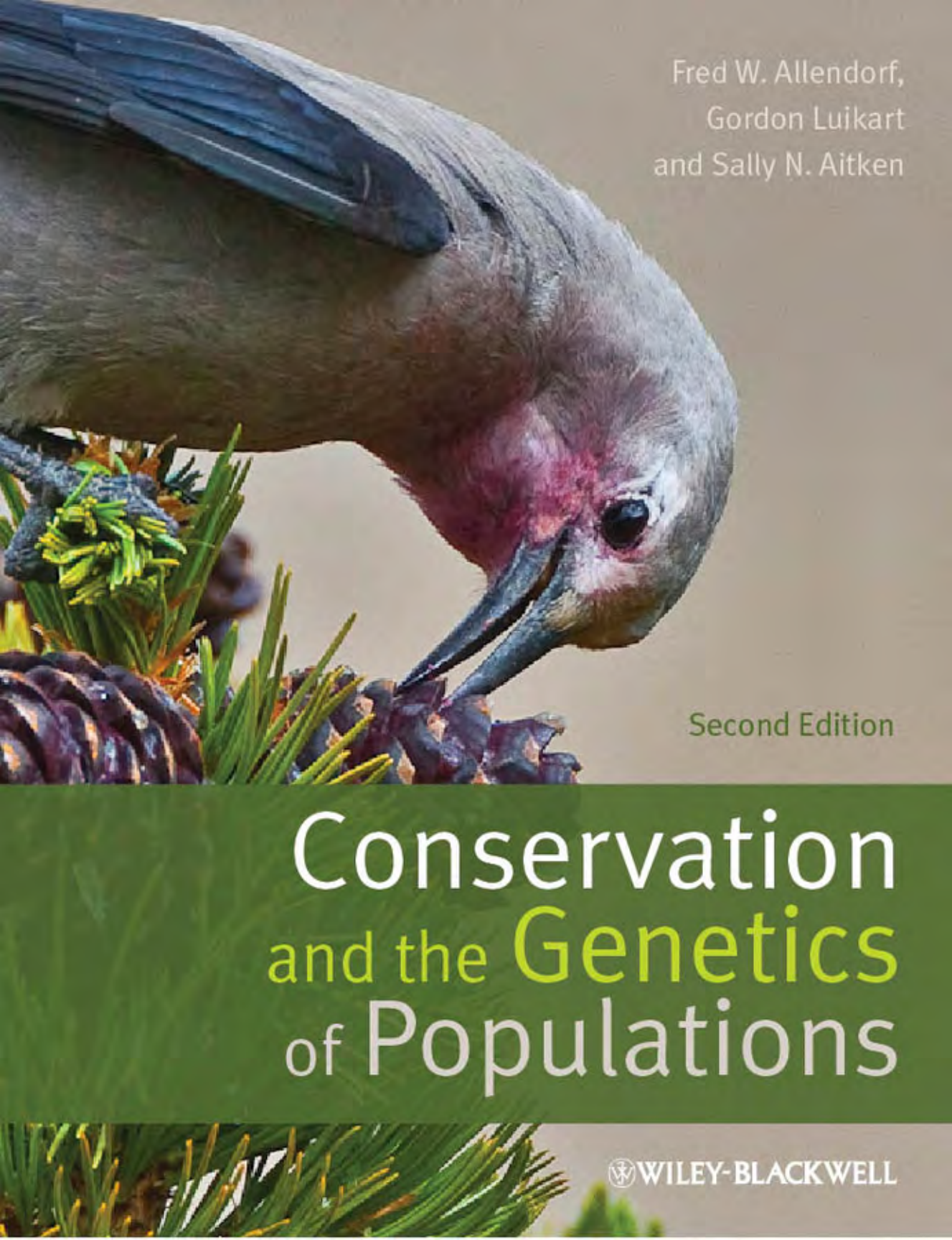




Fred W. Allendorf,
Gordon Luikart
and Sally N. Aitken

Second Edition

Conservation and the Genetics of Populations

 WILEY-BLACKWELL

CONSERVATION AND
THE GENETICS OF
POPULATIONS

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with additional resources

CONSERVATION AND THE GENETICS OF POPULATIONS

Second Edition

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Contents

Guest Box authors, ix

Preface to the second edition, xi

Preface to the first edition, xiii

List of symbols, xv

PART I: INTRODUCTION, 1

1 Introduction, 3

- 1.1 Genetics and civilization, 4
- 1.2 What should we conserve?, 5
- 1.3 How should we conserve biodiversity?, 9
- 1.4 Applications of genetics to conservation, 10
- 1.5 The future, 12

Guest Box 1: L. Scott Mills and Michael E. Soulé, The role of genetics in conservation, 13

2 Phenotypic variation in natural populations, 14

- 2.1 Color pattern, 17
- 2.2 Morphology, 20
- 2.3 Behavior, 23
- 2.4 Phenology, 25
- 2.5 Differences among populations, 27
- 2.6 Nongenetic inheritance, 31

Guest Box 2: Chris J. Foote, Looks can be deceiving: countergradient variation in secondary sexual color in sympatric morphs of sockeye salmon, 32

3 Genetic variation in natural populations: chromosomes and proteins, 34

- 3.1 Chromosomes, 35
- 3.2 Protein electrophoresis, 45

- 3.3 Genetic variation within natural populations, 48
 - 3.4 Genetic divergence among populations, 50
- Guest Box 3: E. M. Tuttle, Chromosomal polymorphism in the white-throated sparrow, 52

4 Genetic variation in natural populations: DNA, 54

- 4.1 Mitochondrial and chloroplast organelle DNA, 56
 - 4.2 Single-copy nuclear loci, 60
 - 4.3 Multiple locus techniques, 68
 - 4.4 Genomic tools and markers, 69
 - 4.5 Transcriptomics, 72
 - 4.6 Other 'omics' and the future, 73
- Guest Box 4: Louis Bernatchez, Rapid evolutionary changes of gene expression in domesticated Atlantic salmon and its consequences for the conservation of wild populations, 74

PART II: MECHANISMS OF EVOLUTIONARY CHANGE, 77

5 Random mating populations: Hardy-Weinberg principle, 79

- 5.1 Hardy-Weinberg principle, 80
 - 5.2 Hardy-Weinberg proportions, 82
 - 5.3 Testing for Hardy-Weinberg proportions, 83
 - 5.4 Estimation of allele frequencies, 88
 - 5.5 Sex-linked loci, 90
 - 5.6 Estimation of genetic variation, 92
- Guest Box 5: Paul Sunnucks and Birgita D. Hansen, Null alleles and Bonferroni 'abuse': treasure your exceptions (and so get it right for Leadbeater's possum), 93

6 Small populations and genetic drift, 96

- 6.1 Genetic drift, 97
- 6.2 Changes in allele frequency, 100
- 6.3 Loss of genetic variation: the inbreeding effect of small populations, 101
- 6.4 Loss of allelic diversity, 102
- 6.5 Founder effect, 106
- 6.6 Genotypic proportions in small populations, 110
- 6.7 Fitness effects of genetic drift, 112
- Guest Box 6: Menna E. Jones, Reduced genetic variation and the emergence of an extinction-threatening disease in the Tasmanian devil, 115

7 Effective population size, 117

- 7.1 Concept of effective population size, 118
- 7.2 Unequal sex ratio, 119
- 7.3 Nonrandom number of progeny, 121
- 7.4 Fluctuating population size, 125
- 7.5 Overlapping generations, 125
- 7.6 Variance effective population size, 126
- 7.7 Cytoplasmic genes, 126
- 7.8 Gene genealogies, the coalescent, and lineage sorting, 129
- 7.9 Limitations of effective population size, 130
- 7.10 Effective population size in natural populations, 132
- Guest Box 7: Craig R. Miller and Lisette P. Waits, Estimation of effective population size in Yellowstone grizzly bears, 134

8 Natural selection, 136

- 8.1 Fitness, 138
- 8.2 Single locus with two alleles, 138
- 8.3 Multiple alleles, 144
- 8.4 Frequency-dependent selection, 147
- 8.5 Natural selection in small populations, 149
- 8.6 Natural selection and conservation, 151
- Guest Box 8: Paul A. Hohenlohe and William A. Cresko, Natural selection across the genome of the threespine stickleback fish, 154

9 Population subdivision, 156

- 9.1 F -Statistics, 158
- 9.2 Spatial patterns of relatedness within local populations, 161
- 9.3 Genetic divergence among populations and gene flow, 163
- 9.4 Gene flow and genetic drift, 165

- 9.5 Continuously distributed populations, 168
- 9.6 Cytoplasmic genes and sex-linked markers, 169
- 9.7 Gene flow and natural selection, 172
- 9.8 Limitations of F_{ST} and other measures of subdivision, 174
- 9.9 Estimation of gene flow, 179
- 9.10 Population subdivision and conservation, 184
- Guest Box 9: M.K. Schwartz and J.M. Tucker, Genetic population structure and conservation of fisher in western North America, 185

10 Multiple loci, 187

- 10.1 Gametic disequilibrium, 188
- 10.2 Small population size, 192
- 10.3 Natural selection, 192
- 10.4 Population subdivision, 196
- 10.5 Hybridization, 196
- 10.6 Estimation of gametic disequilibrium, 199
- 10.7 Multiple loci and conservation, 200
- Guest Box 10: Robin S. Waples, Estimation of effective population size using gametic disequilibrium, 203

11 Quantitative genetics, 205

- 11.1 Heritability, 206
- 11.2 Selection on quantitative traits, 212
- 11.3 Finding genes underlying quantitative traits, 217
- 11.4 Loss of quantitative genetic variation, 220
- 11.5 Divergence among populations, 223
- 11.6 Quantitative genetics and conservation, 225
- Guest Box 11: David W. Coltman, Response to trophy hunting in bighorn sheep, 229

12 Mutation, 230

- 12.1 Process of mutation, 231
- 12.2 Selectively neutral mutations, 235
- 12.3 Harmful mutations, 239
- 12.4 Advantageous mutations, 239
- 12.5 Recovery from a bottleneck, 241
- Guest Box 12: Michael W. Nachman, Color evolution via different mutations in pocket mice, 242

PART III: GENETICS AND CONSERVATION, 245**13 Inbreeding depression, 247**

- 13.1 Pedigree analysis, 248
- 13.2 Gene drop analysis, 252

- 13.3 Estimation of F with molecular markers, 253
- 13.4 Causes of inbreeding depression, 256
- 13.5 Measurement of inbreeding depression, 258
- 13.6 Genetic load and purging, 264
- 13.7 Inbreeding and conservation, 267
- Guest Box 13: Lukas F. Keller, Inbreeding depression in song sparrows, 268

14 Demography and extinction, 270

- 14.1 Estimation of census population Size, 272
- 14.2 Inbreeding depression and extinction, 274
- 14.3 Population viability analysis, 277
- 14.4 Loss of phenotypic variation, 286
- 14.5 Loss of evolutionary potential, 288
- 14.6 Mitochondrial DNA, 289
- 14.7 Mutational meltdown, 289
- 14.8 Long-term persistence, 291
- 14.9 The 50/500 rule, 292
- Guest Box 14: A. G. Young, M. Pickup, and B. G. Murray, Management implications of loss of genetic diversity at the self-incompatibility locus for the button wrinklewort, 293

15 Metapopulations and fragmentation, 296

- 15.1 The metapopulation concept, 297
- 15.2 Genetic variation in metapopulations, 298
- 15.3 Effective population size of metapopulations, 301
- 15.4 Population divergence and connectivity, 303
- 15.5 Genetic rescue, 304
- 15.6 Landscape genetics, 306
- 15.7 Long-term population viability, 311
- Guest Box 15: Robert C. Vrijenhoek, Fitness loss and genetic rescue in stream-dwelling topminnows, 313

16 Units of conservation, 316

- 16.1 What should we protect?, 318
- 16.2 Systematics and taxonomy, 320
- 16.3 Phylogeny reconstruction, 322
- 16.4 Genetic relationships within species, 327
- 16.5 Units of conservation, 336
- 16.6 Integrating genetic, phenotypic, and environmental information, 346
- 16.7 Communities, 348
- Guest Box 16: David J. Coates, Identifying units of conservation in a rich and fragmented flora, 350

17 Hybridization, 352

- 17.1 Natural hybridization, 353
- 17.2 Anthropogenic hybridization, 358
- 17.3 Fitness consequences of hybridization, 360
- 17.4 Detecting and describing hybridization, 364
- 17.5 Hybridization and conservation, 370
- Guest Box 17: Loren H. Rieseberg, Hybridization and the conservation of plants, 375

18 Exploited populations, 377

- 18.1 Loss of genetic variation, 378
- 18.2 Unnatural selection, 381
- 18.3 Spatial structure, 385
- 18.4 Effects of releases, 388
- 18.5 Management and recovery of exploited populations, 391
- Guest Box 18: Guðrún Marteinsdóttir, Long-term genetic changes in the Icelandic stock of Atlantic cod in response to harvesting, 393

19 Conservation breeding and restoration, 395

- 19.1 The role of conservation breeding, 398
- 19.2 Reproductive technologies and genome banking, 400
- 19.3 Founding populations for conservation breeding programs, 403
- 19.4 Genetic drift in captive populations, 405
- 19.5 Natural selection and adaptation to captivity, 407
- 19.6 Genetic management of conservation breeding programs, 410
- 19.7 Supportive breeding, 412
- 19.8 Reintroductions and translocations, 414
- Guest Box 19: Robert C. Lacy, Understanding inbreeding depression: 25 years of experiments with *Peromyscus* mice, 419

20 Invasive species, 421

- 20.1 Why are invasive species so successful?, 422
- 20.2 Genetic analysis of introduced species, 425
- 20.3 Establishment and spread of invasive species, 429
- 20.4 Hybridization as a stimulus for invasiveness, 430
- 20.5 Eradication, management, and control, 431
- 20.6 Emerging diseases and parasites, 433
- Guest Box 20: Richard Shine, Rapid evolution of introduced cane toads and native snakes, 438

21 Climate change, 440

- 21.1 Predictions and uncertainty about future climates, 441
- 21.2 Phenotypic plasticity, 442
- 21.3 Maternal effects and epigenetics, 445
- 21.4 Adaptation, 446
- 21.5 Species range shifts, 448
- 21.6 Extirpation and extinction, 449
- 21.7 Management in the face of climate change, 451
- Guest Box 21: S. J. Franks, Rapid evolution of flowering time by an annual plant in response to climate fluctuation, 453

22 Genetic identification and monitoring, 455

- 22.1 Species identification, 457
- 22.2 Metagenomics and species composition, 464
- 22.3 Individual identification, 465
- 22.4 Parentage and relatedness, 469
- 22.5 Population assignment and composition analysis, 471
- 22.6 Genetic monitoring, 477
- Guest Box 22: C. Scott Baker, Genetic detection of illegal trade of whale meat results in closure of restaurants, 481

Appendix: Probability and statistics, 484

- A1 Paradigms, 485
- A2 Probability, 487
- A3 Statistical measures and distributions, 489
- A4 Frequentist hypothesis testing, statistical errors, and power, 496
- A5 Maximum likelihood, 499
- A6 Bayesian approaches and MCMC (Markov Chain Monte Carlo), 500
- A7 Approximate Bayesian Computation (ABC), 504
- A8 Parameter estimation, accuracy, and precision, 504
- A9 Performance testing, 506
- A10 The coalescent and genealogical Information, 506
- Guest Box A: James F. Crow, Is mathematics necessary?, 511

Glossary, 513

References, 531

Index, 587

Color plates section between page 302 and page 303

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This book has a companion website at:

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Preface to the second edition

Truth is a creation, not a discovery.

R.H. Blyth

This second edition is an updated and expanded version of our book published in 2007. The need for applying genetics to problems in conservation has continued to increase. In addition, many important technological and conceptual developments have changed the field of conservation genetics over the last five years. We have added new chapters on climate change and on genetic effects of harvest (e.g., hunting and fishing), and have extensively revised all other chapters. In an effort to restrict the size of this new edition, we have moved the end of the chapter questions to the book's website. A new edition is needed to keep pace with the changes, to remain a useful overview and synthesis, and to help advance the field. Nearly one-third of the over 1800 references in this book were published after the first edition.

We are excited to have added Sally Aitken as a coauthor. Sally was a reviewer of our first edition for Wiley-Blackwell. Sally's review and suggested changes were so helpful that she should have been an author of that edition!

As we said in the Preface of the first edition, this book is not an argument for the importance of genetics in conservation. Rather, it is designed to provide the reader with the appropriate background and conceptual understanding to apply genetics to problems in conservation. The primary current causes of extinction are anthropogenic changes that affect ecological characteristics of populations (habitat loss, fragmentation, introduced species, etc.). However, genetic information and principles can be invaluable in developing conservation plans for species threatened with such effects. Phil Hedrick (2007) suggested in his review of the first edition that we should have made

more of a sales pitch for the successes of conservation genetics, rather than our very even-handed approach. We do not agree. We are advocates for conservation, not genetics.

We have strived for a balance between theory, empirical data, and statistical analysis in this text. Empirical population genetics depends upon this balance (see Figure 1.1). The effort to measure and understand the evolutionary significance of genetic variation in natural populations began with the rediscovery of Mendel's principles in the early 1900s. For many years, empirical observation of genetic variation lagged far behind the development of sophisticated theory by some of the greatest minds of the twentieth century (e.g., J.B.S. Haldane, R.A. Fisher, and Sewall Wright). Today it is relatively easy to obtain and analyze enormous amounts of information on genetic variation (e.g., markers or genome sequences) in any species.

There are a wide variety of computer programs available to analyze data and estimate parameters of interest. However, the ease of collecting and analyzing data has led to an unfortunate and potentially dangerous reduction in the emphasis on understanding theory in the training of population and conservation geneticists. Understanding theory remains crucial for correctly interpreting outputs from computer programs and statistical analyses. For example, the most powerful software programs that estimate important parameters, such as effective population size (Chapter 7) and gametic disequilibrium (Chapter 10), are not useful if their assumptions and limitations are not understood. We are still disturbed when we read statements in the literature that the loci studied are not linked because they are not in linkage (gametic) disequilibrium.

The tools being used by molecular population geneticists are changing rapidly. Deciding which techniques

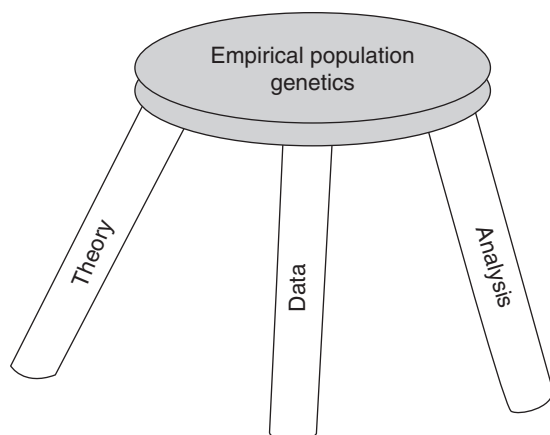


Figure i.1 The application of population genetics to understand genetic variation in natural populations relies upon a balance of understanding the appropriate theory, collecting appropriate data, and understanding its analysis.

to include in Chapter 4 was difficult. We have added new genomics (and other ‘omics’) information and still include some techniques that are no longer in use (e.g., minisatellites) because they are crucial for understanding previous literature. On the other hand, we have not included older techniques that are now known to provide data that are not reliable (e.g., RAPDs).

ACKNOWLEDGMENTS

We would like to thank again everyone acknowledged in the Preface to the previous edition of this book. FWA thanks the Hatfield Marine Science Center and the Hawai‘i Institute of Marine Biology for hosting his extended visits to work on this edition. Chapter 18 is based partially on work supported by the US National

Science Foundation, Grant DEB 074218 to FWA and GL. In addition, we give special thanks to the Minitab Corporation for providing software through their Author Assistance Program, Paul Sunnucks for his many helpful comments on the previous edition, Nils Ryman for help with the Appendix, and Ian Jamieson for help with Table 13.1. In addition, we thank the many colleagues who have helped us by providing comments, information, unpublished data, and answers to questions associated with this edition: Steve Amish, Peter Beerli, Kurt Benirschke, Des Cooper, Rob Cowie, Kirsten Dale, Pam Diggle, Suzanne Edmands, Zac Forsman, Ned Friedman, Oscar Gaggiotti Roxanne Haverkort, Paul Hohenlohe, Marty Kardos, Meng-Hua Li, Ian MacLachlan, Sierra McLane, Juha Merilä, Gordon Orians, Barb Taylor, Mark Tanaka, Dave Towns, C. Susannah Tysor, and Sam Yeaman.

DEDICATION

We dedicate this book to James F. Crow, who died just before his 96th birthday as we were putting the finishing touches on this book. Jim was a great scientist and wonderful human being whose contributions were enormous. We were honored that he agreed to write a Guest Box for the Statistical Appendix. Over the years, we always appreciated Jim’s clear and useful reviews of our papers when they were sent to him. FWA got to know Jim in the last few years while his daughter was attending graduate school in Madison. My most vivid memory of talking with Jim in his tiny office was finding Sewall Wright’s National Medal of Science haphazardly placed on a filing cabinet behind the office door.

12 February 2012

Fred W. Allendorf
Gordon Luikart
Sally N. Aitken

Preface to the first edition

The many beings are numberless; I vow to save them all.

Traditional Zen vow

The one process now going on that will take millions of years to correct is the loss of genetic and species diversity by the destruction of natural habitats. This is the folly our descendants are least likely to forgive us.

Edward O. Wilson, 1984

This book is about applying the concepts and tools of genetics to problems in conservation. Our guiding principle in writing has been to provide the conceptual basis for understanding the genetics of biological problems in conservation. We have not attempted to review the extensive and ever growing literature in this area. Rather we have tried to explain the underlying concepts and to provide enough clear examples and key citations for further consideration. We also have strived to provide enough background so that students can read and understand the primary literature.

Our primary intended audience is broadly trained biologists who are interested in understanding the principles of conservation genetics and applying them to a wide range of particular issues in conservation. This includes advanced undergraduate and graduate students in biological sciences or resource management, as well as biologists working in conservation biology for management agencies. The treatment is intermediate and requires a basic understanding of ecology and genetics.

This book is not an argument for the importance of genetics in conservation. Rather, it is designed to provide the reader with the appropriate background to determine how genetic information may be useful in any spe-

cific case. The primary current causes of extinction are anthropogenic changes that affect ecological characteristics of populations (habitat loss, fragmentation, introduced species, etc.). However, genetic information and principles can be invaluable in developing conservation plans for species threatened with such effects.

The usefulness of genetic tools and concepts in conservation of biological diversity is continually expanding as new molecular technologies, statistical methods, and computer programs are being developed at an increasing rate. Conservation genetics and molecular ecology are under explosive growth, and this growth is likely to continue for the foreseeable future. Indeed we have recently entered the age of genomics. New laboratory and computational technologies for generating and analyzing molecular genetic data are emerging at a rapid pace.

There are several excellent texts in population genetics available (e.g., Hedrick 2005, Hartl and Clark 1997, Halliburton 2004). Those texts concentrate on questions related to the central focus of population and evolutionary genetics, which is to understand the processes and mechanisms by which evolutionary changes occur. There is substantial overlap between those texts and this book. However, the theme underlying this book is the application of an understanding of the genetics of natural populations to conservation.

We have endeavored to present a balanced view of theory and data. The first four chapters (Part I) provide an overview of the study of genetic variation in natural populations of plants and animals. The middle eight chapters (Part II) provide the basic principles of population genetics theory with an emphasis on concepts especially relevant for problems in conservation. The final eight chapters (Part III) synthesize these principles and apply them to a variety of topics in conservation.

We emphasize the interpretation and understanding of genetic data to answer biological questions in