Genetic Variation Within Populations Study Guide Answers

This book addresses research in the rapidly developing integration of conservation biology with population biology.

Rare plant species often occur in populations of relatively small size and thus are at risk of changes in their genetic structure due to the effects of drift and inbreeding. Drift and inbreeding can result in reduced genetic diversity, increased differentiation among populations and an overall decrease in a species' potential to persist when faced with environmental changes. In this study I address these small population paradigms by examining the population genetic dynamics of a rare California grassland annual, Clarkia springvillensis. Using seven isozyme-encoding loci, I assessed the amount and distribution of genetic variation at several spatial scales among three populations and eight subpopulations. Total genetic variation $\rm(H\sb{t}=0.260)$ was lower than species with similar life history traits but equivalent to that of other endemics. Subpopulations were more differentiated from each other $\rm (F\sb{sp}=0.084)$ than were populations $\rm(F\sb{pt}=0.017).$ There was no correlation between genetic and geographic distances and this, along with the significant differentiation of subpopulations, suggest that genetic drift is occurring within populations. However, the effects of drift have not yet become severe; the differentiation exhibited overall was significantly lower than similar species, be they endemic or widespread. Further, I explored the possibility that the seed bank of C. springvillensis could be acting as a buffer against the loss of genetic diversity and the differentiation of populations. The seed bank was surveyed by collecting soil cores in three populations. The genetic constitution of the adults and seed bank cohort was determined by examining eight polymorphic isozyme loci. The total genetic diversity in the seed bank (Ht = 0.355) was significantly higher than in the adults (Ht = 0.260). Additionally, F$\rm\sb{st}$ estimates showed significantly less differentiation among populations' seed banks $\rm(F\sb{st}=0.008)$ than among adults $\rm(F\sb{st}=0.045).$ These results are in agreement with the expectation that seed banks could act to maintain genetic diversity in populations as well as have the effect of slowing differentiation of populations. Finally, I examined the effects of inbreeding throughout the life cycle of 12 maternal lineages in natural and glasshouse populations of C. springvillensis. In the field, inbreeding had no effect on seedling survivorship; habitat and germination time were the important factors. In a glasshouse experiment spanning the full life cycle of the species, there was no evidence of population level inbreeding depression for germination success, survival, total flowers produced or total biomass. However, there was significant variation in response to inbreeding among maternal lines. The variation among families could facilitate a shift in the mating system from outcrossing to selfing. This same variation may also increase the populations probability of persistence despite periods of high inbreeding. The results of this study indicate that the paradigms regarding the genetic dynamics in small populations may not always hold true. Of particular importance is the influence of the seed bank which can maintain genetic variation, slow population differentiation and increase effective population size, thereby buffering populations from predicted consequences of small above ground population size.

Kincaid's lupine (Lupinus oreganus Heller) is a federally listed threatened species native to remnant grassland of western Oregon and southwestern Washington, and is the primary larval host plant of a once thought extinct butterfly, Plebejus icarioides fenderi Macy. Past studies concerning Kincaid's lupine reproduction suggested that populations may suffer reductions in fitness and progeny vigor due to inbreeding depression, but no direct investigation into range-wide patterns of genetic variation has been undertaken. I used nuclear DNA and chloroplast DNA simple sequence repeat (SSR) markers to determine genet size and patterns of non-

adventitious rhizomatous lupine spread, to estimate the number of genets within Kincaid's lupine populations, and to assess whether seed transfer for the purpose of genetic rescue is an appropriate genetics management strategy for Kincaid's lupine. Patterns of allelic diversity at nDNA SSR loci within study patches revealed that non-adventitious spread of rhizomes can extend to at least 27 m and may dominate a portion of a lupine patch or small population. However, genet spread and arrangement in study patches were sufficiently integrated such that interplantlet Bombus foraging flights exceeding 2 m had > 90% probability of occurring between different genets. Within-lupine patch genetic diversity was well-undersampled, refuting the supposition that Kincaid's lupine populations suffer from inbreeding depression due to small effective population sizes. Estimation of Kincaid's lupine abundance through leaf cover and inflorescence number was tightly correlated with plantlet number, a unit of vegetative and sexual growth, within lupine patches but the relationship was not consistent between patches within populations or between populations. We used genet to plantlet ratios (determined through genotyping) and plantlet density to estimate genet population size in Kincaid's lupine patches. Because of the strong correlation between cover and plantlet density, historically collected lupine abundance data could be used to estimate genet population size provided that plantlet density is calibrated to patch-specific cover measurements. Within patches and populations across the range of Kincaid's lupine there was little DNA evidence suggesting severe inbreeding. Only one of 24 populations and five study patches had strong statistical evidence of a recent genetic bottleneck despite the range-wide fragmentation of lupine populations and habitat. Mean population fixation index values for nearly half of the populations were near Hardy-Weinberg equilibrium expectations and only one small lupine population had a F-value > 0.20, suggestive of high inbreeding levels. Half of the populations actually had an excess of heterozygotes, suggesting that genetic diversity is not being lost. Chloroplast DNA coincides well with the observation that genetic diversity is not being lost through inbreeding or genetic bottlenecking in Kincaid's lupine. The mean number of cpDNA haplotypes per population was approximately 4 maternal lineages, which is very high for an animal pollinated plant with heavy seeds that have limited dispersal. Even relatively small populations of Kincaid's lupine had 2 or more cpDNA haplotypes, indicating that populations are not severely inbred. Both nuclear and chloroplast DNA SSR genetic marker diversity suggests that Kincaid's lupine does not require genetic rescue for effective conservation. Due to the longevity of Kincaid's lupine and the apparently large amount of within population genetic diversity, the encouragement of natural recruitment from vegetation management that improves habitat conditions is likely to maintain the relatively large amount of genetic diversity within Kincaid's lupine populations.

Metrosideros polymorpha is the most abundant native plant in the Hawaiian Islands growing at elevations from sea level to the subalpine. M. polymorpha exhibits high levels of apparent local adaptation and ranges in morphology from small shrubs (1m) to relatively large trees (20m). Despite the high morphological variation and broad ecological amplitude in this species, there have been few studies assessing genetic variation among populations of morphological varieties. The objective of this study was to use the molecular technique of inter-simple sequence repeats (ISSRs) to examine the genetic diversity and structure of morphologically distinct neighboring populations of M. polymorpha, growing in bog or bog-like conditions and adjacent or nearby forests across multiple islands. ISSR data using three primers were collected for a total of 287 individuals from five of the major islands. A total of 111 loci were found to be 100% polymorphic. The mean value of Nei's gene diversity for all populations was 0.2436 +/- 0.172. The majority of genetic variation was found within microhabitat within islands, with an average of 91.34% (range 80.87%--95.72%). The average amount of genetic variation attributed to differences among microhabitats across islands was 8.64% (range 4.28%--19.13%). There was a significant correlation between geographic and genetic distance

across all populations, and a UPGMA phenogram shows the Kaua'i bog population to have the greatest genetic distance from all other populations. This study demonstrates that populations of morphologically distinct variants of M. polymorpha contain an average amount of genetic diversity within populations and a low amount of genetic differentiation among populations compared to other flowering plant species. These data reflect the fact that M. polymorpha is a widespread ecological generalist capable of living in a vast range of habitats most likely due to extensive gene flow throughout the Hawaiian Islands. Detectable levels of genetic differentiation among populations appear to be the result of geographic isolation rather than putative adaptation to microhabitats, and therefore the different morphologies of bog vs. forest plants are most likely due to phenotypic plasticity and may not have a strong genetic basis. Abstract: In this study, the relative influences of selection, gene flow, and other evolutionary forces on the spatial structure of genetic variation within a eucalypt species complex (the spotted gums: genus Corymbia, section Politaria) were assessed. The study investigated the spatial genetic structure among four putative species of spotted gum (broad-scale), as well as within a single population (fine-scale) of one species, using both molecular and quantitative markers. The spotted gum complex occurs naturally across a range of 2500 km in eastern Australia. Spatial genetic variation within and between the four putative spotted gum species was examined using both chloroplast and nuclear markers. No significant differentiation was found between the three northern species of the complex, C. citriodora, C. variegata and C. henryi. The southern species, C. maculata, shared no haplotypes with any of the three northern species. These results disagree in part with those reported in a previous allozyme based study in which C. henryi was found to be significantly divergent from C. variegata (with which it is sympatric) and more closely aligned with C. maculata. Re-analysis of the allozyme data provided evidence of selection acting at the PGM2 locus within populations of C. variegata and C. henryi. The exclusion of this locus from the data set led to concordance between the cpDNA and nDNA analyses. Restricted gene flow and evidence of isolation by distance were identified as the dominant processes influencing the contemporary distribution of the cpDNA haplotypes. No geographic structure of haplotypes was found and complex genealogical relationships between haplotypes indicated the combined effects of past fragmentation, range expansion and possible long distance dispersal events. The variation and spatial structure in both neutral molecular markers and quantitative genetic traits were compared to explore the relative influences of dispersal and selection within a single eucalypt population. Both mature trees (n=130) from a natural population of C. variegata and their progeny (n=127) were sampled. A very high outcrossing rate (98%) was estimated for the population based on data from seven microsatellite loci. This suggested regular pollen-mediated gene flow into the population, further supported by the observed high levels of genetic diversity and polymorphism. Significant positive spatial structure was found between parent trees occurring up to 150 m apart in the natural forest, although genetic distance between these individuals suggested limited relatedness (i.e. less than half-sib relatedness). The effect of pollen-mediated gene flow appears, therefore, to swamp any effect of nearest neighbour inbreeding which has been reported in other studies of eucalypt populations and has been attributed to limited seed dispersal. Resistance to the fungal disease Sporothrix pitereka (Ramularia Shoot Blight) was measured on progeny from each of the population study trees. Substantial resistance variability was found, along with a high estimate in heritability of resistance (0.44 plus or minus 0.06), indicating significant additive genetic variation within the population. Spatial analysis showed no significant spatial structure with resistant and susceptible genotypes apparently distributed randomly throughout the population. The lack of concordance between the molecular and quantitative markers suggests that there may be a cost to resistance. Temporal variation in the severity of disease outbreaks may have then led to differential selection of seedlings across many generations, maintaining variability in disease

resistance and facilitating the apparent random distribution of disease resistant and susceptible genotypes throughout the population. C. variegata is an important commercial forestry species. The identification of strong genetic control in the disease resistance trait, as well as significant adverse genetic and phenotypic correlations between susceptibility and growth traits, will aid future breeding programs. Controlled crosses between resistant genotypes from this population should result in strong genetic gains in both resistance and growth, with little costs associated with inbreeding depression due to the highly outcrossed nature of the population.
This book deals with central concepts in population genetics, describing the main evolutionary processes that influence the allele frequency distribution and change. The different chapters discuss topics such as population size and structure, migration, inbreeding and interbreeding, mechanisms of extinction and speciation, along with different data techniques and molecular methods used for detecting DNA sequence variation in the study of genetic polymorphisms. Part of the book includes statistical and computational methods commonly used to process population genetics data, which constitute an essential tool for understanding the concepts discussed. The book will be a useful reference for graduate students and researchers working on population genetics, and other related areas including microbiology, genetics, molecular biology, ecology, anthropology and others.
Biodiversity-the genetic variety of life-is an exuberant product of the evolutionary past, a vast human-supportive resource (aesthetic, intellectual, and material) of the present, and a rich legacy to cherish and preserve for the future. Two urgent challenges, and opportunities, for 21st-century science are to gain deeper insights into the evolutionary processes that foster biotic diversity, and to translate that understanding into workable solutions for the regional and global crises that biodiversity currently faces. A grasp of evolutionary principles and processes is important in other societal arenas as well, such as education, medicine, sociology, and other applied fields including agriculture, pharmacology, and biotechnology. The ramifications of evolutionary thought also extend into learned realms traditionally reserved for philosophy and religion. The central goal of the In the Light of Evolution (ILE) series is to promote the evolutionary sciences through state-of-the-art colloquia-in the series of Arthur M. Sackler colloquia sponsored by the National Academy of Sciences-and their published proceedings. Each installment explores evolutionary perspectives on a particular biological topic that is scientifically intriguing but also has special relevance to contemporary societal issues or challenges. This tenth and final edition of the In the Light of Evolution series focuses on recent developments in phylogeographic research and their relevance to past accomplishments and future research directions.
Human Population Genetics and Genomics provides researchers/students with knowledge on population genetics and relevant statistical approaches to help them become more effective users of modern genetic, genomic and statistical tools. In-depth chapters offer thorough discussions of systems of mating, genetic drift, gene flow and subdivided populations, human population history, genotype and phenotype, detecting selection, units and targets of natural selection, adaptation to temporally and spatially variable environments, selection in age-structured populations, and genomics and society. As human genetics and genomics research often employs tools and approaches derived from population genetics, this book helps users understand the basic principles of these tools. In addition, studies often employ statistical approaches and analysis, so an understanding of basic statistical theory is also needed. Comprehensively explains the use of population genetics and genomics in medical applications and research Discusses the relevance of population genetics and genomics to major social issues, including race and the dangers of modern eugenics proposals Provides an overview of how population genetics and genomics helps us understand where we came from as a species and how we evolved into who we are now
Herbicide resistant invasive weeds provide a unique system in which to study the evolution of

adaptive traits. In most species, it can be difficult to determine which novel traits are adaptive as opposed to fixed due to drift and/or linkage. However, the adaptive trait, herbicide resistance, and the corresponding selective environments are extremely tractable. During the last decade, resistance to the herbicide glyphosate has evolved in weedy populations of Lolium sp (Poaceae) populations in agricultural systems of California, USA. Earlier work indicated that a non-synonymous mutation in the 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) gene is associated with the resistant phenotype within California. The research conducted for this dissertation assessed the processes facilitating the evolution of glyphosate resistance within California populations of Lolium sp and if selection for the adaptive trait is associated with sympatric population divergence. The ability of an organism to adapt to new selection pressures and evolve new traits is dependent on the presence of adaptive genetic variation within populations. Research described in this dissertation assessed whether of genetic variability resulting from hybridization and/or gene duplication contributed to the evolution of glyphosate-resistance in Lolium populations. In Chapter 1, I used neutral nuclear and chloroplast DNA to assess the evolutionary history of Lolium sp., and determine if populations were of hybrid origin. The analysis indicated that California glyphosate-resistant and susceptible plants were not hybrids, but were most closely related to the L. multiflorum group. In Chapter 3, I assessed if duplication of the EPSPS locus contributed to L. multiflorum's potential to evolve resistance to glyphosate. The analysis detected at least two EPSPS loci, one of which has glyphosate-resistant type alleles and one of which only has glyphosate-susceptible type alleles. These data support the hypothesis that new phenotypic functions can evolve from duplicated genes. It has been hypothesized that strong divergent selection can disrupt gene flow between populations and cause sympatric populations to diverge genetically. Since glyphosate treatment is an extremely strong selection agent, I studied if populations under varying intensities of glyphosate treatment had diverged at neutral Simple Sequence Repeat (SSR) loci. As described in Chapter 2, patterns of genetic differentiation and population substructure were not associated with glyphosate-response phenotypes and glyphosate-treatment environments. However, gene flow between individuals differed between glyphosate-response phenotypes. Over time, this variation in gene flow may lead to genetic differentiation. Polymorphism or variation in DNA sequence can affect individual phenotypes such as color of skin or eyes, susceptibility to diseases, and response to drugs, vaccines, chemicals, and pathogens. Especially, the interfaces between genetics, disease susceptibility, and pharmacogenomics have recently been the subject of intense research activity. This book is a self-contained collection of valuable scholarly papers related to genetic diversity and disease susceptibility, pharmacogenomics, ongoing advances in technology, and analytic methods in this field. The book contains nine chapters that cover the three main topics of genetic polymorphism, genetic diversity, and disease susceptibility and pharmacogenomics. Hence, this book is particularly useful to academics, scientists, physicians, pharmacists, practicing researchers, and postgraduate students whose work relates to genetic polymorphisms. Tsetse flies transmit trypanosome species that cause sleeping sickness in humans and nagana in livestock. In the absence of a vaccine against trypanosome parasites and given the high cost of treatment, vector control remains the most effective method for reducing the incidence of trypanosomiasis. In anticipation of area-wide control of G. pallidipes by using genetic methods, a thorough understanding of its breeding structure is required. Capture release-recapture data show that G. pallidipes has a high capacty for dispersal, but genetic data indicate surprisingly high differentiation among populations. Studying local patterns of genetic variation and examining how such variation changes temporarlly can provide insight into the apparent contraditction between ecological and genetic data. The overall objective of my research was to determine microgeographic (200 m - [plus or minus] 10 km) genetic structure of G. pallidipes and compare with population structure at the macrogeographic (tens

to hundreds of kilometers) scale. In addition, I wanted to assess temporal changes in gene diversity and differentiation. Microsatellite DNA loci were characterized and used to study genetic variation within and among natural G. pallidipes populations. The loci were highly polymorphic (mean number of alleles = 20.5 ± 10.1) and unlinked hence useful for population studies. Mating was random within but not among populations at the macrogeographic scale (F[subfield ST] = 0.18). Differentiation among microgeographic populations was minimal (F[subfield ST] = 0.17) indicating a high rate of gene flow at microgeographic scale. Allele frequencies were homogeneous among sampling sites. Analysis of molecular variance (AMOVA) showed that most of the variation (>90%) lay within sites while only 2% of the total variance was attributed to variation among blocks. Allele frequencies were homogenous between seasons. Genetic differentiation was higher in the dry season than in the wet season. However, differentiation between pooled wet and pooled dry season samples did not differ significantly from zero (F[subscript ST] = 0.008, G[subscript ST] = 0.004). AMOVA showed that less than 2% of the variance could be attributed to difference between temporal samples. It is concluded that tsetse populations show little temporal variation probably due to drift. These results provide a better understanding of levels of genetic subdivision and gene flow at the local scale.

This book focuses on the use of molecular tools to study small populations of rare and endangered mammals, and presents case studies that apply an evolutionary framework to address innovative questions in the emerging field of mammalian conservation genomics using a highly diverse set of novel molecular tools. Novel and more precise molecular technologies now allow experts in the field of mammology to interpret data in a more contextual and empirical fashion and to better describe the evolutionary and ecological processes that are responsible for the patterns they observe. The book also demonstrates how recent advances in genetic/genomic technologies have been applied to assess the impact of environmental/anthropogenic changes on the health of small populations of mammals. It examines a range of issues in the field of mammalian conservation genomics, such as the role that the genetic diversity of the immune system plays in disease protection and local adaptation; the use of noninvasive techniques and genomic banks as a resource for monitoring and restoring populations; the structuring of population by physical barriers; and genetic diversity. Further, by integrating research from a variety of areas – including population genetics, molecular ecology, systematics, and evolutionary and conservation biology – it enables readers to gain a deeper understanding of the conservation biology of mammals that are at increasing risk of extinction at local, regional and global scales. As such, it offers a unique resource for a broad readership interested in the conservation biology of mammals and conservation management strategies to better preserve biodiversity.

As the population of older Americans grows, it is becoming more racially and ethnically diverse. Differences in health by racial and ethnic status could be increasingly consequential for health policy and programs. Such differences are are not simply a matter of education or ability to pay for health care. For instance, Asian Americans and Hispanics appear to be in better health, on a number of indicators, than White Americans, despite, on average, lower socioeconomic status. The reasons are complex, including possible roles for such factors as selective migration, risk behaviors, exposure to various stressors, patient attitudes, and geographic variation in health care. This volume, produced by a multidisciplinary panel, considers such possible explanations for racial and ethnic health differentials within an integrated framework. It provides a concise summary of available research and lays out a research agenda to address the many uncertainties in current knowledge. It recommends, for instance, looking at health differentials across the life course and deciphering the links between factors presumably producing differentials and biopsychosocial mechanisms that lead to impaired health.

Most species inhabit environments that are spatially heterogeneous at some scale. If dispersal is low enough relative to spatial variations in the effect of natural selection, then local adaptations may emerge. On the other hand, if dispersal is high enough to prevent isolation by distance, then gene flow among populations will influence both the amount of standing genetic variation maintained within populations and the architecture of this variation. Here, I explore various genetic consequences of evolution in heterogeneous environments. I begin by reviewing two empirical studies exploring how heterogeneous selection and gene flow affect the maintenance of variation within populations. The first of these is an observational study of patterns in natural populations of Pinus contorta (lodgepole pine; Chapter 2), while the second is a manipulative laboratory evolution experiment using Drosophila melanogaster (Chapter 3). I then discuss three theoretical studies on the evolution of locally adaptive trait divergence between populations under migration-selection balance. The first of these develops analytical approximations to predict the invasion probability and persistence time of beneficial mutations in finite populations (Chapter 4). The second of these studies explores the effect of migration-selection balance on the evolution of the genetic architecture underlying a quantitative trait (Chapter 5). The final theoretical study presents an exploration of the discrepancies between quantitative genetic models of mutation-selection balance and observations based on individual-based simulations (Chapter 6). Taken together, this research contributes to our understanding of how gene flow and heterogeneous selection influence the genetics of adaptation and the maintenance of genetic variation.

Zebra finches (Taeniopygia guttata) have been the subject of extensive neurological and behavioral research having served as the dominant model for vocal learning over half a century. Learned vocal communication, or vocal learning, is a trait that is shared by humans and songbirds but is rare or less well developed in other animals. Unlike innate communication, learned vocalizations are acquired early on by juveniles listening and copying what they hear from adults. Little, however, has been done to characterize the intraspecific variation in song behavior in the zebra finch model system. Other systems, such as the lab mouse, Mus musculus, have begun to take advantage of inbred and natural populations to assess genetic variation and to link genotype and behavior. The opportunity exists to do the same in the zebra finch. The first step to better able study song learning in a genetics context is to define trait variation within and among populations. The majority of research conducted on these birds relies on domesticated populations of Taeniopygia guttata castanotis (T. g. castanotis), but wild populations are also available for study, as is a second subspecies, T. g. guttata. With the sequencing of the zebra finch genome a decade ago, zebra finches have risen in importance in the field of population genomics so there is an opportunity to investigate the genetic variation in this system as well. I compared patterns genetic and song variation among these populations to examine how these features have diverged during the early stages of domestication as well as during divergence in allopatry. When comparing the wild and domesticated populations, I find that overall levels of genetic differentiation are low (FST = ~0.02); I also find evidence of selection acting on portions of the genome. Genetic drift also appears to have played a role in shaping patterns of genetic variation. While genetic drift has led to reduced diversity and a loss of rare alleles in domestic populations, it has also done so in the island subspecies, T. g.

guttata: I found further support for a dramatic bottleneck in the island subspecies as the two subspecies have diverged, as there is an overall reduction in diversity. Among the most highly diverged regions of the genome are two genes associated with color. I have identified fixed differences in two well-known pigmentation genes, SLC45A2 and CDKN2A that may contribute to plumage color differences between subspecies. In addition to genetic divergence, I also characterized divergence in song behavior among populations. I find that the island subspecies shows less variation in song among individuals than the mainland birds. Though the island subspecies, T. g. guttata, shows a reduction in variation in song among individuals possibly due to the bottleneck during speciation, the domestication process has actually led to increased variability in song structure in domesticated birds. It is possible that domesticated birds have been freed from the constraints on song structure imposed by mate choice and the need for accurate species recognition. Finally, in order to differentiate between genetic or cultural controls of this difference in variation, I cross-fostered both subspecies to the Bengalese finch, Lonchura striata domestica, to test for differences in song copying behavior. I cannot reject the null hypothesis that zebra finch subspecies copy tutor songs equally well, but it does appear that the high variability in song structure in T. g. castanotis remains following controlled tutoring. Overall, I have begun to characterize the intraspecific behavioral and genetic variation in zebra finches, which has the potential to further our ability to study gene-environment influences on behavior, particularly with regards to the genetic contributions to song copying ability.

Two Centuries of Darwin is the outgrowth of an Arthur M. Sackler Colloquium, sponsored by the National Academy of Sciences on January 16-17, 2009. In the chapters of this book, leading evolutionary biologists and science historians reflect on and commemorate the Darwinian Revolution. They canvass modern research approaches and current scientific thought on each of the three main categories of selection (natural, artificial, and sexual) that Darwin addressed during his career. Although Darwin's legacy is associated primarily with the illumination of natural selection in The Origin, he also contemplated and wrote extensively about what we now term artificial selection and sexual selection. In a concluding section of this book, several science historians comment on Darwin's seminal contributions. Two Centuries of Darwin is the third book of the In the Light of Evolution series. Each installment in the series explores evolutionary perspectives on a particular biological topic that is scientifically intriguing but also has special relevance to contemporary societal issues or challenges. The ILE series aims to interpret phenomena in various areas of biology through the lens of evolution and address some of the most intellectually engaging, as well as pragmatically important societal issues of our times.

The majority of diamondback terrapin (Malaclemys terrapin) genetics studies have focused on Atlantic Coast populations. In contrast, only a few studies have been published examining the genetic structure of Gulf Coast terrapin (Forstner

et al. 2000; Hart 2005; Hauswaldt & Glenn 2005; Coleman 2011). Particularly, information is lacking for populations along the northern Gulf Coast of Mexico within the subspecies ranges of the Texas (M. t. littoralis) and Mississippi (M. t. pileata) diamondback terrapin. Previous to this study, the only northern Gulf Coast populations to have been genetically assessed in published literature were in Nueces Bay, Texas, Cocodrie Bayou, Louisiana, and Mobile Bay, Alabama (Forstner et al. 2000; Hart 2005; Hauswaldt & Glenn 2005; Coleman 2011). To date, no genetic studies have been published on terrapin populations in Galveston Bay, Texas, which is located on the eastern end of the M. t. littoralis subspecies range. This study provides the first genetic information for terrapin populations in Galveston Bay and offers a comparison of genetic variation and diversity among other northern Gulf Coast populations utilizing polymorphic microsatellite DNA markers developed by King and Julian (2004). Reference DNA samples were acquired from previously sampled northern Gulf Coast populations in Nueces, TX, Louisiana, and Alabama, and were compared with Galveston Bay terrapin. Results found in previous studies (Hart 2005; Coleman 2011) were also compared with the results of the reference samples collected in this study, as well as with the genetic diversity found for Galveston Bay. Analyses of molecular variance (AMOVA) were performed to test for genetic differentiation among populations using Wright's F-statistics fixation and differentiation estimator indices. Observed heterozygosities were tested for agreement with Hardy-Weinberg Equilibrium to determine the likelihood of random mating within and among populations. Genetic diversity was assessed based on the number of different alleles observed within each population and compared with results of diversity using Shannon's Information Index. Twenty-one informative alleles on 8 different loci with frequencies of at least 5% were identified for characterizing individuals from northern Gulf Coast terrapin populations and pairs of populations. No significant genetic differentiation was found within Galveston Bay populations. However, with the exception of the Louisiana and Alabama populations, the northern Gulf Coast populations exhibited a significant degree of genetic differentiation among populations and demonstrated a direct, positive correlation with spatial distribution between each pair of populations. Based on the findings of this study, it was concluded that northern Gulf Coast terrapin populations (ranging the coast from Nueces Bay, TX east to Dauphin Island, AL) are distributed within 3 distinct genetic metapopulations, where Louisiana and Alabama terrapin are within a single metapopulation, and the two Texas terrapin populations (Nueces and Galveston) were each within a distinct metapopulation. Additionally, based on the populations sampled in this study, the minimal spatial distance segregating any neighboring pair of genetically distinct northern Gulf Coast metapopulations was found to be approximately 300 kilometers. No significant difference in genetic diversity was found among the northern Gulf Coast populations. The findings of this study emphasize the importance of how additional terrapin population genetics studies in non-sampled areas, in

combination with previously collected data, can alter and refine scientific understanding of how species genetic metapopulations interact.

This book presents a long-term study in genetic isolates of indigenous small ethnics of Dagestan, located in the North-East part of Caucasus in Russia. Dagestan is characterized by extreme cultural and linguistic differences in a small geographic area and contains 26 indigenous ethnic groups. According to archeological data these indigenous highland ethnics have been living in the same area for more than ten thousand years. Our long-term population-genetic study of Dagestan indigenous ethnic groups indicates their close relation to each other and suggests that they evolved from one common ancestral meta-population. Dagestan has an extremely high genetic diversity between ethnic populations and a low genetic diversity within them. Such genetic isolates are exceptional resources for the detection of susceptibility genes for complex diseases because of the reduction in genetic and clinical heterogeneity. The founder effect and gene drift in these primary isolates may have caused aggregation of specific haplotypes with limited numbers of pathogenic alleles and loci in some isolates relative to others. The book presents a study in four ethnically and demographically diverse genetic isolates with aggregation of schizophrenia that we ascertained within our Dagestan Genetic Heritage Research Project. The results obtained support the notion that mapping genes of any complex disease (e.g., schizophrenia) in demographically older genetic isolates may be more time and cost effective due to their high clinical and genetic homogeneity, in comparison with demographically younger isolates, especially with genetically heterogeneous outbred populations.

Analysis of Genetic Variation in Animals includes chapters revealing the magnitude of genetic variation existing in animal populations. The genetic diversity between and within populations displayed by molecular markers receive extensive interest due to the usefulness of this information in breeding and conservation programs. In this concept molecular markers give valuable information. The increasing availability of PCR-based molecular markers allows the detailed analyses and evaluation of genetic diversity in animals and also, the detection of genes influencing economically important traits. The purpose of the book is to provide a glimpse into the dynamic process of genetic variation in animals by presenting the thoughts of scientists who are engaged in the generation of new idea and techniques employed for the assessment of genetic diversity, often from very different perspectives. The book should prove useful to students, researchers, and experts in the area of conservation biology, genetic diversity, and molecular biology.

Asclepias meadii, or Mead's milkweed, was once a widespread tallgrass prairie species but is now a federally threatened species due to habitat destruction. In 2006, Missouri Department of Conservation began introducing new plants from Kansas and other Missouri populations into the Wah'kon-tah prairie system. The purposes of this study are: 1) to assess the genetic diversity of five Missouri

populations/prairies of A. meadii; 2) compare the genetic diversity of Asclepias meadii to three widespread congeners, Asclepias incarnata, A. tuberosa, and A. viridis; and 3) to assess the changes, if any, that have occurred in the clonal structure of A. meadii at Wah'kon-tah and Niawathe prairies using amplified fragment length polymorphisms (AFLP). This is a relatively quick technique that yields a large number of polymorphic fragments useful for population genetic studies. Unlike previous studies, there were no clones detected at any of the prairies. Rockhill Prairie showed the most AFLP diversity (Shannon's diversity; I=0.164), and South Fork had lowest (I=0.096). Proffit Mountain showed the highest unbiased He (0.094) and South Fork the lowest (0.066). Compared to other Asclepias species, A. meadii showed the least genetic diversity (I=0.127 and UHe=0.081) whereas A. tuberosa showed the most (I=0.256 and UHe=0.167). Both A. meadii and A. tuberose maintain more genetic variation, AMOVA, within populations (93% and 94%) than do A incarnata and A. viridis (88% and 87%). To maintain sexually viable populations, management should be aimed at maintaining or increasing genetically diverse populations.

Abstract : 'Northern Hardwoods,' are a characteristic composition of multiple tree species and a part of the rich and diverse northeastern forests. Hardwoods e.g. oaks (Quercus: Fagaceae and Sugar maple), serve as foundation species and offer ecological and economical gains to wildlife and humans. Most of the forest trees go through many biotic and abiotic stresses, for example climate change in their long life span. To overcome these threats and to adapt to changing conditions, tree species need to maintain variation especially in adaptive genes. Therefore, it is necessary to analyze genetic diversity within forest tree populations and take appropriate forest management practice decisions. Genetic tools, such as microsatellite markers developed using next generation DNA sequencing technologies, can be used to address these challenges. Here we report the development of nuclear microsatellite markers in one of the most important hardwood tree species, sugar maple (Acer saccharum Marsh.) (Chapter II). We also use genic microsatellite markers to study the introgression patterns of adaptive alleles in two interfertile red oak species, Quercus rubra and Quercus ellipsoidalis (Chapter III). Using the paired-end low coverage Illumina sequencing technology, we developed a set of seven nuclear microsatellite markers (nSSRs) in sugar maple (Acer saccharum Marsh.). Initially, we screened 96 markers in a panel of six unrelated individuals, out of which seven markers produced polymorphic PCR products. These markers were utilized to analyze genetic variation and gene flow in one sugar maple population in an urban setting consisting of 48 individuals. Additionally, 96 seeds from one open pollinated adult tree were used for the gene flow analysis. In addition to these seven markers, we also tested six previously published microsatellites. Paternity analyses displayed effective dispersal of pollen in the sugar maple population with 76% of gene flow from outside the stand. There was no fine-scale genetic structure observed in this population, which also suggested effective dispersal of both seeds and pollen. To

check the transferability of these markers to other Acer species, four individuals from each species of Acer rubrum L., Acer saccharinum L., Acer platanoides L., and Acer ginnala Maxim. were tested at these markers. All markers amplified PCR products in these four species. However, only two markers, AS47 and SM37, were locus-specific and polymorphic in one species (A. ginnala). These markers can serve as an important tool to study genetic variation patterns in sugar maple populations in the face of climate change. Quercus rubra L. and Q. ellipsoidalis E. J. Hill are two interfertile red oak species with different adaptations to drought. I have studied the introgression of adaptive microsatellite alleles at a CONSTANS-Like gene (COL) as a response to micro-environment between these two hybridizing species in two sympatric populations. My results indicated that divergent selection in contrasting environments resulted in high interspecific differentiation at COL. However, interspecific differentiation was lower in sympatric stands, where both species occur in similar environments. The introgression of allele 138 from Q. ellipsoidalis into Q. rubra was higher compared to introgression of allele 141 from Q. rubra into Q. ellipsoidalis in contrast to earlier studies in parapatric populations. My results suggest that the introgression of adaptive genes between two red oak species is strongly affected by environmental selection.

Essay from the year 2002 in the subject Biology - Genetics / Gene Technology, grade: 1.1 (A+), Oxford University (New College), 13 entries in the bibliography, language: English, abstract: In the mid-1980s one of the most important studies by Sibley and Ahlquist on our relationship to apes and monkeys found that our closest relatives are the chimpanzees and the bonobos. The study of genetic diversity within both human and chimpanzee populations has been of major interest as researchers have been and are still trying to find out about the differences in genetic diversity between the two otherwise so closely related species. The genetic diversity refers to the amount of genetic variation found in a population. It has been discovered that chimpanzees have a greater total genetic diversity than humans, but that there are exceptions such as in the major histocompatibility complex in which chimpanzees display a low genetic diversity. I am going to explore how the total genetic diversity is surveyed in and distributed among human and chimpanzee populations and I am going to compare their levels of total diversity. I am also going to explore whether different types of polymorphism reveal the same patterns of distribution within and among populations. Population genetics is the basis of evolutionary studies, and has been widely used in several researches. This recent field of science has important applications for the management of populations (natural and domesticated), as well as for evolutionary studies of the various factors that affect gene frequencies over time and spatial distribution.In this work, presented in three sections (Population and Quantitative Genetics, Genetic Diversity in Crop Management, Population Genetics for Conservation Studies), the reader will find cutting-edge information in carefully selected and revised works.This book is intended for all researchers, academics, and students who are interested in the intriguing area of population genetics.

Drawing on startling new evidence from the mapping of the genome, an explosive new account of the genetic basis of race and its role in the human story Fewer ideas have

been more toxic or harmful than the idea of the biological reality of race, and with it the idea that humans of different races are biologically different from one another. For this understandable reason, the idea has been banished from polite academic conversation. Arguing that race is more than just a social construct can get a scholar run out of town, or at least off campus, on a rail. Human evolution, the consensus view insists, ended in prehistory. Inconveniently, as Nicholas Wade argues in A Troublesome Inheritance, the consensus view cannot be right. And in fact, we know that populations have changed in the past few thousand years—to be lactose tolerant, for example, and to survive at high altitudes. Race is not a bright-line distinction; by definition it means that the more human populations are kept apart, the more they evolve their own distinct traits under the selective pressure known as Darwinian evolution. For many thousands of years, most human populations stayed where they were and grew distinct, not just in outward appearance but in deeper senses as well. Wade, the longtime journalist covering genetic advances for The New York Times, draws widely on the work of scientists who have made crucial breakthroughs in establishing the reality of recent human evolution. The most provocative claims in this book involve the genetic basis of human social habits. What we might call middle-class social traits—thrift, docility, nonviolence—have been slowly but surely inculcated genetically within agrarian societies, Wade argues. These “values” obviously had a strong cultural component, but Wade points to evidence that agrarian societies evolved away from hunter-gatherer societies in some crucial respects. Also controversial are his findings regarding the genetic basis of traits we associate with intelligence, such as literacy and numeracy, in certain ethnic populations, including the Chinese and Ashkenazi Jews. Wade believes deeply in the fundamental equality of all human peoples. He also believes that science is best served by pursuing the truth without fear, and if his mission to arrive at a coherent summa of what the new genetic science does and does not tell us about race and human history leads straight into a minefield, then so be it. This will not be the last word on the subject, but it will begin a powerful and overdue conversation.

Analyses of 43 blue spruce populations at age 12 (9 years in the field) revealed significant differences among populations for survival, height, vigor, crown diameter, frost injury, and foliage color. Use of regions increases the probability of locating better seeds sources, but high variability among individual populations within regions limits their value in specifying where better seed sources can be collected. Phenotypes should be selected in best stands within regions.

Studies of natural populations reveal that tremendous phenotypic variation in immune function exists within species. Selection on extant variation drives the short term evolution of the immune response, potentially resulting in the temporary maintenance of genetic variation in populations or in the fluctuation of allele frequencies. Immune response genes also frequently show evidence of elevated rates of adaptive evolution between species. I used two approaches to study how genetic variation within a population is related to long term evolutionary patterns. From an in-depth study of the pathogen recognition molecule Eater, I find evidence for a recent partial selective sweep in a single population of Drosophila melanogaster. The putatively selected allele has a significantly higher level of gene expression, suggesting that gene regulation rather than protein structure is the target of selection. In a broader study of over 200 immune genes using target enrichment and high-throughput sequencing, I find that

genes with the highest rates of adaptive evolution between species have low levels of variation within a population. This suggests that selective sweeps, which reduce variation, occur in rapidly evolving genes. Genes that recognize infection and transduce signal within the immune response have low levels of variation consistent with selective sweeps, supporting the idea that these two aspects of the immune system are subject to elevated pathogen pressures. Our ability to understand the selective pressures that shape the antibacterial immune response is limited by our lack of knowledge about the epidemiology of disease in natural populations. I have performed a survey of natural bacterial pathogens in wild populations of D. melanogaster in Ithaca, New York, with the aim of understanding the rates, distributions, and identities of bacterial infections in the wild. I find that 0.3% to 2% of wild flies are infected with a diverse array of opportunistic pathogens. The identification and subsequent characterization of natural pathogens will lead to a better understanding of the selective pressures that drive the evolution of the insect immune response. A complete understanding of the evolution of resistance to infection requires consideration of the short term evolutionary dynamics measured through population genetics and phenotypic study of individuals and their pathogens within populations.

Virus as Composition, Complexity, Quasispecies, Dynamics, and Biological Implications, Second Edition, explains the fundamental concepts surrounding viruses as complex populations during replication in infected hosts. Fundamental phenomena in virus behavior, such as adaptation to changing environments, capacity to produce disease, and the probability to be transmitted or respond to treatment all depend on virus population numbers. Concepts such as quasispecies dynamics, mutations rates, viral fitness, the effect of bottleneck events, population numbers in virus transmission and disease emergence, and new antiviral strategies are included. The book's main concepts are framed by recent observations on general virus diversity derived from metagenomic studies and current views on the origin and role of viruses in the evolution of the biosphere. Features current views on key steps in the origin of life and origins of viruses Includes examples relating ancestral features of viruses with their current adaptive capacity Explains complex phenomena in an organized and coherent fashion that is easy to comprehend and enjoyable to read Considers quasispecies as a framework to understand virus adaptability and disease processes

Coral reef declines have been recorded for all major tropical ocean basins since the 1980s, averaging approximately 30-50% reductions in reef cover globally. These losses are a result of numerous problems, including habitat destruction, pollution, overfishing, disease, and climate change. Greenhouse gas emissions and the associated increases in ocean temperature and carbon dioxide (CO_2) concentrations have been implicated in increased reports of coral bleaching, disease outbreaks, and ocean acidification (OA). For the hundreds of millions of people who depend on reefs for food or livelihoods, the thousands of communities that depend on reefs for wave protection, the people whose cultural practices are tied to reef resources, and the many economies that depend on reefs for fisheries or tourism, the health and maintenance of this major global ecosystem is crucial. A growing body of research on coral physiology, ecology, molecular biology, and responses to stress has revealed potential tools to increase coral resilience. Some of this knowledge is poised to provide practical interventions in the short-term, whereas other discoveries are poised to facilitate research that may

later open the doors to additional interventions. A Research Review of Interventions to Increase the Persistence and Resilience of Coral Reefs reviews the state of science on genetic, ecological, and environmental interventions meant to enhance the persistence and resilience of coral reefs. The complex nature of corals and their associated microbiome lends itself to a wide range of possible approaches. This first report provides a summary of currently available information on the range of interventions present in the scientific literature and provides a basis for the forthcoming final report.
This book is unique in covering a wide range of design and analysis issues in genetic studies of rare variants, taking advantage of collaboration of the editors with many experts in the field through large-scale international consortia including the UK10K Project, GO-T2D and T2D-GENES. Chapters provide details of state-of-the-art methodology for rare variant detection and calling, imputation and analysis in samples of unrelated individuals and families. The book also covers analytical issues associated with the study of rare variants, such as the impact of fine-scale population structure, and with combining information on rare variants across studies in a meta-analysis framework. Genetic association studies have in the last few years substantially enhanced our understanding of factors underlying traits of high medical importance, such as body mass index, lipid levels, blood pressure and many others. There is growing empirical evidence that low-frequency and rare variants play an important role in complex human phenotypes. This book covers multiple aspects of study design, analysis and interpretation for complex trait studies focusing on rare sequence variation. In many areas of genomic research, including complex trait association studies, technology is in danger of outstripping our capacity to analyse and interpret the vast amounts of data generated. The field of statistical genetics in the whole-genome sequencing era is still in its infancy, but powerful methods to analyse the aggregation of low-frequency and rare variants are now starting to emerge. The chapter Functional Annotation of Rare Genetic Variants is available open access under a Creative Commons Attribution 4.0 International License via link.springer.com.
Now updated for its second edition, Population Genetics is the classic, accessible introduction to the concepts of population genetics. Combining traditional conceptual approaches with classical hypotheses and debates, the book equips students to understand a wide array of empirical studies that are based on the first principles of population genetics. Featuring a highly accessible introduction to coalescent theory, as well as covering the major conceptual advances in population genetics of the last two decades, the second edition now also includes end of chapter problem sets and revised coverage of recombination in the coalescent model, metapopulation extinction and recolonization, and the fixation index.
This book assesses the scientific value and merit of research on human genetic differences--including a collection of DNA samples that represents the whole of human genetic diversity--and the ethical, organizational, and policy issues surrounding such research. Evaluating Human Genetic Diversity discusses the potential uses of such collection, such as providing insight into human evolution and origins and serving as a springboard for important medical research. It also addresses issues of confidentiality and individual privacy for participants in genetic diversity research studies.
Using Science to Improve the BLM Wild Horse and Burro Program: A Way Forward reviews the science that underpins the Bureau of Land Management's oversight of free-

ranging horses and burros on federal public lands in the western United States, concluding that constructive changes could be implemented. The Wild Horse and Burro Program has not used scientifically rigorous methods to estimate the population sizes of horses and burros, to model the effects of management actions on the animals, or to assess the availability and use of forage on rangelands. Evidence suggests that horse populations are growing by 15 to 20 percent each year, a level that is unsustainable for maintaining healthy horse populations as well as healthy ecosystems. Promising fertility-control methods are available to help limit this population growth, however. In addition, science-based methods exist for improving population estimates, predicting the effects of management practices in order to maintain genetically diverse, healthy populations, and estimating the productivity of rangelands. Greater transparency in how science-based methods are used to inform management decisions may help increase public confidence in the Wild Horse and Burro Program.

Introductory guide to human population genetics and microevolutionary theory Providing an introduction to mathematical population genetics, Human Population Genetics gives basic background on the mechanisms of human microevolution. This text combines mathematics, biology, and anthropology and is best suited for advanced undergraduate and graduate study. Thorough and accessible, Human Population Genetics presents concepts and methods of population genetics specific to human population study, utilizing uncomplicated mathematics like high school algebra and basic concepts of probability to explain theories central to the field. By describing changes in the frequency of genetic variants from one generation to the next, this book hones in on the mathematical basis of evolutionary theory. Human Population Genetics includes: Helpful formulae for learning ease Graphs and analogies that make basic points and relate the evolutionary process to mathematical ideas Glossary terms marked in boldface within the book the first time they appear In-text citations that act as reference points for further research Exemplary case studies Topics such as Hardy-Weinberg equilibrium, inbreeding, mutation, genetic drift, natural selection, and gene flow Human Population Genetics solidifies knowledge learned in introductory biological anthropology or biology courses and makes it applicable to genetic study. NOTE: errata for the first edition can be found at the author's website: http://employees.oneonta.edu/relethjh/HPG/errata.pdf

The Fourth Edition of Genetics of Populations is the most current, comprehensive, and accessible introduction to the field for advanced undergraduate and graduate students, and researchers in genetics, evolution, conservation, and related fields. In the past several years, interest in the application of population genetics principles to new molecular data has increased greatly, and Dr. Hedrick's new edition exemplifies his commitment to keeping pace with this dynamic area of study. Reorganized to allow students to focus more sharply on key material, the Fourth Edition integrates coverage of theoretical issues with a clear presentation of experimental population genetics and empirical data. Drawing examples from both recent and classic studies, and using a variety of organisms to illustrate the vast developments of population genetics, this text provides students and researchers with the most comprehensive resource in the field.