Genetic Variation Within Populations Study Guide Answers

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.

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.

Phytophthora ramorum NA1 is an invasive plant pathogen causing disease on more than 130 plant hosts. Since, its introduction to California in the mid 1990s, the pathogen has spread to forests causing Sudden Oak Death and Ramorum blight of ornamentals in the nursery trade. Current knowledge indicates that P. ramorum NA1 reproduces asexually and yet, recent genome studies has identified considerable genetic variation within the recently established population. Various isolates of P. ramorum NA1 have mutations that span many base pairs to nearly entire chromosomes which we refer to as Structural Variants (SVs). My research goals were as stated: 1) to identify the mechanism for which genetic variation arises and to understand how these polymorphisms contribute to future generations of the population, and 2) to study forest conditions that drive or are correlated with genetic variation in the population of P. ramorum NA1. To construct an experimental framework for studying the evolution of P. ramorum NA1, I reviewed the literature of fungi and oomycetes that had a similar history: 1) asexually reproducing, 2) invasive or emerging populations, and 3) cause infections on plant or animals. Because we do not know how new mutations arise in P. ramorum NA1 populations in natural landscapes, I reviewed the most well-known mechanisms that generate new polymorphisms and phenotypes in asexuals such as somatic mutations, Horizontal gene or chromosome transfer, cryptic sex, hybridization, heterokaryosis, and epigenetic processes. I then outlined the different methods to distinguish between these modes of evolution by using population structure and genomic signatures for each type of mechanism. In order to understand how the population of P. ramorum NA1 is responding to its new range, I examined various methods for detecting selection and adaptation focusing on genomic scans that identify correlations with environmental axes. Lastly, I discussed future questions to explore in asexual systems. After reviewing population genetic studies of asexual populations, I tested the most likely hypotheses explaining the genetic variation in P. ramorum NA1: 1) somatic mutations, 2) Horizontal Gene Transfer, and 3) cryptic sex. First, the genealogy of the population and history of the mutations needed to be compared to identify any

discordances suggesting recombination between individuals in the population. The population structure and phylogenies of Structural Variants did not show recombination between individuals supporting somatic mutations as the mechanism for novel genetic variation. Ancestral state reconstruction show that a subset of SVs persists longer in the population and the majority of SVs arise multiple times in the phylogeny known as genetic parallelism. An analysis of the location of SVs in the genome and GO enrichment analyses indicate that these mutations occur in genes related to pathogenicity, DNA replication and repair, response to stress, motility, and carbohydrate metabolism. Results therefore show that Structural Variants repeatedly evolve in the population and are implicated in the evolution of the pathogen's biology. In order to understand why Structural Variants are repeatedly evolving in the population, I studied the environmental conditions important to the life cycle of P. ramorum NA1 and their association with observed phenotypic and genotypic variation. I hypothesized that genetic parallelism was a signature of forest conditions driving new genotypic and phenotypic variation in the population. To study the correlation between genetic parallelism and environmental factors, we focused on the subpopulations in Sonoma Co. and Big Sur in Monterey Co. These demes do not experience migration, are geographically distinct, and, yet, have individuals that have parallel SVs. Isolates within these two demes were collected based on their phenotype in culture. The "non-wild type" (NWT) is the only easily scorable phenotype of P. ramorum NA1 and is associated with SVs. However, NWT was found to be most strongly correlated with the number of deletions, a type of SV, and not with parallel SVs. Therefore, the environmental conditions associated with NWT (similarity in annual temperature, minimum temperature during the coldest month, Spring precipitation, and the frequency of California bay laurel between demes) was slightly different than the parameters associated with parallel SVs (similarity in minimum temperature during the coldest month, total stem density of P. ramorum's main hosts, and solar radiation during the hottest month between Sonoma Co. and Monterey Co.). Though genetic parallelism is not associated with NWT phenotype, correlation with the distribution of hosts and climate variables suggest that P. ramorum NA1's evolution is driven by forest ecology.

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.

Analysis of Genetic Variation in Animals

Spatial Structure and Population Genetic Variation in a Eucalypt Species Complex

Assessing Rare Variation in Complex Traits

Short Term Evolution in the Immune Response of Drosophila Melanogaster
Using Science to Improve the BLM Wild Horse and Burro Program

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.

Mixture between populations is an evolutionary process that shapes genetic variation.

Intermixing between groups of distinct ancestries creates mosaics of chromosomal segments inherited from multiple ancestral populations. Studying populations of mixed ancestry (admixed populations) is of special interest in population genetics as it not only provides insights into the history of admixed groups but also affords an opportunity to reconstruct the history of the ancestral populations, some of whom may no longer exist in unmixed form. Furthermore, it improves our understanding of the impact of population migrations and helps us discover links between genetic and phenotypic variation in structured populations.

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.

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.

Population Genetics

Genetic Variation in Blue Spruce

Genetic variation patterns of Shorea contorta and Parashorea malaanonan (Dipterocarpaceae) in the Philippines

Understanding Racial and Ethnic Differences in Health in Late Life

Genetics of Populations

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.

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.
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.

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.

Volume X: Comparative Phylogeography

A Study of Genetic Variability in Larval and Adult Populations of Dungeness Crab (Cancer Magister)

The Ecological Genetics of Rarity

Human Population Genetics and Genomics

Human Population Genetics

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.

The rapid decline of the Philippine forests has resulted in highly fragmented tree populations. In response to this, plantation programs boomed during the 80s and early 90s of the last century. Plantation forests, however, were mostly established with reproductive materials from unknown sources with presumably restricted genetic diversity. In this study, genetic variation patterns at microsatellite (SSR) and AFLP markers were investigated and compared between planted and natural populations of the ecologically important and critically endangered tropical rainforest tree species: Shorea contorta and Parashorea malaanonan (Dipterocarpaceae). The study was important to conserve the remaining genetic diversity within populations of the investigated dipterocarps. Further, it provided useful data for better planning actions when it comes to reinforcement of existing species populations and re-introduction of the species. In addition, it gave information for a genetically sound seed collection efforts to support the continuous forest restoration programs in the country.

What are the genomic signatures of adaptations in DNA? How often does natural selection dictate changes to DNA? How does the ebb and flow in the abundance of individuals over time get marked onto chromosomes to record genetic history? Molecular population genetics seeks to answer such questions by explaining genetic variation and molecular evolution from micro-evolutionary principles. It provides a way to learn about how evolution works and how it shapes species by incorporating molecular details of DNA as the heritable material. It enables us to understand the logic of how mutations originate, change in abundance in populations, and become fixed as DNA sequence divergence between species. With the revolutionary advances in genomic data acquisition, understanding molecular population genetics is now a fundamental requirement for today's life scientists. These concepts apply in analysis of personal genomics, genome-wide association studies, landscape and conservation genetics, forensics, molecular anthropology, and selection scans. This book introduces, in an accessible way, the bare essentials of the theory and practice of molecular population genetics.

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.

A Study of Genetic Variation Found in the Segregating Populations Following Inter-varietal Crosses in American Upland Cotton

An Assessment of Genetic Variation Within Missouri's Populations of Asclepias Meadii Torr. Ex Grey (Apocynaceae) and a Comparison with Three Widespread Asclepias Species

A Study of Genetic Structure, Inbreeding and Seed Bank Dynamics in a Rare Annual Plant

Local Adaptation and Maintenance of Variation in Heterogeneous Environments

Genetic Variation

The Fourth Edition of Genetics of Populations is the most current, comprehensive, and accessible introduction to the field for advanced undergraduate 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 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 u a variety of organisms to illustrate the vast developments of population genetics, this text provides students and researchers with the most comprehens resource in the field.

Genetic Variation: A Laboratory Manualis the first compendium of protocols specifically geared towards genetic variation studies, and includes thoroug discussions on their applications for human and model organism studies. Intended for graduate students and professional scientists in clinical and rese settings, it covers the complete spectrum of genetic variation—from SNPs and microsatellites to more complex DNA alterations, including copy numbe

variation. Written and edited by leading scientists in the field, the early sections of the manual are devoted to study design and generating genotype da the use of resources such as HapMap and dbSNP, as well as experimental, statistical, and bioinformatic approaches for analyzing the data. The final sections include descriptions of genetic variation in model organisms and discussions of recent insights into human genetic ancestry, forensics, and hu variation.

Spatial and temporal genetic variation was assessed using mitochondrial DNA from adult and megalopae of Dungeness crabs, Cancer magister, from Fraser Delta in British Columbia, Washington, Oregon, and California. Megalopae were continuously sampled using light traps in one location, Coos Ba Oregon, and compared with adults sampled across the species' range. While small-scale spatial and temporal variation were evident, there was no significant fit to the Isolation-by-Distance model when considering adult and larvae populations sampled over a coastal length of ~1700 km (Mantel r = 0.059, p = 0.289). Smaller bays showed higher genetic diversity than larger bays, contrary to typical expectations. MtDNA diversity measures (assesse canonical correlation analysis) were correlated with bay size and depth, suggesting that hydrological patterns or fishing harvests in local areas (or a combination of both) influenced the observed genetic signature. The Dungeness crab ancestral population likely went through a historic population expansion associated with recent glacial relaxation, as evidenced by mismatch distributions and predominance of singleton haplotypes. In larval sampl we commonly observed numerous individuals of a haplotype, which suggests that families of larvae remain aggregated during dispersal. Sampled offsp revealed a low fraction of the adult gene pool (in accordance with the Hedgecock effect), yet high variability in recruitment over time. A realized long distance dispersal of larvae and the additive effects of recruitment from different sources over time may have prevented significant genetic differentiatio within the C. magister range.

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 ar gain deeper insights into the evolutionary processes that foster biotic diversity, and to translate that understanding into workable solutions for the regio and global crises that biodiversity currently faces. A grasp of evolutionary principles and processes is important in other societal arenas as well, such a 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 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 serie focuses on recent developments in phylogeographic research and their relevance to past accomplishments and future research directions.

Genetic Variation Within and Among Populations of Draba Burkel Sp. Nov. (Brassicaceae) in Northern Utah: a Conservation Genetics Study Using Enzyme Electrophoresis

Mechanisms of Evolution

Design and Analysis of Genetic Studies

A Comparative Assessment of Genetic Variation of Diamond Terrapin (Malaclemys Terrapin) in Galveston Bay, Texas in Relation to Other Northern Gu Coast Populations

A Test of Populations in Nebraska

This volume considers the genetic variability of human populations, particularly in the tropics: its

origins and maintenance, and its contribution to the phenotypic variability of complex characters. The first section deals with the ways of analysing genetic variation and provides a valuable review of relevant developments in molecular biology. The origin and maintenance of genetic diversity is considered in the second section with data presented for Pacific, African, Asian and Central American populations. The final section concerns characters in which the genetic contribution to variability is complex and shows how such characters may be used to elucidate biological problems of affinity and differentiation, of adaptation and survival. Published as part of the Decade of the Tropics research programme of the International Union of Biological Sciences, this volume will be of particular interest to human geneticists, physical and biological anthropologists.

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.

Though much widespread in distribution, the nematode worm Caenorhabditis elegans exhibits low levels of genetic variation at the DNA sequence level, a paradox which may be partly explained by its typical self-fertilization mode of reproduction. However recent work on the genetic structure of natural populations of C. elegans from France, Scotland and Portugal suggests a substantial level of outcrossing together with finding of a very strong local population structure. To find out whether this same occurrence extrapolates to other wild isolates of worm populations, the present study was carried on worm populations from California. Here, genetic variation is studied by detecting single nucleotide polymorphisms in a random genome-wide manner using Amplified Fragment Length Polymorphism analysis (AFLP). The worms used in this study are natural isolates of C. elegans collected from parks and gardens around the Los Angeles area in southern California. Some populations sampled were a few meters apart, enabling the assessment of variation and population structure on a very local scale. As previous studies, a low overall genetic diversity was found with these worm populations. The finding of a strong population structure and high linkage disequilibrium both within and between chromosomes was also concurrent with the findings from other wild isolates. All these findings elucidate the extra-ordinary evolutionary dynamics of these sets of worm from the wild.

Three of the four major mechanisms of evolution, natural selection, genetic drift, and gene flow are examined. There are 5 tenets of natural selection that influence individual organisms: Individuals within populations are variable, that variation is heritable, organisms differ in their ability to survive and reproduce, more individuals are produced in a generation than can survive, and survival & reproduction of those variable individuals are non-random. Organisms respond evolutionarily to changes in their environment and other selection pressures, including global climate change. The importance of spatial structure of a population in relation to how it affects the strength of gene flow and/or genetic drift, as well as the genetic variation and evolution of populations, is shown. Gene flow tends to reduce variation between populations and increase it within populations, whereas genetic drift tends to reduce genetic variation, especially in small, isolated populations. The mechanisms of evolution can lead to speciation, which requires both time and genetic isolation of populations, in addition to natural selection or genetic drift.

Discuss the distribution of genetic diversity found in human and chimpanzee populations

NEUTRAL AND ADAPTIVE GENETIC VARIATION IN NORTH AMERICAN HARDWOOD TREE SPECIES

Studies in Population Genetics

Calanoida) : a DNA Sequence Analysis of the Mitochondrial Cytochrome Oxidase I Gene

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.

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

Spatial patterns of genetic variation are shaped by a variety of population genetic processes, and can therefore be a rich source of information about population history. The work presented here focuses on two drivers of spatial variation: recent secondary contact after isolation, and responses to spatially varying selection. The first chapter describes expected genome-wide patterns of coancestry resulting from secondary contact between two differentiated populations, with the continuous movement of individuals by diffusive local migration. Using analytic

expressions derived for expected linkage disequilibrium (LD), an inference framework was developed to estimate the timing of secondary contact and gene flow. This was applied to genomic data from spatially distributed admixed human populations, providing an alternative to commonly used admixture models. The following chapters examine patterns of spatial variation that are influenced by selection. While continued gene flow acts to homogenize allele frequencies between different populations, differential selection across space can maintain consistent patterns of geographic variation. These patterns are historically well studied, especially in the context of local adaptation. Here, genome-wide patterns of geographic variation in D. simulans is described, in order to better understand the process of local adaptation in this species, and in Drosophlia in general. Chapter two compares and contrasts patterns of differentiation between pairs of northern and southern populations of D. simulans in Australia and North America, with a focus on patterns of convergence and parallelism. There is evidence for parallel differentiation between the two continents in regions of the genome associated with regulation of gene expression. Contrary to patterns observed in the closely related Drosophila melanogaster, the spatial distribution of genetic variation in D. simulans does not support temperate adaptation outside of the species ancestral range. The results of this study suggest that populations on the two continents may have experienced independent, and different, adaptive trajectories, and that there may be limited power to detect parallel differentiation from comparing pairs of populations. Following the results of chapter two, chapter three presents a more detailed examination of genetic variation in D. simulans collected along the North American east coast and Central America. By analyzing patterns of genetic variation in 8 North American and one Panamanian population, this study identifies genetic variants that are associated with environmental gradients along the sampled transect. This study finds some evidence for the potential role of gene regulation in local adaptation, and significant overlap with D. melanogaster of genes containing latitudinally associated alleles. This study also reveals geographically inconsistent patterns of genetic variation along the cline, highlighting the need for further sampling, both temporally and geographically, in order to obtain a better understanding of population dynamics and adaptation in this species. (Gene lists and Gene Ontology enrichments for chapter 3 are available online as Supplemental file 1 and Supplemental file 2).

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

Natural Genetic Variation in Arabidopsis Thaliana Photosynthesis

Effect of Strong Selection on Genetic Diversity and Population Structure of Lolium Sp. (Poaceae)

A Preliminary Study of Genetic Variation Within and Among Populations of Diaptomus Leptopus (Copepoda

A Research Agenda

Insights from Studies of Population Genetics and the Epidemiology of Bacterial Infection

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 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.

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.

Human Population GeneticsJohn Wiley & Sons

A Primer of Molecular Population Genetics

Geographic Patterns of Genomic Variation Shaped by Demography and Selection

A Laboratory Manual

Genetic Study of Population Mixture and Its Role in Human History

A Way Forward

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.

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.

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.

Genetic diversity is one of the measures of biodiversity and has consequences in biological variation. It is crucial to understand the evolutionary and adaptative processes in all living species. This book is an interdisciplinary and integrated work that will contribute to the knowledge of academics from different areas of biological sciences. This collection of scientific papers was chosen and analyzed to

offer readers a broad and integrated view of the importance of genetic diversity in the evolution and adaptation of living beings, as well as practical applications of the information needed to analyze this diversity in different organisms. This book was edited by geneticist researchers and provides academics with up-to-date and quality information on the subject.

A Genetic Comparison of Bog Vs. Forest Populations of Metrosideros Polymorpha (Myrtaceae) in Hawai'i

Genetic Variation and Population Structure in Wild Isolates of Caenorhabditis Elegans Collected from California

Evaluating Human Genetic Diversity

In the Light of Evolution

Genomic Architecture of Schizophrenia Across Diverse Genetic Isolates