Genetic Variation Within Populations Study Guide

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A Primer of Molecular Population Genetics Cuvillier Verlag

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.

Assessing Rare Variation in Complex Traits Momentum Press

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).

Mechanisms of Evolution Oxford University Press

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.

Genetic variation patterns of Shorea contorta and Parashorea malaanonan (Dipterocarpaceae) in the Philippines Oxford University Press, USA

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.

A Study of Genetic Variation in Natural Populations of Drosophila Melanogaster Springer

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.

Evaluating Human Genetic Diversity Springer

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.

Population Genetic Studies of the Tsetse Fly, Glossina Pallidipes (Diptera: Glossinidae) GRIN Verlag

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.

In the Light of Evolution National Academies Press

What can social science, and demography in particular, reasonably expect to learn from biological information? There is increasing pressure for multipurpose household surveys to collect biological data along with the more familiar interviewer-respondent information. Given that recent technical developments have made it more feasible to collect biological information in non-clinical settings, those who fund, design, and analyze survey data need to think through the rationale and potential consequences. This is a concern that transcends national boundaries. Cells and Surveys addresses issues such as which biologic/genetic data should be collected in order to be most useful to a range of social scientists and whether amassing biological data has unintended side effects. The book also takes a look at the various ethical and legal concerns that such data collection entails.

Adaptive Genetic Variation in the Wild Academic Press

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.

Behavioral and Genetic Divergence Among Wild and Domesticated Populations of the Zebra Finch (Taeniopygia Guttata) John Wiley & Sons

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.

A Companion to Anthropological Genetics John Wiley & Sons

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.

A Genetic Monitoring and Evaluation Program for Supplemented Populations of Salmon and Steelhead in the Snake River Basin Cambridge University Press

Studying genetic variation presents a dilemma. While the genetic variation of greatest interest is that causing variation in traits and disease risk in natural populations, natural populations have characteristics that make them challenging to study. In this work, I have assessed the use of cell culture methods as a solution to some of these challenges. In particular, I studied genetic variation in the budding yeast Saccharomyces cerevisiae that was generated by selection in the lab as a model for natural genetic variation. I have found that even simplistic selection programs in the laboratory, including the use of chemical mutagenesis to introduce genetic variation, can be used to rapidly generate genetic variation with the same characteristics as that observed in natural populations of budding yeast. I also explored the use of human-derived lymphoblastoid cell lines as source of genetic variation that eliminates some of the most challenging problems that arise from the use of humans as research subjects. In addition to the ethical limitations, there are also severe technical limitations to the study of human subjects, not least of which is the difficulty of direct experimentation to confirm hypotheses. I found that lymphoblastoid cell lines are a reliable experimental system in which phenotypic variation, at the cellular level, primarily represents differences between lines, a significant portion of which is due to additive genetic variation. Due to the growth of publicly available genotype data, these lines can be used to locate genetic variants with phenotypic effects by linkage-association mapping. In addition to the shared database resources, cell lines are amenable to distribution from central repositories, suggesting that cell culture could form the basis of a community resource for the study of human genetic variation. While cell culture methods have share weaknesses with traditional genetic model systems, the use of a variety of cell culture approaches, including microorganisms and human-derived cell lines, represents an important, complementary approach to the investigation of genetic variation both for basic, mechanistic questions and for understanding the genetic causes of diversity in human phenotypes.

Cell Culture Models of Genetic Variation Oxford University Press

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.

Genomic Architecture of Schizophrenia Across Diverse Genetic Isolates IntechOpen

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.

Insights Into Natural Selection and Recombination from Patterns of Genetic Variation National Academies Press

Explore the latest research in anthropological genetics and understand the genome’s role in cultural and social development A Companion to Anthropological Genetics illustrates the role of genetic analysis in advancing the modern study of human origins, populations, evolution, and diversity. Broad in scope, this essential reference work establishes and explores the relationship between genetic research and the

major questions of anthropological study. Through contributions by leading researchers, this collection explores molecular genetics and evolutionary mechanisms in the context of macro- and microevolution, paleontology, phylogeny, diet, and disease, with detailed explanations of quantitative methods, including coalescent and approximate Bayesian computation. With an emphasis on contextualizing new and developing genetic research within anthropological frameworks, this text offers critical perspective on the conditions of molecular evolution that accompany cultural and social transformation, while also addressing critical disciplinary questions, such as the ethical issues surrounding ancestry testing and community-based genetic research. Acts as an essential reference on the contributions of genetic science to the field of anthropology Features new work by leading researchers of the field Explores the evolution of immunity, including the genetics and epigenetics of pathogens, chronic illness, and disease resistance Provides in-depth examination of mutation and dietary adaptation, including AMY1, lactase persistence, and sensory polymorphisms Explains essential quantitative and phylogenetic methods for aligning genomic analysis with evolution and migration time scales Offering thorough coverage on leading questions and developing research, A Companion to Anthropological Genetics is a comprehensive resource for students and scholars.

Genomic and Ecological Basis of Parallel Evolution in the California Population of the Asexual Pathogen Phytophthora Ramorum NA1 National Academies Press

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.

Population Genetics of Ranid Frogs Springer Nature

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.

Short Term Evolution in the Immune Response of Drosophila Melanogaster Oxford University Press

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.

Human Population Genetics and Genomics John Wiley & Sons

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.

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

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.