

Analysis Of A Squirrel Gene Pool Answer Key

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The evolution of new phenotypes and species is a population genetic process that is governed by four fundamental forces: natural selection, drift, mutation, and gene flow. Ecological genetics is the reciprocal interaction between population genetic theory and empirical observations from nature and the laboratory. Here I present a study in which I synthesize ecological information with population genetic studies in order to better understand how and why organisms diversify at the genetic, phenotypic, and species level. Pine squirrels (Genus: *Tamiasciurus*) are an important study organism for investigating the early stages of adaptation and speciation in nature because they are comprised of only recently divergent lineages, form narrow hybrid zones, show sharp geographic variation in several phenotypic traits of ecological interest, such as fur coloration and cranial morphology associated with bite force, and are a model organism for behavioral and ecological research. Pine squirrels (also known as tree squirrels) are ubiquitous across coniferous forests of North America and are comprised of only two recognized species: the Douglas squirrel (*T. douglasii*) and the North American red squirrel (*T. hudsonicus*). In my first chapter, I show with molecular divergence analyses using multilocus genetic data that these two species split less than a half million years ago. I also use phylogenetic inference and isolation with migration models to resolve the biogeographic puzzle of red squirrels occurring on Vancouver Island despite the closest mainland regions being occupied by Douglas squirrels. A species tree analysis using 15 nuclear loci indicates that the origin of squirrels on the island was likely from *T. hudsonicus* populations that occurred in interior montane regions that apparently persisted south of continental ice during the LGM. Surprisingly, phylogenetic analysis with mtDNA shows that all island squirrels carry the mtDNA of the sister species *T. douglasii*. We found historical migration between *T. douglasii* and island *T. hudsonicus*, but no historical migration between *T. douglasii* and mainland *T. hudsonicus* using IM models. These findings show a complex colonization and migration history between both mainland species and the island population. In my second chapter, I examined hybrid zone dynamics between the two squirrel species along an environmental gradient in the North Cascade Mountains of southern British Columbia and northern Washington. I found that genetic and phenotypic variation had steeper clines than a neutral genetic marker, which suggests that divergent selection is overriding gene flow in maintaining distinction between these species. Furthermore, all phenotypic clines were centered in a forest ecotone, thereby implicating environmental factors as being responsible for the location of the species boundary. Furthermore, I detected hybridization occurring to at least the F2 generation, which supports the notion that hybrid inviability is not as strong as environmental forces in maintaining distinction between species at this hybrid zone. In my third chapter, I show differential patterns of clinal variation in several ecologically important traits within Douglas squirrels (*T. douglasii*) along a forest gradient in Oregon. Ventral fur color shows a relatively sharp clinal transition from deep orange in the coastal region to a whitish-yellow, which coincides with a gradient in tree canopy openness. In contrast, cranial morphology varies continuously and gradually and does not show any sharp transitions, which is surprising given the abrupt changes in size and hardness of their primary food source, the cones from which they extract seeds. Collectively, my dissertation research provides an integrative examination of the contemporary processes of selection and gene flow that have shaped phenotypic variation and the genetic structure of pine squirrels in western North America.

Each species—from the familiar gray squirrel of American backyards to the exotic and endangered woolly flying squirrel of Pakistan—is described in a detailed account that includes distinguishing characteristics, ecology, natural history, conservation status, and current threats to its existence. *Squirrels of the World* includes • stunning color photographs that document rare and unusual squirrels as well as common varieties • evolution, morphology, ecology, and conservation status • colorful range maps marking species distribution • images of the skull of each genus of squirrel • extensive references

Sciurus niger (Rodentia: Sciuridae) is a large tree squirrel which inhabits the southeastern portion of North America. Currently there are ten recognized subspecies which are distinguished based on differences in morphology and ecology. While molecular work has been undertaken for a few subspecies of *S. niger*, the patterns of genetic differentiation of the entire species have yet to be examined. This study attempts to characterize the genetic structure of *S. niger* in order to help determine the validity of current subspecies designations and offer insight into the post-glacial colonization patterns of the species. A 296 base pair fragment of the mitochondrial control region (dloop) was sequenced from 55 specimens of *S. n. vulpinus*, 13 samples of *S. n. niger*, and 13 samples of *S. n. rufiventer*. Fifteen previously reported haplotypes (Lance et al. 2003) representing *S. n. cinereus*, *S. n. rufiventer*, and *S. n. vulpinus* were incorporated into the analysis. Additionally, a data set of 89 sequences generated at the Van Den Bussche Laboratory of Molecular Systematics and Conservation Genetics were added to this data set. These sequences included representatives of the following 8 subspecies: *S. n. bachmani*, *S. n. cinereus*, *S. n. limitis*, *S. n. ludovicianus*, *S. n. niger*, *S. n. rufiventer*, *S. n. subauratus*, and *S. n. vulpinus*. The compiled data set of 258 individuals belonging to 8 subspecies yielded 125 unique haplotypes,

indicating extremely high levels of diversity in the control region. Several tree-based methods recovered two distinct shallow clades which do not correspond to geographic regions or subspecies. A parsimony-based minimum spanning network revealed two haplotype clusters which correspond to the two clades found in the tree-based methods. The haplotypes are closely linked in a starshaped phylogenetic network; several of the most frequent haplotypes were internal, while the majority were unique to single populations and presented distal positions in the network. Overall there was a lack of genetic structure amongst populations with most of the variance explained by within population genetic diversity. Despite poor branch support, the congruent recovery of the two *S. niger* clades via both clustering-based and optimality criterion-based methods supports the separation of haplotypes into two major haplogroups. These results indicate that the currently recognized subspecies based on alpha taxonomic characters are not concordant with the mitochondrial history of *S. niger*. Instead, my findings suggest that the control region haplotype distribution in fox squirrels may be the result of repeated and rapid habitat expansions/retractions during glacial events in the Pleistocene. The shallow divergence between haplotypes across wide geographic distances suggest that the patterns of morphological and ecological differentiation we observe within *S. niger* may have occurred much more recently than previously thought"--Abstract.

ENDOGENOUS RETROVIRAL SEQUENCES REGULATE TISSUE-SPECIFIC EXPRESSION OF A HUMAN SALIVARY AMYLASE GENE IN TRANSGENIC MICE.

A comprehensive and invaluable resource, *Methods for Ecological Research on Terrestrial Small Mammals* is a must-have for any ecologist working on small mammals.

specific for human amylase transcripts and expression of human growth hormone was determined by a radioimmunoassay. The intraspecific genetic variation and diversity within the Humboldt's flying squirrel (*Glaucomys oregonensis*) has not yet been characterized despite its elevation to full species in 2017. The San Bernardino flying squirrel (*G. o. californicus*) is thought to be the southernmost population of *G. oregonensis* and is restricted to the San Bernardino and San Jacinto Mountains in California, but recent surveys indicate they have been extirpated from the latter locality. In order to provide baseline genetic data across the geographic range of *G. oregonensis*, I had the following objectives: 1) investigate the intraspecific molecular variation in *G. oregonensis* with a focus on the subspecies distributed in California; 2) evaluate the genetic diversity within *G. o. californicus*; 3) estimate if gene flow is occurring between the rest of the species and *G. o. californicus*. Population genetic and phylogenetic analyses, incorporating nine microsatellite loci and the partial or entire mitochondrial cytochrome-b gene, were performed on a total of 147 samples (tissue, hair, and museum specimen) using the Illumina high-throughput sequencing (HTS) platform; thereby bioinformatically coding alleles based on read count. My results support previously published work describing a south to north colonization of the species after the Last Glacial Maximum and highlight the genetic distinctiveness of *G. o. californicus*. The ensuing data from this study contributes valuable information toward understanding the genetic diversity within *G. oregonensis*, provides material to inform future conservation decisions for *G. o. californicus*, and has novel implications for future HTS microsatellite genotyping.

In this volume of *Cell and Molecular Responses to Stress* articles provide up-to-date information on key areas of signal sensing (sensing of pain, heat, cold, light, infrared radiation), molecules involved in the intracellular transmission of these signals, metabolic responses to stress including changes in gene expression and production of specialized proteins that aid cell responses to factors including interrupted blood supply (ischemia), oxygen limitation (hypoxia/anoxia), freezing and dehydration, amino acid limitation, radiation and processing drugs. There are chapters which also provide insights into new technologies (such as cDNA arrays), analysis of metabolic control theory (a key method for analysing stress effects on cells), and examine how enzymes evolve in the face of stress.

Over half of the world's population now lives in urban areas. Few who live in cities understand that cities, too, are ecosystems, as beholden to the laws and principles of ecology as are natural ecosystems. *Understanding Urban Ecology: An Interdisciplinary Systems Approach* introduces students at the college undergraduate level, or those in advanced-standing college credit high school courses, to cities as ecosystems. For graduate students it provides an overview and rich literature base. Urban planners, educators, and decision makers can use this book to help in designing a more sustainable or "green" future. The authors use a systems approach to explore the complexity and interactions of different components of a city's ecology with an emphasis on the energy and materials required to maintain such concentrated centers of human activity and consumption. The book is written by seventeen specialized contributors and includes ten accompanying detailed field exercises to promote hands-on experience, observation, and quantification of urban ecosystem structure and function. The chapters describe one by one the different subsystems of the urban environment, their individual components and functions, and the interactions among them that create the social-ecological environments in which we live. The book's emphasis on social-ecological metabolism provides students with the knowledge and methods needed to evaluate proposed policies for urban sustainability in terms of ecosystem capacity, potential positive and negative feedbacks, the laws of thermo-dynamics, and socio-cultural perception and adaptability.

This title offers a fascinating look at the vocabulary of science and technology. Thoughtfully chosen by the editors of the American Heritage® Dictionaries, these words will stimulate inquisitive minds to explore new terrain and challenge long-standing science buffs to measure up. Covering a wide variety of scientific fields—from evolution and ecology to physics and computer science—the words are representative of the vocabulary required to understand the most important concepts of science. Each term is defined and explained in clear, nonscientific language, with examples showing the reader the importance of the word both in its field and in daily life. Many entries have extra features explaining word origins or providing fun facts and enlightening details. Key illustrations make the abstract comprehensible. Subjects discussed include absolute zero, dendrochronology, game theory, histone, Kuiper belt, Munchausen syndrome, piezoelectric effect, rain shadow, time dilation, and xerophyte. A great graduation gift or reward for the expert in the house, *100 Science Words Every College Graduate Should Know* is sure to delight, surprise, and inspire everyone interested in the language of science and technology.

Genetic connectivity is a crucial element of self-sustaining wildlife populations. Anthropogenic barriers, such as interstate highways, can disrupt gene flow by preventing dispersal between groups of individuals. Another gene flow disruptor is isolation by distance (IBD): the principle that population differentiation increases as spatial distance increases, because individuals are more

likely to mate with individuals that are geographically proximate rather than distant. Investigating landscape genetics of wildlife populations is an important step towards understanding the landscape features and spatial scales that are relevant to maintaining connectivity. In Chapter 1, I explored the effects of interstate highways on genetic connectivity for six species of mammals in Indiana. These species included raccoon (*Procyon lotor*), Virginia opossum (*Didelphis virginiana*), fox squirrel (*Sciurus niger*), eastern gray squirrel (*S. carolinensis*), eastern chipmunk (*Tamias striatus*), and white-footed mouse (*Peromyscus leucopus*). These species represent a range of attributes, several of which affect dispersal ability across the interstate highway. Site characteristics, such as culverts and bridges, were included in the analysis. Population clustering was evaluated using Bayesian population assignment software and population genetic metrics. The results of the population genetic analyses indicated that five of the study species experienced a decrease in gene flow in relation to interstate highways. Smaller species exhibited population differentiation at more sites than the larger species; however, interstate highways were not a barrier to genetic connectivity for fox squirrels. My results are concordant with previous road ecology research; the barrier effects of high-traffic roads are variable, depending on the study species and potential crossing points. These findings may be carefully extrapolated to predict how species of concern may be impacted by high-traffic roads.

Ecosystems are the stage on which the play of evolution is acted, and ecosystems are complex, spatially structured and temporally varying. The purpose of this Research Topic is to explore critical challenges and opportunities for the transition from landscape genetics to landscape genomics. Landscape genetics has focused on the spatial analysis of small genetic datasets, typically comprised of less than 20 microsatellite markers, taken from clusters of individuals in putative populations or distributed individuals across landscapes. The recent emergence of large scale genomic datasets produced by next generation sequencing methods poses tremendous challenge and opportunity to the field. Perhaps the greatest is to produce, process, curate, archive and analyze spatially referenced genomic datasets in a way such that research is led by a priori hypotheses regarding how environmental heterogeneity and temporal dynamics interact to affect gene flow and selection. The papers in the Research Topic cover a broad range of topics under this area of focus, from reviews of the emergence of landscape genetics, to best practices in spatial analysis of genetic data. The compilation, like the emerging field itself, is eclectic and illustrates the scope of both the challenges and opportunities of this emerging field.

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Molecular Biology of the Hepatitis B Virus presents a comprehensive account of the various molecular aspects of the life cycle of the hepatitis B virus (HBV). Topics covered include the animal model systems, sequence data on the hepadnavirus genomes, the transcripts coded for the viral genome and sequence elements involved in regulating their expression, hepadnavirus replication, and analysis of the various HBV gene products and their role in virion synthesis and assembly. Other important features of the book include its discussions of the consequences of long term exposure to hepadnavirus infection and its association with hepatocellular carcinoma, the use of recombinant technologies in the generation of second generation vaccines, and the utilization of recombinant technologies to analyze an immune mediated disease. Researchers studying hepadnaviruses will find a wealth of information in this essential reference volume.

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Biodiversity Conservation and Habitat Management is a component of Encyclopedia of Natural Resources Policy and Management in the global Encyclopedia of Life Support Systems (EOLSS), which is an integrated compendium of twenty one Encyclopedias. Biodiversity is declining worldwide at a very unprecedented rate as a complex response to several human-induced changes in the global environment. The magnitude of these changes is so large and their effects are so strongly linked to the altered ecosystem processes and to human (ab-)use of natural resources that biodiversity loss is today perceived as one of the most important issues that humankind should face with extreme urgency. Disseminating information, raising awareness, and propelling concern within a diversified target audience (general public, schools, local authorities, and government agencies) are also essential to develop shared responsibility and to encourage collaborative efforts and compliance. This has been the main objective of "Biodiversity Conservation and Habitat Management". The Theme on Biodiversity Conservation and Habitat Management provides the essential aspects and a myriad of issues of great relevance to our world in eight major topics of discussion, and is focused on 1) History and Overview of Biodiversity Conservation and Protected Areas, 2) Management of Forests and other Wooded Habitats, 3) Management of

Savannahs and Other Open Habitats, 4) Management of Wetlands, 5) Management of Tourism and Human Recreation Pressure, 6) Conservation Strategies, Species Action Plans and Translocation, 7) Captive Breeding and Gene Banks, and 8) Eradication and Control of Invasive Species. These two volumes are aimed at the following five major target audiences: University and College students Educators, Professional practitioners, Research personnel and Policy analysts, managers, and decision makers and NGOs.

This book summarises the newest information on seasonal adaptation in animals. Topics include animal hibernation, daily torpor, thermoregulation, heat production, metabolic depression, biochemical adaptations, neurophysiology and energy balance. The contributors to this book present interdisciplinary research at multiple levels ranging from the molecular to the ecophysiological, as well as evolutionary approaches. The chapters of this book provide original data not published elsewhere, which makes it the most up-to-date, comprehensive source of information on these fields. The book's subchapters correspond to presentations given at the 14th International Hibernation Symposium in August 2012 in Austria. This is a very successful series of symposia (held every four years since 1959) that attracts leading researchers in the field. Like the past symposia, this meeting – and consequently the book – is aimed not only at hibernation but at covering the full range of animal adaptations to seasonal environments. For the next four years, this book will serve as the cutting-edge reference work for graduate students and scientists active in this field of physiology and ecology. .

"Alaskan Arctic ground squirrels, *Spermophilus paryii*, hibernate about seven months per year. During two-week torpor periods, respiration, circulation, metabolism, and catabolism are dramatically decreased, except for brief periods of interbout euthermia. These divergent hibernation states provide a particularly compelling model for variance-based studies of global gene expression. A guiding hypothesis in this Thesis is that Arctic ground squirrels exit interbout euthermia and enter torpor with an invariant metabolic scaffolding of various metabolites that are erected to serve as a ready metabolome for the challenges of the next brief return to euthermia. To develop this hypothesis further, I performed an exploratory data analysis of high-density mouse cDNA micro arrays cross-hybridized with Arctic ground squirrel mRNA to measure transcriptomes in brown adipose, skeletal muscle, and liver tissues. The results revealed that variation in transcript expression profiles were tissue specific and may reflect the degree to which tissues are active during hibernation. These results are encouraging. They justify a more thorough evaluation of the utility of using global variation in transcript expression patterns. In combination with a priori biological knowledge, these patterns will guide future studies into more detailed analyses of hibernation-state dependent and functionally relevant transcripts"--Leaf iii.

Papers from a symposium on the endangered Mt. Graham red squirrel, called in response to the building of an observatory on the mountain by the University of Arizona, offers a comprehensive picture of the ecological conditions and the impacts of natural and man-made changes on the squirrel and its mountain home.

Volume 47 in the internationally acclaimed *Advances in Clinical Chemistry* contains chapters submitted from leading experts from academia and clinical laboratory science. Authors are from a diverse field of clinical chemistry disciplines and diagnostics, ranging from basic biochemical exploration to cutting-edge microarray technology. Leading experts from academia and clinical laboratory science Volume emphasizes novel laboratory advances with application to clinical laboratory diagnostics and practical basic science studies Here is a manual for an environmental scientist who wishes to embrace genomics to answer environmental questions. The volume covers: gene expression profiling, whole genome and chromosome mutation detection, and methods to assay genome diversity and polymorphisms within a particular environment. This book provides a systematic framework for determining environmental impact and ensuring human health and the sustainability of natural populations.

Zoologists have categorized primates into a single order, and no one doubts today that they share a common ancestry. Humans and Old and New World non human primate species, from the lemurs of Madagascar to the African anthropoid apes, represent diverging branches of an evolutionary common trunk. Along with species-specific characters, all primates have retained a number of ancestral traits, relics of their common origin. The comparative study of these species-specific and ancestral traits makes it possible to reconstruct the evolutionary pathways of humans and nonhuman primates. The discovery of the human blood groups and, later, of the Major Histocompatibility Complex (MHC) had a seminal effect on the field of human genetics, providing the first sound examples of Mendelian polymorphisms. The use of blood group and MHC alleles as genetic markers in biological anthropology generated a conceptual revolution and persuaded researchers to begin to think in terms of populations and not only in terms of typology. The counterparts of these human red and white cell antigens were found and studied in nonhuman primates, and progress in this field is summarized in this book.

A series of international symposia on viral hepatitis and liver disease has been held triennially, and called the "Olympics" of this research field. Our book presents the results of the eighth of these "Olympiads" which for the first time, was held in Asia (May 1993, Tokyo). Due to the rapid progress in research on both basic and clinical aspects of viral hepatitis and liver disease, the state of the art in this field is continually being updated, and our book provides a broad and in-depth survey of current work. The major topics in our book include molecular biology of the five known hepatitis viruses (HAV, HBV, HCV, HDV, and HEV), clinical implications of genetic variants of HBV and HCV, interferon treatment of HCV-related liver disease, and worldwide epidemiology and control of viral hepatitis. New subjects not seen in previous books, such as genotypes of HCV, are also covered. Expanding knowledge about the heterogeneity of the HCV genome has revealed a great variety of genotypes as well as their association with host pathogenesis and their varying responsiveness to interferon therapy. The first promising results of efforts to develop a hepatitis C vaccine are also presented. Finally, compared with its predecessors, our book contains many more papers from Asian countries, where the prevalence of viral hepatitis and liver disease is the highest in the world.

A world of categories devoid of spirit waits for life to return. Saul Bellow, *Humboldt's Gift* The stock-in-trade of communicating hypotheses about the historical path of evolution is a graphical representation called a phylogenetic tree. In most such graphics, pairs of branches diverge from other branches, successively marching across abstract time toward the present. To each branch is tied a tag with a name, a binomial symbol that functions as does the name given to an individual human being. On phylogenetic trees the names symbolize species. What exactly do these names signify? What kind of information is communicated when we claim to have knowledge of the following types?

"*Tetonia mathewzi* was ancestral to *Pseudotetonia ambiguus*. " "The sample of fossils attributed to *Homo habilis* is too variable to contain only one species. " "Interbreeding populations of savanna baboons all belong to *Papio anubis*. " "*Hylobates lar* and *H. pileatus* interbreed in zones of geographic overlap. " While there is nearly universal agreement that the notion of the species is fundamental to our understanding of how evolution works, there is a very wide range of opinion on the conceptual content and meaning of such particular statements regarding species. This is because, oddly enough, evolutionary biologists are quite far from agreement on what a species is, how it attains this status, and what role it plays in evolution over the long term.

Mammalian hibernation is characterized by a deep reduction in basal metabolic rate and body temperature in order to maximize energy savings during times of low food availability and harsh environmental conditions. These physiological extremes are lethal to non-hibernators, yet because hibernators are broadly distributed among mammalian lineages, the genes that underlie the phenotype are hypothesized to be

common to all mammals, although differentially expressed. Because of their natural phenotypic plasticity, hibernators are excellent models for identifying natural solutions to improve the human medical outcomes of a number of conditions. Hence, my research has focused on elucidating the genes that underlie the phenotype of the model hibernator, the 13-lined ground squirrel. Specifically, differential gene expression was analyzed in two organs of the hibernator, the heart and brown adipose tissue (BAT). In the heart, differential protein expression among eight dynamic seasonal and physiological stages of the hibernator's year was defined via 2D-DiGE and tandem mass-spectrometry methodology, while in BAT, differential transcript expression among 10 different seasonal and physiological states of the hibernator's year was characterized via a digital transcriptome analysis. The results of these analyses reveal that both the heart and BAT undergo a seasonal reprogramming, with gene products involved in fatty acid catabolism and the stress response increasing during the winter period of hibernation. Additionally, in heart, cofilin-2 becomes dephosphorylated during the cold body temperature and metabolically-depressed state of torpor, and this may serve as a mechanism to preserve ATP while the heart continually functions during torpor. In BAT, many of the significant transcript changes during winter hibernation exhibited an unexpected pattern - apparently increasing despite low body temperature when transcription is suppressed during torpor and early arousal. Measurements of total, short poly(A) and long poly(A) RNA abundance in 13 candidate genes by RT-qPCR revealed three patterns of BAT RNA dynamics in hibernation. The results have led to the generation of a new hypothesis, which proposes that while most transcripts degrade during torpor, a subset involved in BAT function are stabilized via lengthened poly(A) tails, so that they are prioritized for rapid translation during the highly metabolically active period of arousal.

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