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# Analysis Of A Squirrel Gene Pool Answers

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Wildlife Abstracts

ScholarlyEditions

A world of catagones devmd  
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

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name, a binominal 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? "Tetonius mathewzi was ancestral to Pseudotetonius ambiguus. " "The sample of fossils attributed to Homo habzlis 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 speczes 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 biolo

gists 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. Ecology of Endangerment ScholarlyEditions 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

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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.

*The Last Refuge of the Mt. Graham Red Squirrel* Jones & Bartlett Learning  
Reflecting what a new

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generation of conservation biologists is doing and thinking, this vital and far ranging second edition explores where conservation biology is heading. It challenges many conventions of conservation biology by exposing certain weaknesses of widely accepted principles. Combining contributions from both the school and the new breed of conservation biologists, this insightful text focuses primarily on topics that are integral to the daily activities of conservation biologists. Several chapters address ecosystem restoration and biotic invasions as well as the mechanics of population viability analyses, which are now a routine facet of conservation efforts. A case history approach is implemented throughout the book, with the use of practical real-world examples. Furthermore, an in-depth look at quantitative analyses is

presented, allowing for models and mathematical analyses to pinpoint limitations in existing data and guide research toward those aspects of biology that are most likely to be critical to the dynamics of a species or an ecosystem.

Cross-Base Highway Project, New Roadway Construction Between I-5 at the Thorne Lane Interchange and WA-7 at 176th St. South EOLSS Publications

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

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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.

### **Viral Hepatitis and Liver Disease**

University of Arizona Press

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

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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. *The Least Cost Path From Landscape Genetics to Landscape Genomics* Springer Science & Business Media Phylogenetic and

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Population Genetic  
Analysis of the  
Humboldt's Flying  
Squirrel Using High-  
throughput Sequencing  
Data  
Biodiversity  
Conservation and  
Habitat Management -  
Volume II Springer  
Science & Business  
Media  
Issues in Genetic  
Medicine / 2011  
Edition is a  
ScholarlyEditions™  
eBook that delivers  
timely,  
authoritative, and  
comprehensive  
information about  
Genetic Medicine.  
The editors have  
built Issues in  
Genetic Medicine:  
2011 Edition on the  
vast information  
databases of  
ScholarlyNews.™ You  
can expect the

information about  
Genetic Medicine in  
this eBook to be  
deeper than what you  
can access anywhere  
else, as well as  
consistently  
reliable,  
authoritative,  
informed, and  
relevant. The content  
of Issues in Genetic  
Medicine: 2011  
Edition has been  
produced by the  
world's leading  
scientists,  
engineers, analysts,  
research  
institutions, and  
companies. All of the  
content is from peer-  
reviewed sources, and  
all of it is written,  
assembled, and edited  
by the editors at  
ScholarlyEditions™  
and available  
exclusively from us.  
You now have a source

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you can cite with authority, confidence, and credibility. More information is available at <http://www.ScholarlyEditions.com/>.

### **ISE The Living World**

Phylogenetic and Population Genetic Analysis of the Humboldt's Flying Squirrel Using High-throughput Sequencing Data 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



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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. Evolutionary Dynamics of Pine Squirrels (*Tamiasciurus*) in Western North America 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

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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

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squirrels on the island dynamics between the  
was likely from T. two squirrel species  
hudsonicus populations along an environmental  
that occurred in gradient in the North  
interior montane Cascade Mountains of  
regions that southern British  
apparently persisted Columbia and northern  
south of continental Washington. I found  
ice during the LGM. that genetic and  
Surprisingly, phenotypic variation  
phylogenetic analysis had steeper clines  
with mtDNA shows that than a neutral genetic  
all island squirrels marker, which suggests  
carry the mtDNA of the that divergent  
sister species T. selection is  
douglasii. We found overriding gene flow  
historical migration in maintaining  
between T. douglasii distinction between  
and island T. these species.  
hudsonicus, but no Furthermore, all  
historical migration phenotypic clines were  
between T. douglasii centered in a forest  
and mainland ecotone, thereby  
T.hudsonicus using IM implicating  
models. These findings environmental factors  
show a complex as being responsible  
colonization and for the location of  
migration history the species boundary.  
between both mainland Furthermore, I  
species and the island detected hybridization  
population. In my occurring to at least  
second chapter, I the F2 generation,  
examined hybrid zone which supports the

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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. Genetic Structure and Phylogeography of the Fox Squirrel, *Sciurus niger*, as Inferred from a Mitochondrial Gene "*Sciurus niger* (Rodentia: Sciuridae) is a large tree squirrel which inhabits the southeastern portion of North America. Currently there are ten recognized

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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

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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

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during glacial events in the Pleistocene. The shallow divergence between haplotypes across wide geographic distances suggest that the patterns of morphological and ecological differentiation the we observe within S. niger may have occurred much more recently than previously thought"--Abstract. Ground Squirrel Antipredator Behavior Time, Chance and Divergence ENDOGENOUS RETROVIRAL SEQUENCES REGULATE TISSUE-SPECIFIC EXPRESSION OF A HUMAN SALIVARY AMYLASE GENE IN TRANSGENIC MICE. specific for human amylase transcripts and expression of human growth hormone was determined by a radioimmunoassay. Cross-Base Highway Project, New Roadway Construction Between I-5 at the Thorne Lane Interchange and WA-7 at 176th St. South Environmental Impact Statement The Least Cost Path From Landscape Genetics to Landscape Genomics 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

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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)



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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.

**Research Grants Index**

Frontiers Media SA

"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

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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.

Habitat Modeling,  
Landscape Genetics,  
and Habitat  
Connectivity for the  
Mohave Ground Squirrel

to Guide Renewable  
Energy Development

John Wiley & Sons  
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

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processing drugs. There molecular data has are chapters which increased greatly, and also provide insights Dr. Hedrick's new into new technologies edition exemplifies (such as cDNA arrays), his commitment to analysis of metabolic keeping pace with this control theory (a key dynamic area of study. method for analysing Reorganized to allow stress effects on students to focus more cells), and examine sharply on key how enzymes evolve in material, the Fourth the face of stress. Edition integrates Nucleic acids. Part 2 coverage of Elsevier theoretical issues The Fourth Edition of with a clear Genetics of presentation of Populations is the experimental most current, population genetics comprehensive, and and empirical data. accessible Drawing examples from introduction to the both recent and field for advanced classic studies, and undergraduate and using a variety of graduate students, and organisms to researchers in illustrate the vast genetics, evolution, developments of conservation, and population genetics, related fields. In the this text provides past several years, students and interest in the researchers with the application of most comprehensive population genetics resource in the field. principles to new A Genetic

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Investigation of Six  
Mammal Species in

Indiana Springer  
Science & Business  
Media

"*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  
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*rufiventer*. Fifteen  
previously reported  
haplotypes (Lance et  
al. 2003) representing  
*S. n. cinereus*, *S. n.*  
*rufiventer*, and *S. n.*  
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following 8 subspecies: linked in a starshaped S. n. bachmani, S. n. phylogenetic network; cinereus, S. n. several of the most limitis, S. n. frequent haplotypes ludovicianus, S. n. were internal, while niger, S. n. the majority were rufiventer, S. n. unique to single subauratus, and S. n. populations and vulpinus. The compiled presented distal data set of 258 positions in the individuals belonging network. Overall there to 8 subspecies was a lack of genetic yielded 125 unique structure amongst haplotypes, indicating populations with most extremely high levels of the variance of diversity in the explained by within control region. population genetic Several tree-based diversity. Despite methods recovered two poor branch support, distinct shallow the congruent recovery clades which do not of the two S. niger correspond to clades via both geographic regions or clustering-based and subspecies. A optimality criterion- parsimony-based based methods supports minimum spanning the separation of network revealed two haplotypes into two haplotype clusters major haplogroups. which correspond to These results indicate the two clades found that the currently in the tree-based recognized subspecies methods. The based on alpha haplotypes are closely taxonomic characters

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are not concordant with to the exotic and the mitochondrial endangered woolly history of *S. niger*. flying squirrel of Pakistan—is described Instead, my findings suggest that the in a detailed account control region that includes haplotype distribution distinguishing characteristics, in fox squirrels may ecology, natural be the result of history, conservation repeated and rapid status, and current habitat threats to its expansions/retractions existence. Squirrels of during glacial events the World includes• in the Pleistocene. stunning color The shallow divergence photographs that between haplotypes document rare and across wide geographic unusual squirrels as distances suggest that well as common the patterns of varieties• evolution, morphological and morphology, ecology, ecological differentiation the we and conservation observe within *S.* status• colorful range *niger* may have maps marking species occurred much more distribution• images recently than of the skull of each previously genus of squirrel• thought"--Abstract. extensive references

*Environmental Genomics* *Proceedings of the*  
 JHU Press *International*  
 Each species—from the *Symposium on Viral*  
 familiar gray squirrel *Hepatitis and Liver*  
 of American backyards

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*Disease: Molecules  
Today, More Cures  
Tomorrow, Tokyo, May  
10-14, 1993 (1993  
ISVHLD) Springer  
Science & Business  
Media*

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

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ecological research. occurring on  
Pine squirrels (also Vancouver Island  
known as tree despite the closest  
squirrels) are mainland regions  
ubiquitous across being occupied by  
coniferous forests of Douglas squirrels. A  
North America and are species tree analysis  
comprised of only two using 15 nuclear loci  
recognized species: indicates that the  
the Douglas squirrel origin of squirrels  
(*T. douglasii*) and on the island was  
the North American likely from *T.*  
red squirrel (*T. hudsonicus*  
*hudsonicus*). In my populations that  
first chapter, I show occurred in interior  
with molecular montane regions that  
divergence analyses apparently persisted  
using multilocus south of continental  
genetic data that ice during the LGM.  
these two species Surprisingly,  
split less than a phylogenetic analysis  
half million years with mtDNA shows that  
ago. I also use all island squirrels  
phylogenetic carry the mtDNA of  
inference and the sister species *T.*  
isolation with *douglasii*. We found  
migration models to historical migration  
resolve the between *T. douglasii*  
biogeographic puzzle and island *T.*  
of red squirrels *hudsonicus*, but no



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historical migration flow in maintaining  
between *T. douglasii* distinction between  
and mainland these species.  
*T. hudsonicus* using IM Furthermore, all  
models. These phenotypic clines  
findings show a were centered in a  
complex colonization forest ecotone,  
and migration history thereby implicating  
between both mainland environmental factors  
species and the as being responsible  
island population. In for the location of  
my second chapter, I the species boundary.  
examined hybrid zone Furthermore, I  
dynamics between the detected  
two squirrel species hybridization  
along an occurring to at least  
environmental the F2 generation,  
gradient in the North which supports the  
Cascade Mountains of notion that hybrid  
southern British inviability is not as  
Columbia and northern strong as  
Washington. I found environmental forces  
that genetic and in maintaining  
phenotypic variation distinction between  
had steeper clines species at this  
than a neutral hybrid zone. In my  
genetic marker, which third chapter, I show  
suggests that differential patterns  
divergent selection of clinal variation  
is overriding gene in several

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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.

*Squirrels of the World*  
Frontiers Media SA

The study of proteomics provides researchers with a better understanding of disease and physiological processes in animals. Methods in Animal Proteomics will provide animal scientists and veterinarians currently researching these topics in domestic animals a firm foundation in the

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basics of proteomics methodology, while also reviewing important advances that will be of interest to established researchers in the field. Chapters will provide practical information on a range of topics including protein identification and separation, bioinformatics, and applications to disease and reproduction research. This text will be written by leading international proteomics experts and essential for researchers in the fields of animal biology and veterinary medicine.

**Species, Species Concepts and Primate Evolution** Springer Science & Business Media

A comprehensive and

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

**Ground Squirrel Antipredator Behavior**

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

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for determining environmental impact and ensuring human health and the sustainability of natural populations. Molecular Biology and Evolution of Blood Group and MHC Antigens in Primates

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

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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

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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.

**Environmental Impact Statement**

specific for human amylase transcripts and expression of human growth hormone was determined by a radioimmunomatrix assay.

*The Transcriptional Program of Ground Squirrel Hepatitis Virus*

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.