Analysis Of A Squirrel Gene Pool Answers

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

Sensing, Signaling and Cell Adaptation

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.

Genetic Structure and Phylogeography of the Fox Squirrel, Sciurus Niger, as Inferred from a Mitochondrial Gene

Springer Science & Business Media

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 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.

Time, Chance and Divergence

Frontiers Media SA

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.

ENDOGENOUS RETROVIRAL SEQUENCES REGULATE TISSUE-

SPECIFIC EXPRESSION OF A HUMAN SALIVARY AMYLASE GENE IN TRANSGENIC MICE. Scholarly Editions

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.

Final Project Report Springer Science & Business Media

"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 metabalome 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 tran scriptomes 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.

Methods in Animal Proteomics University of Arizona Press

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

Using Landscape Genetics to Assess Population Connectivity in a Habitat Generalist 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 you can cite with authority, confidence, and credibility. More information is available at http://www.ScholarlyEditions.com/.

Ground Squirrel Antipredator Behavior

Frontiers Media SA

A series of international symposia on viral hepatitis and liver disease has been held triannially, 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 Genetic In

vestigation of Six Mammal Species in Indiana Elsevier 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.

Issues in Genetic Medicine: 2011 Edition Springer Science & Business Media Understanding the nature of genetic variation in natural populations is an underlying theme of population genetics. In recent years population genetics has benefited from the incorporation of landscape and environmental data into pre-existing models of isolation by distance (IBD) to elucidate features influencing spatial genetic variation. Many of these landscape genetics studies have focused on populations separated by discrete barriers (e.g., mountain ridges) or species with specific habitat requirements (i.e., habitat specialists). One difficulty in using a landscape genetics approach for taxa with less stringent habitat requirements (i.e., generalists) is the lack of obvious barriers to gene flow and preference for specific habitats. My study attempts to fill this information gap to understand mechanisms underlying population subdivision in generalists, using the squirrel treefrog (Hyla squirella) and a system for classifying 'terrestrial ecological systems' (i.e. habitat types). I evaluate this dataset with microsatellite markers and a recently introduced method based on ensemble learning (Random Forest) to identify whether spatial distance, habitat types, or both have influenced genetic connectivity among 20 H. squirella populations. Next, I hierarchically subset the populations included in the analysis based on (1) genetic assignment tests and (2) Mantel correlograms to determine the relative role of spatial distance in shaping landscape genetic patterns. Assignment tests show evidence of two genetic clusters that separate populations in Florida's panhandle (Western cluster) from those in peninsular

Florida and southern Georgia (Eastern cluster). Mantel correlograms suggest a patch size of approximately 150 km. Landscape genetic analyses at all three spatial scales yielded improved model fit relative to isolation by distance when including habitat types. A hierarchical effect was identified whereby the importance of spatial distance (km) was the strongest predictor of patterns of genetic differentiation above the scale of the genetic patch. Below the genetic patch, spatial distance was still an explanatory variable but was only approximately 30% as relevant as mesic flatwoods or upland oak hammocks. Thus, it appears that habitat types largely influence patterns of population genetic connectivity at local scales but the signal of IBD becomes the dominant driver of regional connectivity. My results highlight some habitats as highly relevant to increased genetic connectivity at all spatial scales (e.g., upland oak hammocks) while others show no association (e.g., silviculture) or scale specific associations (e.g., pastures only at global scales). Given these results it appears that treating habitat as a binary metric (suitable/non-suitable) may be overly simplistic for generalist species in which gene flow probably occurs in a spectrum of habitat suitability. The overall pattern of spatial genetic and landscape genetic structure identified here provides insight into the evolutionary history and patterns of population connectivity for H. squirella and improves our understanding of the role of matrix composition for habitat generalists.

Molecular Biology and Evolution of Blood Group and MHC Antigens in Primates JHU Press

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 anthro poid apes, represent diverging branches of an evolutionary common trunk. Along with sp ecies-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 evolu tionary pathways of humans and nonhuman primates. The discovery of the human blood groups and, later, of the Major Histocom patibility Complex (MHC) had a seminal effect on the field of human genetics, providing the first sound examples of mendel ian polymorphisms. The use of blood group and MHC alleles as genetic markers in biological anthropology gen erated a conceptual revolution and persuaded researchers to begin to think in terms of populations and not only intems of typology. The counterparts of these human red and white cell antigens were found and studied in nunhuman primates, and progress in this field is summarized in this book.

Emerging Infectious Diseases ScholarlyEditions

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

The Least Cost Path From Landscape Genetics to Landscape Genomics Jones & Bartlett Learning 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.

Genetics of Populations EOLSS Publications "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 the we observe within S. niger may have occurred much more recently than previously thought"--Abstract.

Issues in Biochemistry and Biophysics Research: 2011 Edition 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-mad changes on the squirrel and its mountain home.

Environmental Impact Statement 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 goegraphic 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.

The Intersection of Life History Chracteristics and Anthropogenic Barriers

Refecting what a new 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 the are integral to the daily activities of conservation biologists. Several chapters address ecosystem restoration and biotic invasions as well as the 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. *Research Awards Index* A world of categones 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 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.