

Analysis of a Squirrel Gene Pool

Suppose that a squirrel population lives in a wooded region in your state and has a genetic diversity that has remained at about the same level since 1970. You have collected 20 mice from this squirrel colony and are at the beginning of the analysis. These animals are members of one and the same species that inhabit wooded areas throughout the state. The only difference is in the color of their fur. The mice are divided into two groups: the light-colored mice and the dark-colored mice. The light-colored mice are called "homozygous" and the dark-colored mice are called "heterozygous". The light-colored mice are called "homozygous" and the dark-colored mice are called "heterozygous".



Suppose that you have collected 20 mice from this squirrel colony and are at the beginning of the analysis.

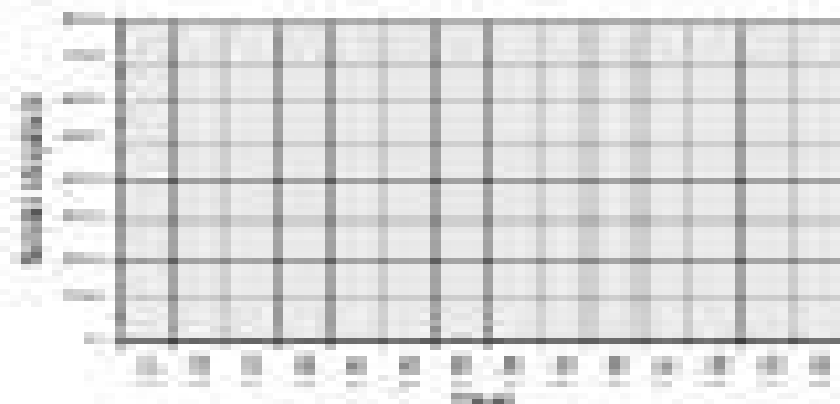
Year	Light	Dark	Total	Light	Dark	Total
1970	10	10	20	10	10	20
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Population Genetic Analysis of the Humboldt's Flying Squirrel Using High-throughput Sequencing Data Stella Chi Yuan,2020

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 **Evolutionary Dynamics of Pine Squirrels**

(*Tamiasciurus*) in Western North America Andreas Shintaro Chavez,2013 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.

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