

Analysis of a Squirrel Gene Pool

Suppose that, after a natural disaster, a small population of 20 squirrels is left on an island. Between 1970 and 1990, they produced at least another 1000 squirrels and at least 1000 more. These squirrels are genetically different from the original 20 squirrels. The genetic differences are caused by the fact that the squirrels are genetically different from the original 20 squirrels. The genetic differences are caused by the fact that the squirrels are genetically different from the original 20 squirrels.



Suppose that, after a natural disaster, a small population of 20 squirrels is left on an island.

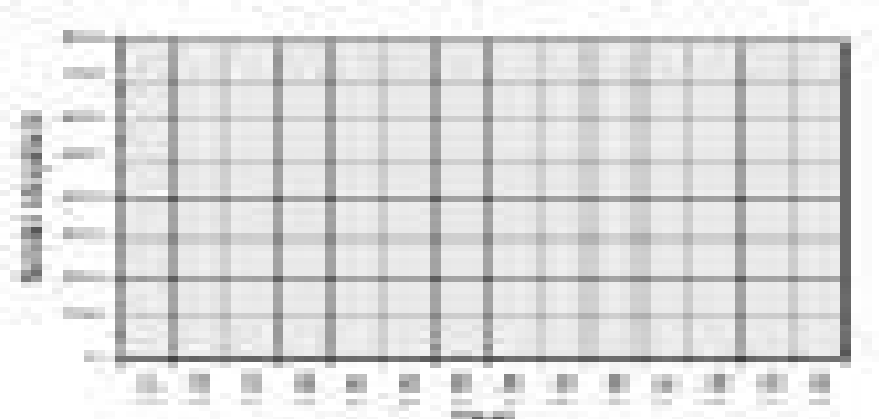
Year	Genotype	Phenotype	Frequency	Genotype	Phenotype	Frequency
1970	AA	Red	0.50	aa	Black	0.50
1975	AA	Red	0.40	aa	Black	0.60
1980	AA	Red	0.30	aa	Black	0.70
1985	AA	Red	0.20	aa	Black	0.80
1990	AA	Red	0.10	aa	Black	0.90
1995	AA	Red	0.05	aa	Black	0.95
2000	AA	Red	0.02	aa	Black	0.98
2005	AA	Red	0.01	aa	Black	0.99
2010	AA	Red	0.00	aa	Black	1.00

Genotype	Phenotype
AA	Red
Aa	Red
aA	Red
aa	Black

1. Suppose you wanted to know the frequency of the red allele in the squirrel population in 1970. How would you find it?

Suppose that there were 1000 squirrels in the population in 1970. How many red squirrels would there be?

Suppose that there were 1000 squirrels in the population in 1970. How many black squirrels would there be?



Analysis Of A Squirrel Gene Pool Answers

**United States. Superintendent of
Documents**



Analysis Of A Squirrel Gene Pool Answers:

The Journal of Wildlife Management ,1997

Monthly Catalogue, United States Public Documents ,1982

Monthly Catalog of United States Government Publications United States. Superintendent of Documents,1982 February issue includes Appendix entitled Directory of United States Government periodicals and subscription publications September issue includes List of depository libraries June and December issues include semiannual index Bibliography of Agriculture with Subject Index ,1988-10 **African Wildlife** ,1971 **Bibliography of Agriculture** ,1988-10 Phylogenetic and

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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