

Analysis of a Squirrel Gene Pool

Suppose that, after observing that a certain population of squirrels varied only slightly between 1975 and 1995, you decided to make careful studies between 1995 and 2000. In the meantime, there remains the possibility of gene flow which might obscure the subtle changes caused by natural selection. The data described are consistent for some factors which are being analyzed separately to determine whether or not the population is changing. The following are the observed results for the first factor which was analyzed, with results for other factors to be described in subsequent sections.



Approximate population sizes and approximate relative fitness values are given.

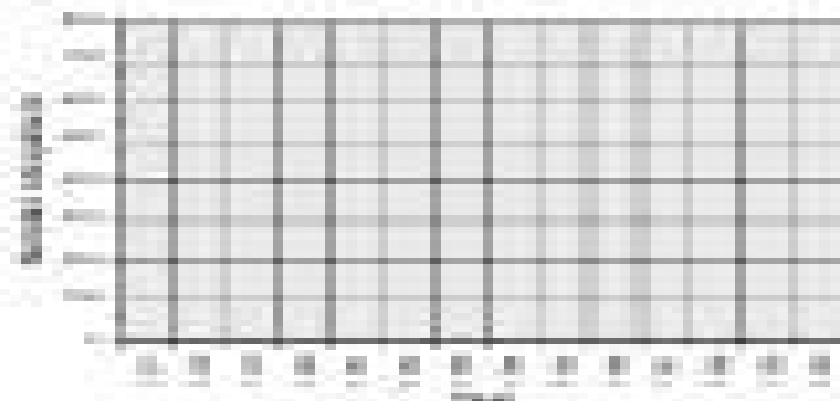
Year	Size	Mean	Genes	Size	Size	Size
1975	500	1.00	1000	50000	100000	100000
1976	510	1.01	1010	50500	101000	101000
1977	520	1.02	1020	51000	102000	102000
1978	530	1.03	1030	51500	103000	103000
1979	540	1.04	1040	52000	104000	104000
1980	550	1.05	1050	52500	105000	105000
1981	560	1.06	1060	53000	106000	106000
1982	570	1.07	1070	53500	107000	107000
1983	580	1.08	1080	54000	108000	108000
1984	590	1.09	1090	54500	109000	109000
1985	600	1.10	1100	55000	110000	110000
1986	610	1.11	1110	55500	111000	111000
1987	620	1.12	1120	56000	112000	112000
1988	630	1.13	1130	56500	113000	113000
1989	640	1.14	1140	57000	114000	114000
1990	650	1.15	1150	57500	115000	115000
1991	660	1.16	1160	58000	116000	116000
1992	670	1.17	1170	58500	117000	117000
1993	680	1.18	1180	59000	118000	118000
1994	690	1.19	1190	59500	119000	119000
1995	700	1.20	1200	60000	120000	120000

Year	Size	Size
1975	100000	100000
1976	101000	101000
1977	102000	102000
1978	103000	103000
1979	104000	104000
1980	105000	105000
1981	106000	106000
1982	107000	107000
1983	108000	108000
1984	109000	109000
1985	110000	110000
1986	111000	111000
1987	112000	112000
1988	113000	113000
1989	114000	114000
1990	115000	115000
1991	116000	116000
1992	117000	117000
1993	118000	118000
1994	119000	119000
1995	120000	120000

1. Select appropriate changes from the following to describe the changes in the gene pool through time (you may select more than one):

Steady state, directional selection, stabilizing selection, disruptive selection, genetic drift, founder effect, bottleneck.

Approximate the magnitude of change in the population size and the magnitude of change in the fitness of the population.



Analysis Of A Squirrel Gene Pool Answers

G Psacharopoulos



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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web google earth chrome ile tarayıcınızdan istediğiniz yere saniyeler içinde uçun ve yüzlerce 3d şehri keşfedin