October 19, 2010

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 09-AFC-9

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Eric Solorio Project Manager California Energy Commission 1516 Ninth Street Sacramento, CA 95814

RE: Mohave Ground Squirrel (MGS) Habitat Connectivity Study – Ridgecrest Solar 1, LLC AFC - Docket No. 09-AFC-9, BLM ROW #CACA-49016

Enclosed is the Draft Study Plan for the Mohave Ground Squirrel (MGS) Connectivity Study. This is just one task of the study's scope but includes the science and methodology behind the proposed study.

Your earliest attention to reviewing the document would be appreciated. We expect at least one more workshop to resolve questions and to finalize the study scope/work plan. Solar Millennium requests the agencies to approve a study whereby it can abide by the results. Comments in advance of another workshop would facilitate a more productive session and scope resolution.

If you have questions, please get in touch.

Sincerely,

Billy Owens Sr. Director, Project Development

Enclosure



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### APPLICATION FOR CERTIFICATION For the *Ridgecrest Solar Power Project*

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### Docket No. 09-AFC-9

### PROOF OF SERVICE (Revised 7/9/2010)

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### **DECLARATION OF SERVICE**

I, <u>Elizabeth Copley</u>, declare that on <u>October 19, 2010</u>, I served and filed copies of the attached <u>Ridgecrest Solar Power Project (Docket No. 09-AFC-9) Mohave Ground Squirrel (MGS) Draft Study Plan</u>. The original document, filed with the Docket Unit, is accompanied by a copy of the most recent Proof of Service list, located on the web page for this project at:

#### [http://www.energy.ca.gov/sitingcases/solar\_millennium\_ridgecrest].

The documents have been sent to both the other parties in this proceeding (as shown on the Proof of Service list) and to the Commission's Docket Unit, in the following manner:

#### (Check all that Apply)

#### For service to all other parties:

- X sent electronically to all email addresses on the Proof of Service list;
- by personal delivery;
- <u>X</u> by delivering on this date, for mailing with the United States Postal Service with first-class postage thereon fully prepaid, to the name and address of the person served, for mailing that same day in the ordinary course of business; that the envelope was sealed and placed for collection and mailing on that date to those addresses **NOT** marked "email preferred."

#### AND

#### For filing with the Energy Commission:

<u>X</u> sending an original paper copy and one electronic copy, mailed and emailed Respectively, to the address below (preferred method);

#### OR

\_\_\_\_\_ depositing in the mail an original and 12 paper copies, as follows:

#### **CALIFORNIA ENERGY COMMISSION**

Attn: Docket No. 09-AFC-9 1516 Ninth Street, MS-4 Sacramento, CA 95814-5512 docket@energy.state.ca.us

I declare under penalty of perjury that the foregoing is true and correct.

Ecopy

# Ridgecrest Solar Power Project Mohave Ground Squirrel Habitat Connectivity Study *Draft Study Plan* October 19, 2010

## **Study Objectives**

On behalf of Solar Millennium, LLC, AECOM, Dr. Philip Leitner, and Dr. Fraser Shilling propose to develop and implement a study of Mohave ground squirrel (MGS, *Xerospermophilus mohavensis*) habitat connectivity near Ridgecrest, CA.

- To understand the actual occupancy and environmental factors correlated with occupancy of Mohave ground squirrel (MGS) at and immediately surrounding the proposed Ridgecrest Solar Power Plant (RSPP) site.
- 2) To understand the potential connectivity needs of MGS in the region and movement requirements both within and among populations.
- 3) To estimate the impact of development of the Ridgecrest site on MGS movement and population connectivity

## **Study Background**

Solar Millennium proposes to construct a Solar Power Plant in Ridgecrest, California. Concerns about the effects of the proposed RSPP on MGS habitat connectivity have been raised and discussed during environmental review of the project. However, empirical data to evaluate the existing importance of the site for local and regional MGS movements, dispersal, and population connectivity do not currently exist. This study plan was developed to assess the current value of the site to MGS and MGS population connectivity.

The study plan proposes to conduct field sampling for MGS at the RSPP site and adjacent lands to compare MGS occupancy and connectivity in the region. Under the direction of Dr. Philip Leitner, MGS habitat occupancy and movement will be assessed by collecting and analyzing a combination of data describing MGS presence, distribution, movements, and genetic relationships. Live-trapping of MGS and collecting environmental variables at trapping locations can provide information on the distribution of MGS in the study region and environmental factors that may be associated with MGS occupancy. By the use of radio-telemetry, the studies will provide insight into landscape movement patterns of both adult and juvenile MGS within the study region. Genetic data collected from animals within the study region can be compared with existing genetic data from adjacent MGS populations to evaluate patterns of gene flow among these populations.

The study plan also proposes to implement analytical tools to analyze and model MGS movement opportunities and habitat connectivity. Dr. Fraser Shilling would serve as a scientific advisor on habitat connectivity modeling throughout the study. Two primary approaches will be used: 1) statistical predictions of movement across the landscape using movement data from field sampling and 2) spatially-explicit modeling of potential movement across the landscape and among populations using a combination of findings from the field studies, habitat suitability maps and landscape disturbance.

By integrating these data and approaches, it will be possible to assess the relative importance of the RSPP site for connectivity as compared to other areas within the study region.

### **Study Location**

The study region is shown in Figure 1. It includes an area of approximately 373 km<sup>2</sup> (144 mi<sup>2</sup>) lying to the south and southwest of the City of Ridgecrest. The region is defined so as to include the RSPP project site and adjoining areas that could provide connectivity between known MGS populations. It extends from the RSPP project site approximately 4 miles to the west, 7 miles to the east and 10 miles to the south into Fremont Valley. Figure 1 shows the distribution of BLM and private land ownership within the study region, as well as the location of lands characterized by steep terrain (>15% slope).

Six study areas located within the study region are indicated by letter designations (A-F) in Figure 1; the study areas are shown at a larger scale in Figures 2-4. The study areas are distinct landscape units with extensive areas of low to moderate topography (<15% slope) and alluvial soils that are likely to be occupied by MGS, and were therefore selected for field sampling of MGS. Table 1 indicates the size of each of the study areas. Field studies including live-trapping and radio-telemetry will be focused within these 6 study areas.

Table 1. Size of 6 study areas in acres and hectares		
Study Area	Acres	Hectares
А	5,979	2,420
В	7,403	2,996
С	5,988	2,423
D	5,730	2,319
E	14,130	5,718
F	9,013	3,648
Total	48,243	19,523

## **Study Site Selection**

Study sites for MGS trapping will be selected within each study area. Each of the study areas is overlaid with a sampling grid consisting of 1 x 1 km cells as illustrated in Figures 2-4. Those cells with >50% of their surface area consisting of BLM land that is <15% slope are considered suitable as field study sites. Such cells should have within their boundaries sufficient area that is public land accessible for study and that have a good likelihood of MGS occupancy. Each cell in a study area will be assigned a sequential number and the required set of study sites will be selected by use of a random numbers table. The number of study sites selected within each of the 6 study areas will be proportional to the number of suitable cells available. This approach will ensure that all study areas are sampled at the same level of intensity. Table 2 outlines the number of suitable 1 x 1 km cells available within each study area and shows the expected number of sites that would be sampled. In general, approximately 39% of the suitable cells will be selected within each study area, for a total of 60 study sites.

Table 2. Number of suitable 1x1 km cells in each of the 6 study areas and the number of study sites to be randomly selected within each study area			
Study Area	Suitable 1x1 km Cells	Study Sites to be Selected	
А	14	5	
В	26	10	
С	14	5	
D	22	9	
E	51	20	
F	28	11	
Total	155	60	

A trapping grid will be located within each of the randomly-selected study sites (1 x 1 km cells). Each trapping grid will consist of 20 traps in 2 lines of 10 traps. There will be 100 m spacing between the lines and 50 m spacing between traps in a line. Each trapping grid will cover 4.5 ha and if a 100 m boundary strip around the grid is assumed, the effective trapping area will be 19.5 ha. Radio-tracking studies indicate that MGS movements of 100 m are common during daily foraging activity, so that any individuals within the effective trapping area should be available for capture.

## **Field Sampling Methods**

All live-trapping, handling, and radio-collar procedures will follow the guidelines established by the American Society of Mammalogists (Gannon et al. 2007). All personnel capturing, handling, and marking MGS will be approved for these activities by the CDFG and will possess a valid Scientific Collecting Permit. All trapping would occur under the supervision of Dr. Leitner.

## Trapping

Live-trapping of MGS will be conducted to assess the occurrence and distribution of MGS in the study region. The trapping effort would attempt to determine if MGS, including resident adults, are present in the study areas.

MGS trapping will occur in three trapping periods, each of which is approximately 6 weeks in length. The first trapping period will be from about Feb. 1-Mar. 15, the second from Mar. 16-Apr. 30, and the third from May 1-June 15. These periods define 3 distinct phases in MGS spatial behavior: mating season when adult males undertake extensive daily movements in search of mates, then the period in which adult females are pregnant and lactating and movement of both sexes is limited, and finally the period in which juveniles are becoming more mobile, leading in some cases to long-distance (>1 km) dispersal. Trapping will be conducted for 4 consecutive days at each of the 60 study sites during each of the 3 trapping periods. The 60 study sites will be sampled in random order during each trapping period, thus avoiding temporal bias. The capture data will be analyzed separately for each trapping period.

Two types of traps will be used during this study. Pymatuning traps ( $10 \times 10.5 \times 39 \text{ cm}$ ) have wire mesh sides and back, while the tops, bottoms, and door are solid sheet metal. Sherman traps are smaller ( $8 \times 9 \times 31 \text{ cm}$ ), made entirely of sheet aluminum, and have perforated sides for ventilation. Traps will be baited with a commercial livestock feed that includes rolled oats, rolled barley, cracked corn, and molasses. Early in the field season, traps will be placed beside or under shrubs within 1-3 m of the trapping station markers. Later, when daytime temperatures are higher, traps will be placed under cardboard covers to shade them from direct sun. Shade temperatures will be monitored and traps

closed if temperatures exceed  $32^{\circ}$ C (~90°F). Traps will be opened in the morning between 0700 and 0900 hours. They will be checked for captures during the middle of the day and then checked and closed for the evening between 1600 and 1800 hours.

All captured MGS will be weighed, reproductive condition and age (adult/juvenile) will be determined, a PIT tag will be implanted for individual identification, and a 2 mm tissue sample will be taken from the ear for genetic analysis. All animals will be released at the point of capture and, if appropriate, captured animals will be equipped with radio-collars for radio-telemetry. Data obtained during daily trapping events will be recorded in a database each evening.

## **Environmental Data Collection**

Important environmental variables associated with each study site and trapping grid will be characterized by two distinct and complementary methods: 1) field collection of environmental variables known to be important in describing habitat suitability for MGS and 2) GIS measurement of distance from all roads, potential OHV activity, proximity to legacy and contemporary agriculture, local shrub cover and diversity (calculated from aerial photographs), and summed potential disturbance from multiple synergistic or individually-acting sources. Table 3 lists the types of environmental data that will be collected by field sampling methods at the study sites.

Table 3. Environmental properties that will be collected in the field for each study site(60 trapping grids)		
Perennial woody vegetation (shrub layer)	Total shrub cover estimate	
	Shrub cover estimate per species	
	Shrub species present	
	Total shrub density estimate	
	Shrub density estimate per species	
Herbaceous vegetation	Herbaceous species present	
	Herbaceous cover estimate (native vs. non-native species)	
	Herbaceous productivity (above-ground dry herbaceous standing crop	
Physiographic characteristics	Surface type – wash, terrace, alluvial slope, desert pavement	
	Slope and aspect	

Shrub vegetation will be sampled on each trapping grid by establishing a 2 meter-x -25 meter plot at each of 5 randomly chosen trap stations. At each plot, all individual shrubs will be identified to species and their dimensions recorded. This will allow calculation of density and cover by species and for all shrubs present.

Herbaceous vegetation will be sampled on each trapping grid by establishing two 0.5 meter-x-0.5 meter plots at each of 5 randomly chosen trap stations, one plot between shrubs and 1 plot under shrub canopy. In each plot, the herbaceous species present will be recorded and cover will be estimated for each species. Data will be reported separately for native and non-native species. All above-ground herbaceous material will then be harvested, air-dried, and weighed to obtain a measure of annual productivity. Herbaceous sampling will be carried out during April and May when maximum growth has been attained.

Data will be taken in the field on the physiographic properties associated with each trapping grid, including type of landform.

## **Radio-telemetry**

Radio-telemetry will be conducted in order to assess MGS movement patterns within each study area and the larger study region. By radio-tracking adult males during the breeding season, it will be possible to identify landscape characteristics important for local gene flow. Radio-tracking adult females will allow identification of natal burrows where juveniles can be captured and radio-collared. This task would attempt to identify potential MGS movement extent and direction and landscape characteristics supporting movement by tracking juveniles as they disperse to new habitats within the study region.

The exact model and manufacturer of the radio-collars will be determined following approval of the study plan. The total mass of each collar, including transmitter, battery, and attachment device, will be no greater than 5 grams so that the unit does not exceed ~5% of the animal's body mass. This will prevent adverse effects on the behavior and well-being of the subject. There are several other considerations in selecting a radio-collar. These include the type of antenna, the battery life, and the transmission range.

Adult males will be radio-collared during the spring mating season and located up to 3-4 times per day during this period to determine movement patterns during searches for mates. Males can cover as much as 1 km<sup>2</sup> during this period. Adult females will be radio-collared during the spring mating season and tracked up to 3-4 times per day through the period of pregnancy and lactation in order to document their movements and to assist in locating litters of juveniles for further study. Female home ranges are relatively stable in size during their active season, usually ranging from 0.5-2.0 hectares (Harris and Leitner 2004). Juvenile males and females will be radio-collared during late May and their movements will be followed to determine the frequency and direction of long-distance dispersal events. A substantial proportion of juveniles of both sexes can move from 1-8 km from their birthplace during their first summer (Harris and Leitner 2005). All radio-collared animals will be followed until they enter dormancy (June-August) and their final locations recorded. It will be assumed that animals have entered dormancy if there is no movement of the radio signal for 5 consecutive days during the typical immergence period. It can be difficult to differentiate mortality from normal dormancy, but every effort will be made to re-locate animals the following spring and remove radio-collars or install new radios as appropriate.

## **Collection of Incidental Data**

Incidental observations of desert tortoises (*Gopherus agassizii*) encountered during MGS field sampling will be documented. While no systematic surveys will be conducted for this species, every effort will be made to record all occurrences that are observed in the course of regular field studies. A standard data sheet will be used and information will be collected on date, time, and location (UTM coordinates) of the occurrence. When possible, data on sex, size, behavior, and health will also be recorded. Observers will carefully avoid disturbing or harassing desert tortoises while collecting relevant data. This information will be entered into a special database and made available to the responsible agencies, including California Department of Fish and Game, U.S. Fish and Wildlife Service, and Bureau of Land Management.

## **Genetic Tissue Sampling**

During live-trapping, tissue samples will be taken from the ear pinna of all captured MGS. The tissue samples will be taken with a disposable 2 mm biopsy punch and stored in labeled microvials in 95% ethanol. Microvials will be kept under refrigeration to enhance preservation until transferred to the laboratory at the University of Nevada Reno (UNR) for processing.

## Potential Data Analysis Methods for Phase 1

Proposed methods for data analysis will depend on the success of field sampling (i.e., no or few MGS captures versus greater than a few MGS captures). Because there is no empirical data for MGS in the study region and there exists a great amount of annual variation in the reproductive success of MGS, it may be that no MGS or very few MGS are captured and radio tracked during Phase 1. Therefore, the proposed methods described below are intended to evaluate the value of the study region to MGS habitat connectivity under scenarios in which: 1) greater than a few MGS individuals are captured and radio tracked or 2) no or very few MGS are captured and radio tracked. These scenarios function as "bookends" around the most likely range of possible data-collection scenarios. Under scenario #1, a greater emphasis would be placed on using raw field data collected from MGS captures and radio tracking to evaluate habitat connectivity in the study region using statistical modeling and landscape genetics approaches and a lesser emphasis would be placed on connectivity modeling based on simulated movement through the landscape. Under scenario #2, a greater emphasis would be placed on conducting habitat connectivity modeling using existing habitat suitability data for MGS throughout their range and habitat suitability parameters for the study region to evaluate habitat connectivity in the study region to evaluate habitat connectivity in the study region.

### Scenario 1: Greater than a few MGS individuals are captured and radio tracked

### Analysis of Trapping Data

MGS trapping data will be used to estimate percent occupancy and detectability in the various study areas of the study region. Models describing occupancy patterns will be developed and tested using appropriate statistical software packages. The appropriate statistical software will be determined following a review of available packages and may include PRESENCE (Hines, 2006). Environmental variables can be used as covariates in testing hypotheses regarding habitat suitability. The analysis would seek to correlate MGS occupancy patterns with collected environmental variables and compare MGS occupancy among study sites and study areas within the region.

### Analysis of Movement Data

Radio-telemetry data will be mapped using GIS software to indicate the extent and location of movements within the study region. These data will be used in combination with genetic information to describe the extent to which adult male movements and juvenile dispersal contribute to gene flow within and among MGS populations within the study region.

Occupancy and movement data will be used in predictive models for the regions for occupancy, movement, and genetic flow among populations. Occupancy for previously delineated areas will be initially determined using PRESENCE or a more robust statistical software. This model requires multiple sampling events at individual sites and large numbers of samples to estimate occupancy and to minimize variance. The model GENPRES will be used with data from other studies to design the sampling process.

Data from radio-collared adults and juveniles can also be used in movement models to understand the types of landscape attributes that may influence actual movement of animals. These data can be used in a variety of ways to simulate movement and to understand the importance of movement pathways. One approach is to use network theory to approximate or simulate movement among populations (nodes) across landscapes (connectors among nodes). Another approach would be to describe potential movements using landscape attributes that are known to be important for occupancy or movement, including potential barriers. This would be accomplished with a combined landscape condition/disturbance map and least-cost path approach in GIS. In both cases, the model would use remotely-sensed and field-collected data about environmental correlates to animal occupancy and movement. The disturbance data and model would include transportation infrastructure; residential, commercial, and industrial development; population density; electrical transmission corridors; and recreation areas and trails. These models are usually best built as custom models to answer questions defined by the project. Corridor modeling uses habitat suitability and disturbance information to

approximate how animals would move through a landscape, assuming enough is known about the species' behavior. There is a wide variety of corridor models available: 1) Least cost corridor uses a simulated object moving across a landscape, where each incremental step is toward a lower-cost or more suitable location; 2) Graph theoretic approaches which estimate the relative value of different potential connections among objects (such as population locations, or places on a landscape); 3) FunConn approximates movement of different organisms using information about the landscape and rules about organismal movement behavior.; and 4) Circuitscape uses electrical circuit theory and habitat/disturbance maps to predict where organismal movement and connections are more and less likely among places on a landscape.

#### Analysis of Genetic Data

### Laboratory Genetic Analysis

Whole genomic DNA will be extracted using QIAGEN DNeasy extraction kits (QIAGEN Inc., Valencia, CA, USA) and the standard animal tissue protocol. Seventeen microsatellite loci will be amplified with the following primer sets: GS14 and GS26 (Stevens et al. 1997); IGS 110b and IGS 6 (May et al. 1997); B109 and B126 (Garner et al. 2005); SmohB110, SmohC109, SmohC114, SmohC9, SmohB3, SmohC10, SmohD102, SmohD116, SmohA114, SmohB108, and SmohB118 (Bell and Matocq 2010). Individual reactions will be a multiplex of 3-4 loci that will be combined with a fluorescent size standard prior to running on an ABI 3100 (Applied Biosystems) in the Nevada Genomics Center at UNR. We will identify allele sizes using genemarker (Softgenetics). To confirm allele calls, duplicate genotypes will be generated for 20% of the individuals at each locus.

### Analysis of Genetic Relatedness

Hardy-Weinberg equilibrium will be tested locus by locus by using an extension of Fisher's exact test (1,000,000 step Markov Chain and 10,000 dememorization steps) as implemented in the ARLEQUIN software package (version 3.11; Excoffier et al. 2005). Linkage disequilibrium will be tested using a likelihood ratio test as implemented in ARLEQUIN by permuting alleles among individuals 10,000 times. In addition to reporting the average numbers of alleles per locus within each locality (uncorrected,  $A_u$ ) a rarefaction approach will be used as implemented in the ADZE software package (version 1.0; Szpiech et al. 2008) to take into account differing sample sizes (corrected,  $A_c$ ).

The possibility of recent reductions in effective population size will be investigated using the BOTTLENECK software package (version 1.2.02; Cornuet and Luikart 1997). When effective population size is reduced, allelic diversity will decline more rapidly than heterozygosity resulting in an excess of heterozygosity relative to that expected based on the number of observed alleles were the population at drift-mutation equilibrium. Deviation from drift-mutation equilibrium will be assessed under the Two-Phase Mutation Model (10,000 iterations; probability of single step mutations = 0.90) using a Wilcoxon sign-rank test.

To identify the number of genetic clusters represented in these data without imposing prior spatial information, a Bayesian assignment approach will be used as implemented in the program STRUCTURE ver. 2.2 (Pritchard et al. 2000; Falush et al. 2003). The most probable number of clusters will be identified based on the rate of change in log probability of the data over successive  $K(\Delta K)$  as suggested by Evanno et al. (2005).

The scale of genetic structuring in this system will be identified using spatial autocorrelation methods as implemented in GENALEX (Peakall and Smouse 2006). To further identify fine-scale spatial-genetic patterns the program SPAGEDI (Hardy and Vekemans 2002) will be used to calculate Queller and Goodnight's individual pairwise relatedness coefficient, r (Queller and Goodnight 1989) and will apply a reduced major axis regression to untransformed data in IBD (Bohonak 1999). Significant relationships will be tested using a Mantel test and 1000 randomizations.

Recent patterns and rates of genetic migration will be identified among local populations using the program BAYESASS (Wilson and Rannala 2003). This analysis is designed to identify migrants within the past 1-2 generations and thus will be comparable to field telemetry data in assessing fine scale dispersal. Analysis of Gene Flow across the LandscapePopulation genetic structure is generally used to depict population subdivision based on genetics studies. Ideally, no genetic structure should be detected in a single mendelian population because every individual is hypothesized to move freely without any physical, genetic, or social preference and to mate randomly (Hamilton, 2009, p.105). However, this does not hold true for actual populations because complex restrictions and preferences (e.g., the mating chance of two individuals often depends on their location. Hamilton, 2009, p.105).

Road-induced genetic divergence among populations or among segments of a population has been documented for many vertebrate species. This effect probably depends on road type and use. Gerlach & Musolf (2000) found that a recent highway (~25 years-old) contributed to a significant population subdivision of bank vole (*Clethrionomys glareolus*), while other road barriers including an old railway (~50 years-old) and a rural road (~25 years-old) did not. Despite many studies of road-crossing effectiveness by wildlife, individual animal crossing of roads may not be sufficient to guarantee the persistence of an entire population, because a species-specific minimum number of individual movement is required to assure gene flow (Corlatti et al., 2009). Developed urban and agricultural areas can also fragment populations. Even for a highly mobile bird, the golden-cheeked warbler (*Dendroica chrysoparia*), the isolation caused by agricultural lands clearly caused one population to diverge from other sampling populations (Lindsay et al., 2008). It is not known many migrants per generation must cross roads to counteract the effect of fragmentation or genetic drift. This issue has not been resolved for wild populations in a generally applicable way (Holderegger & DiGiulio, 2010).

To detect effects of roads, highways, and other development barriers on the genetic structure of vertebrate populations, it is necessary to collect enough samples from individuals of different geographical populations from appropriate landscape and taxonomic groups, and then choose suitable genetic markers for population structure analysis (Manel et al., 2003; Holderegger & Wagner, 2006). Based on the collected genetic data, a variety of genetic analyses and statistical analyses are performed to determine the spatial genetic pattern and its correlation with roads, highways, and other land-uses (see Manel et al., 2003 for more detailed information).

In this study, analysis of genetic information from field-collected samples will utilize microsatellite markers to document genetic diversity of populations, to explore regional gene flow patterns, and to estimate importance of different portions of the study region for connectivity. Between 15 and 30 samples (mixture of both males and females) from each population are typically needed to detect genetic effects (Karban and Huntzinger, 2006). The analysis of genetic marker patterns can provide information on potential MGS movement corridors within the study region.

Once genetic data are obtained, a variety of population genetic analysis and statistical analysis can be performed to determine spatial genetic pattern and its correlation with development and natural landscape characteristics. For analyzing spatial genetic pattern, as Manel et al., (2003) summarized, there are usually two sets of six approaches. The first set of approaches is to assess genetic differentiation ( $F_{st}$  values) among populations over large geographic area when geographical populations are known in advance. The other set of approaches is to assess spatial genetic patterns at an individual level without defining geographical populations in advance. Among the latter set, the Bayesian assignment, which is implemented in STRUCTURE software version 2.3.3 (http://pritch.bsd.uchicago.edu/structure.html; Pritchard et al., 2000; Falush et al., 2003; Falush et al., 2007), is widely used to test the effect of roads and highways on genetic structure.

### Scenario 2: no or very few MGS are captured and radio tracked

The suite of connectivity models and statistical analysis tools described in scenario 1 above can be used to develop an integrated connectivity model that incorporates landscape disturbance, habitat suitability, MGS occupancy and movement, and genetic information. This analysis and modeling approach would be useful for estimating priority areas for occupancy, movement/dispersal, and conservation.

Three types of modeling could be used and include: habitat suitability modeling, disturbance modeling, and corridor modeling.

**Habitat suitability modeling** is widely used; it is expected that suitability modeling conducted for this study could be done so that it is compatible with a model currently being developed by CEC. Habitat suitability is likely to be determined in both cases by comparing occupancy, and possibly relative population density, with remotely-sensed and field-identified environmental characteristics.

**Disturbance modeling** uses information about human activities in a raster or grid modeling environment and analyzes these data according to questions driving the analysis and the requirements of the organism or process affected by the disturbance. The disturbance data would include transportation infrastructure; residential, commercial, and industrial development; population density; electrical transmission corridors; and recreation areas and trails. These models are usually best built as custom models to answer questions defined by the species, ecosystem, and disturbances of concern.

**Corridor modeling** uses habitat suitability and disturbance information to approximate how animals would move through a landscape, assuming enough is known about the species' behavior. There is a wide variety of corridor models available: 1) Least cost corridor uses a simulated object moving across a landscape, where each incremental step is toward a lower-cost or more suitable location; 2) Graph theoretic approaches which estimate the relative value of different potential connections among objects (such as population locations, or places on a landscape); 3) FunConn approximates movement of different organisms using information about the landscape and rules about organismal movement behavior.; and 4) Circuitscape uses electrical circuit theory and habitat/disturbance maps to predict where organismal movement and connections are more and less likely among places on a landscape.

### References

Bell, K.C. & Matocq, M.D. 2010. Development and characterization of polymorphic microsatellite loci in the Mohave ground squirrel (*Xerospermophilus mohavensis*) *Conserv Genet Resour* doi: 10.1007/s12686-010-9229-y.

Bohonak, A.J. 2002. IBD (Isolation By Distance): A program for analyses of isolation by distance. *J Heredity* 93, 153-154.

Corlatti, L., Hackländer, K., and Frey-Roos, F. 2009. Ability of wildlife overpasses to provide connectivity and prevent genetic isolation. Conservation Biology 23: 548-556.

Cornuet, J.M. & Luikart, G. 1997. Description and power analysis of two tests for detecting recent population bottlenecks from allele frequency data. *Genetics* 144, 2001-2014.

Evanno, G., Regnaut, S. & Goudet, J. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Mol Ecol* 14, 2611-2620.

Excoffier, L., Laval, G. & Schneider, S. 2005. Arlequin ver. 3.0: An integrated software package for population genetics data analysis. *Evol Bioinforma Online* 1, 47-50.

Falush, D., Stephens, M., and Pritchard, J.K. 2003 Inference of population structure using multilocus genotype data: loci and correlated allele frequencies. Genetics 164: 1567-1587.

Falush, D., Stephens, M., and Pritchard, J.K. 2007 Inference of population structure using multilocus genotype data: dominant markers and null alleles. Molecular Ecology Notes 7: 574 -578.

Gannon, W.L., R.S. Sikes, and the Animal Care and Use Committee of the American Society of Mammalogists. Guidelines of the American Society of Mammalogists for the use of wild mammals in research. Journal of Mammalogy 88:809-823.

Garner, A., Rachlow, J.L., Waits, L.P. 2005. Genetic diversity and population divergence in fragmented habitats: conservation of Idaho ground squirrels. *Conserv Genet* 6, 759-774.

Gerlach, G., and Musolf, K. 2000. Fragmentation of landscape as a cause for genetic subdivision in bank voles. Conservation Biology 14:1066–1074.

Hamilton, M.B. 2009. Population Genetics. Chichester: Wiley-Blackwell.

Hardy OJ, Vekemans X. 2002. SpaGeDi: a versatile computer program to analyze spatial genetic structure at the individual or population levels. *Mol Ecol Notes*. 2, 618-620.

Harris, J.H., and P. Leitner. 2004. Home-range size and use of space by adult Mohave ground squirrels, *Spermophilus mohavensis*. Journal of Mammalogy 85:517-523.

Harris, J.H., and P. Leitner. 2005. Long distance movements of juvenile Mohave ground squirrels, *Spermophilus mohavensis*. Southwestern Naturalist 50:188-196.

Hines, J.E. 2006. PRESENCE2. Software to estimate patch occupancy and related parameters. USGS-PWRC. (http://www.mbr-pwrc.usgs.gov/software/presence.html)

Holderegger, R., and DiGiulio, M. 2010. The genetic effects of roads: A review of empirical evidence. Basic and Applied Ecology. doi:10.1016/j.baae.2010.06.006.

Karban, R., and Huntzinger, M. 2006. How to do ecology. A concise handbook. Princeton, NJ: Princeton University Press.

Lindsay, D.L., Barr, K.R., Lance, R.F., Tweddale, S. A., Hayden, T. J., and Leberg, P. L. 2008 Habitat fragmentation and genetic diversity of an endangered, migratory songbird, the golden-cheeked warbler (*Dendroica chrysoparia*). Molecular Ecology 17: 2122-2133.

Manel, S., Schwartz, M.K., Luikart, G., and Taberlet, P. 2003. Landscape genetics: Combining landscape ecology and population genetics. Trends in Ecology and Evolution 18: 1807-1816.

May, B., Gavin, T.A., Sherman, P.W., & Korves, T.M. 1997. Characterization of microsatellite loci in the northern Idaho ground squirrel, *Spermophilus brunneus brunneus. Mol Ecol* 6, 399-400.

Peakall R, Smouse PE. 2006. GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. *Mol Ecol Notes* 6, 288-295.

Pritchard, J.K., Stephens, M., and Donnelly, P. 2000. Inference of population structure using multilocus genotype data. Genetics 155: 945-959.

Queller DC, Goodnight KF. 1989. Estimating relatedness using molecular markers. Evol. 43, 258-275.

Stevens, S., Coffin, J., & Strobeck, C. 1997. Microsatellite loci in Columbian ground squirrels, *Spermophilus columbianus. Mol Ecol* 6, 493-495.

Szpiech, Z.A., Jakobsson, M., Rosenberg, N.A. 2008. ADZE: A rarefaction approach for counting alleles private to combinations of populations. *Bioinformatics* 24, 2498-2504.

Wilson, G.A., B. Rannala. 2003. Bayesian Inference of Recent Migration Rates Using Multilocus Genotypes. Genetics 163, 1177-1191.







