



## **Proposal For Large Mammal Advisory Committee 2014**

### **Inland Deserts Region (R6)**

#### **MONITORING DESERT MULE DEER USING DNA-BASED CAPTURE-RECAPTURE**

Proposed Start and Completion Date: July 1, 2014 – June 30, 2018

#### Executive Summary:

A well-designed monitoring strategy is required to obtain accurate data about population size, trends, and to develop and evaluate management strategies for big game species. To this end, California Department of Fish and Wildlife collects baseline monitoring data on the state's mule deer (*Odocoileus hemionus*) herds. Monitoring desert mule deer (*Odocoileus hemionus eremicus*) abundance in Deer Zone D12, which is in southeastern California within the Sonoran Desert, has proved difficult. This herd is important to hunters and has traditionally been fully subscribed. Although a difficult hunt, this unit produces some of the largest bucks in California. The difficulty with monitoring this herd is due to their location and behavior; they exist at very low densities, are patchily distributed, and are reluctant to leave cover. These characteristics result in low detection probabilities, which in turn, result in poor estimates of population abundance.

One method for estimating population abundance and vital rates, in situations like this, is a DNA-based mark-recapture method, which uses non-invasive collection of genetic samples, such as tissue, hair, and feces to obtain DNA. Our objective is to implement a monitoring effort for desert mule deer in D12, which provides annual estimates of population abundance, composition, and potentially annual survival and rate of population change using fecal DNA-based mark-recapture methods. Our secondary objective is to address mule deer population dynamics in areas proposed for energy development, as well as to evaluate habitat mitigation. Sampling sites are proximate to proposed energy development. This method also has high potential for use in developing a monitoring plan for all areas where desert mule deer are harvested.

#### Statement of Need

One of California Department of Fish and Wildlife's (CDFW) responsibilities is to manage mule deer populations. To this end, collection of baseline monitoring data for big game species is essential. Monitoring desert mule deer (*Odocoileus hemionus eremicus*) abundance in Deer Zone D12, which is in southeastern California within the Sonoran Desert, has proved difficult (Thompson and Bleich 1993). This herd is important to hunters and has traditionally been fully subscribed. Due to the high demand for tags in this zone, in 2010 this hunt was classified as a Premium hunt and tags are issued through the annual Big Game Drawing. Although a difficult hunt, this unit produces some of the largest bucks in California (CDFW, unpublished data). Local hunters and conservation groups have expressed concerns regarding our understanding and management of these desert mule deer. Our objective is to implement a monitoring plan for desert mule deer in D12, which provides annual estimates of

population abundance, composition, and potentially annual survival and rate of population change. In addition, the ability to estimate population size and demographic vital rates is crucial for understanding impacts of energy development, as well as their habitat mitigation measures, on desert mule deer populations.

## Introduction

A well-designed monitoring strategy is required to obtain accurate data about population size, trends, and to develop and implement appropriate management strategies for mule deer (*Odocoileus hemionus*). The CDFW is responsible for the management of deer herds, which includes estimating deer abundance and composition. These estimates are used, in addition to other indices, to determine deer tag quotas. The desert mule deer (*Odocoileus hemionus eremicus*) is a subspecies restricted to the Sonoran Desert in the southeastern corner of California in Imperial, Riverside, and San Bernardino Counties; these deer are hunted in Deer Zone D12. This hunt has traditionally been fully subscribed, but is a difficult hunt. Hunter success is low, but this hunt produces some of the largest bucks in California (CDFW, unpublished data). In addition to knowledge for management, understanding the impacts of habitat fragmentation and isolation on mule deer populations is important because they are more vulnerable, due to their low population densities, to stochastic events, such as recurrent drought. Recognizing the variable nature of desert wildlife populations, Marshal et al. (2004, 2006a) emphasized the importance of conserving the habitat that will allow desert wildlife populations to fluctuate naturally for their long-term conservation.

Desert mule deer are difficult to survey and monitor because they exist at very low densities (Thompson and Bleich 1993, Marshal et al. 2006b), are patchily distributed, and are reluctant to leave cover (Celentano and Garcia 1984). These characteristics result in low detection probabilities, which in turn, result in poor estimates of population abundance. Despite these difficulties, a previous study successfully estimated population size. Marshal et al. (2006b) used marked deer and camera traps at water sources in early summer to estimate population abundance and herd composition of desert mule deer in the Sonoran Desert area of southeastern California. This method worked well, with annual sampling CVs ranging from approximately 6–27%, and averaging approximately 14%. However, this method requires the physical capture and collaring of animals, and the annual replenishment of marked animals, making it a logistically involved and expensive process.

Another promising newer method for estimating population size and vital rates is DNA-based mark-recapture (which is called capture-recapture in the literature). Non-invasive collection of genetic samples, such as tissue, hair, and feces is used to obtain DNA for microsatellite genotyping (Talberlet et al. 1996, Mills et al. 2000, Waits and Paetkau 2005). These data can be used in mark-recapture models to estimate population size and other vital rates (Lukacs and Burnham 2005a;b, Miller et al. 2005, Lukacs et al. 2007). Using noninvasive DNA samples in mark-recapture models is attractive because individuals can be identified without handling and marking animals, thereby decreasing costs associated with demographic monitoring, and is particularly useful for animals difficult to either capture or count, such as desert mule deer.

Recently, Ball et al. (2007) presented an improved laboratory method for sampling fecal pellets, which used sloughed intestinal epithelial cells that are present on the surface of fecal pellets. For free-ranging deer, Brinkman et al. developed (2010) and field tested (2011) a protocol for extracting DNA from fecal pellets for Sitka black-tailed deer. Since the advent of the Brinkman et al. (2011) work, fecal DNA has been successfully used to estimate population size and vital rates for similar ungulate species (e.g., Poole et al. 2011, Hettinga et al. 2012, Harris et al. 2010). Finally, fecal DNA is being used by CDFW biologists to estimate population abundance for the Pacific Deer Herd (El Dorado and Placer counties) and has been used successfully to estimate abundance of black-tailed deer in Mendocino County, California by UC Davis researchers (Lounsberry et al. 2013). Thus, fecal DNA-based methods for identifying individuals have been well established for ungulates.

These data will be applicable for robust-design closed-capture models, which provide estimates of demographic parameters for periods between closed-capture sessions (Kendall and Pollock 1992, Kendall et al. 1995). In addition to estimating population abundance ( $N$ ), robust-design closed-capture models can estimate annual survival ( $S$ ) and finite rate of population change ( $\lambda$ ). In addition, if there are adequate data, additional movement parameters can also be estimated (Kendall et al. 1997, Schwarz and Stobo 1997). The demographic parameters of  $S$  and  $\lambda$  are often more sensitive than  $N$  for detecting changes or declines in populations, and are important for effective population monitoring. It is  $S$  and  $\lambda$  that will be most useful in future years to evaluate population trends and reaction to management actions, such as changes in harvest.

The advantages of using fecal DNA based mark-recapture over camera mark-recapture is a reduction in logistical planning and field time, and potentially cost savings over time. That is, while DNA samples are about \$25/sample at present, this cost is likely to decrease through time. In addition, as field workers gain experience with sample collection and can more readily identify poor quality samples, fewer samples will be submitted for processing for additional cost savings. Finally, desert mule deer are notoriously difficult to capture due to the factors listed above, making non-invasive sampling preferable to methods that require physical capture to mark individuals.

### Objectives

The overall goal of this project is to provide baseline population monitoring data of desert mule deer in D12 to improve their management and meet CDFW responsibilities. To this end, our primary objective is to implement a monitoring strategy to estimate abundance and herd composition. Our secondary objectives include estimating annual  $S$  and  $\lambda$  for potentially more accurate monitoring as well to provide insight to population dynamics. Finally, we hope to leverage these data as pre-treatment data that can be used as part of a BACI study design to evaluate impacts of energy developments on desert mule deer populations. Beyond our primary and secondary goals, this technique has an additional benefit of being adaptable to monitoring other desert ungulates.

Our overall goal is to provide precise population abundance estimates for monitoring and to detect when the population falls below a specified minimum size. Based on population abundance estimates and their sampling variance from a previous desert mule deer study in D12 (Marshall et al. 2006b), we

designed our sampling scheme with a targeted coefficient of variation of  $\leq 15\%$  for estimates of population abundance. The sampling scheme is designed to have 80% power to detect when population abundance is  $\leq 50$ , given  $\alpha = 0.10$ . We defined 50 as a critical minimum population size based on the Marshal et al. (2006b) study, but this value will be adjusted as relevant to sampled populations.

## Methods

The primary focus of monitoring will be in the Chuckwalla Mountains area of D12, which is the northwest part of the Sonoran Desert in southeastern California. The 1,200 km<sup>2</sup> study area is 40 km southwest of Blythe, in Riverside County, California. We will sample in areas with the highest probabilities of encountering desert mule deer. Specifically, we will delineate transects centered on artificial water sources located in the study area and collect samples during the hottest and driest time of the summer (June–early July) when deer are most likely to rely on artificial water sources (Marshal et al. 2006a). Field work will be completed prior to monsoon rains (late July–August), which is when deer disperse to natural water sources following forage greenup (Celentano and Garcia 1984, Hervert and Krausman 1986, Rautenstrauch and Paul 1989). Because we will analyze these data using closed-capture models, which require demographic closure, we will collect samples as close in time as logistically feasible to minimize the chance of deaths or movements occurring during the study period. Results from field observations indicate most fawns are born in early September (Celentano and Garcia 1984), thus births should not violate closure during the study period. In addition, Marshal et al. (2006b) sampled during the same time period and in similar areas from 1999–2004 and concluded there was little violation of the assumptions of a closed capture model, and that any bias was minimal.

Success rates of classifying individuals from fecal pellet samples declines with pellet age, with the most successful samples <2 weeks of age (Brinkman et al. 2009, Poole et al. 2011). In addition, Hervert and Krausman (1986) found that female desert mule deer visited water sources 1 time per day and bucks visited every 1–4 days. Thus, sampling of transects every 5–7 days should capture desert mule deer that use the drinkers and ensure samples are certain to be <2 weeks of age.

For the first year, we will only be able to use these data in closed-capture models to estimate population size ( $N$ ), probability of capture ( $p$ ), and probability of recapture ( $c$ ). Capture histories will be constructed for each deer encountered during the study. For this study, there will be 6 1-week long closed capture sessions in June–early July (6 weeks total length). The periods between closed-capture are sufficiently long (approximately 10.5 months) such that birth, death, immigration, and emigration can occur, so that  $S$  and  $\lambda$  can be estimated, via the closed-capture robust design, after the first year.

Because Marshal et al. (2006b) found high annual variation in population abundance estimates ( $\hat{N}$ ), it is unlikely we will be able to detect trends in abundance, which is a typical metric by which sample size calculations are done. Consequently, we focused our design on achieving adequate precision to detect when abundance falls below a given management threshold. We used inputs for our sample size simulations based on the Marshal et al. (2006b) study in which population estimates ranged 56–106 and averaged 65, and the CV for sampling variance ranged 6–27% and averaged 14%. To start, we designed our sampling plan based on an average CV = 15%,  $\hat{N} = 65$ ,  $\alpha = 0.10$ , and 80% power to detect when

population size was  $<50$  for the lower 90% CI of  $\hat{N}$ . We used this threshold of 50 based on the lower end of the Marshal et al. (2006b) study, but the threshold (and sampling design) will be adjusted as needed for different populations. We used the simulator in Program MARK to determine potential sampling schemes to achieve these goals. After analyzing the first year of data, we will adjust our sampling plan as necessary to be able to identify when the population drops below the minimum population threshold. Our specific sampling plan will be provided upon request.

### Products

Annual progress reports will be submitted to the Wildlife Branch each spring, with quarterly updates as needed. Reports will include annual estimates of population size, herd composition, survival, and finite rate of population change, as well as preliminary evaluation of the project towards meeting initial objectives, financial costs, and any other issues. A final report will be submitted by April 2018 to the Resource Assessment Program and to the CDFW regional offices that addresses each of the stated goals.

A monitoring plan will be written and include field protocols for regular monitoring, with mapped details. By March 2018, we plan to submit our findings for publication in Journal of Wildlife Management, or another appropriate peer reviewed journal, with a title like “Monitoring the elusive desert mule deer; adapting DNA-based mark-recapture methods from the elusive forest black-tailed deer”.

### Collaborators

Project lead is Ms. Jane McKeever and Project Supervisor is Dr. Tom Stephenson. Dr. Mary Conner, Research Associate Professor, Utah State University, will provide contracted support for monitoring study design, data analyses, and manuscript preparation as part of LMAC Project NC8001-26. Local biologists, Mr. Gerald Mulcahy and Mr. Austin Smith, will provide assistance during field seasons and with study area decisions.

### Program Planning

In the spring, prior to the summer field season, personnel will have a planning meeting, which will include site visits. During late May of each year, artificial water sources in the sampling area and ambient temperature will be monitored to determine start date of field sampling. Two months after DNA analyses have been received, a meeting will convene to discuss results of analyses and changes needed. Other meetings will be scheduled as needed.

### Other Resources Requested from CDFW

Samples will be archived if necessary. All data and analyses will be submitted to the Wildlife Branch.

### Issues to be Resolved

Administrative approval is needed. Also, funding from Boone and Crocket Club and California Deer Association will be sought. The plan is for this to be a jointly funded project; we are requesting Boone

and Crocket Club funding for research specific to solar development and habitat. Although the plan is to use outside funds for fecal DNA analysis, if that's not possible a CDFW contract will need to be approved.

**Required Products**

Raw data from field work and genetic analysis will be provided within one month of completion. Annual Progress Reports will be provided by May 1 of each year; Final Report will be provided by June 1, 2018. Publications for Journal of Wildlife Management, or another appropriate peer reviewed journal is expected in March 2018.

**Personnel Requirements and commitments from CDFW**

Three Environmental Scientists (ES) (McKeever, Mulcahy, and Smith) will be available intermittently over the two month (June and July) field season, requiring up to 40% of time each. Two scientific Aids will be hired for three months (100% of time). Project Lead will spend an additional 10% of time each month for coordinating analyses and project review/reporting. Contracting, prepared by Project Lead, will initially take a significant amount of time. In May of each year, an additional 10% of time will be needed from ES staff.

**Budget Detail - per year budget detail by activity/task:**

With start date of July 1, 2014, the first year of the project will not cover the entire sampling season; therefore, an additional year of funding is requested. Project staff will need the assistance of two temporary help positions for 3 months of time (June - August) for field work and sample processing each year. Budget includes sampling supplies, travel and O&E for permanent and temp help staff. The estimated annual cost for contracted fecal DNA genetic analysis is \$20,000. Through the RFP process, genetic analyses will be contracted with a lab, the cost of which will be proposed from outside funding.

<b>Item Description</b>	<b>Year 1 2014/2015</b>	<b>Year 2 2015/2016</b>	<b>Year 3 2016/2017</b>	<b>Year 4 2017/2018</b>
<b><u>Personnel Expense</u></b>				
Dr. Mary Conner	Paid by LMAC Project: NC8001-26 (Contract P126003)			
Temporary Help 2 Scientific Aids for 3 months each (except Year 1)	July 1 start 4 months @ \$8,000	6 months @ \$12,000	6 months @ \$12,000	6 months @ \$12,000
<b><u>Personnel Subtotal</u></b>	<b><u>\$8,000</u></b>	<b><u>\$12,000</u></b>	<b><u>\$12,000</u></b>	<b><u>\$12,000</u></b>
<b><u>Operating Expense</u></b>				
Field Supplies	\$3,000	\$1,000	\$1,000	\$1,000

Lab Costs @ \$25/sample w/ increase in sampling in Year 4 and 5.	\$15,000	\$20,000	\$20,000	\$20,000
Publications costs			\$1,000	\$2,000
Travel (Per Diem/Mileage)	\$4,000	\$8,000	\$8,000	\$8,000
Miscellaneous (Field Supplies/Travel)	\$1,000	\$1,000	\$1,000	\$1,000
<u>Operating Expense Subtotal</u>	<u>\$23,000</u>	<u>\$30,000</u>	<u>\$31,000</u>	<u>\$32,000</u>
<b>Total Estimated Project Cost</b>	<b>\$31,000</b>	<b>\$42,000</b>	<b>\$43,000</b>	<b>\$44,000</b>
<b>Total Est. BGMA Funds Requested</b>	<b>\$31,000</b>	<b>\$42,000</b>	<b>\$43,000</b>	<b>\$44,000</b>

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