Proposal Format: Large Mammal Advisory Committee 2014

Marin County Deer Abundance 2015-2016

Proposed Start and Completion Date:

June 2015 – August 2018

Statement of Need

Robust deer population estimates are needed for conservation and management of the state's deer. Population data for deer in Marin County is minimal and what little there is comes from road survey data. For purposes of deer conservation and defensible tag quotas CDFW needs to collect better population data.

Introduction

We will evaluate the ability of an integrated application of random sampling (Thompson 2012), fecal DNA transects (Lounsberry et al. 2015), and camera traps (O' Connell 2011) to estimate deer abundance across a large geographic area. To accomplish this, we will model abundance using a closed, mark-recapture model (Kéry and Schaub 2011) of the DNA data and an N-mixture model (Royle 2004) of the camera trap data.

Surveys will occur on 68 randomly selected plots located throughout Marin County public lands and private lands associated with the Marin Agricultural Land Trust (MALT). These lands sum to 770 km^2 amounting to 57% of the total land area of Marin County (Figure 1). Deer in Marin County are believed to be non-migratory.

Objectives

- Establish 2 camera trap stations/plot and 1 pellet collection transect on randomly selected plots in Marin County (years 1-3).
- Deploy iridium collars on 20 male and 20 female deer for home range estimation (year 1).
- Use cameras to attempt abundance estimation (Years 1-3).
- Collect and analyze DNA samples to determine unique individuals and gender (Years 1-3).
- Use results of DNA analysis to run CMR model (Years 1-3).
- Use home range information to attempt to scale up local density and abundance estimates (Years 1-3).

Methods

We intersected hexagons from the U.S. Forest Service's Forest and Inventory Analysis sampling frame that completely intersects our study area (Bechtold and Patterson 2005). We

plan to survey all of the 68 hexagons of which survey lands (public and MALT) sum to at least 10 % of hexagon area. We randomly selected a survey start point within survey lands within each hexagon.

Starting in June 2015 through August 2018, we will conduct a camera trap survey at the start and finish locations for each DNA pellet transect location and left up for 30 days. The images will be reviewed to create a detection history of the minimum number of individually distinguishable deer per station per 24-hour survey period by gender/juvenile/antler classes.

Similar to the protocol of Lounsberry et al. (2015), we will concurrently establish a 2-m wide belt transect up to 1.2 km in length in the vicinity of each random site that follows deer trails (when present). On the first sampling occasion, we will collect all fresh pellets with a mucous sheen and attempt to clear all pellets from 2 m beyond either side of the transect. We will return each week (for a total of 4 visits) to collect newly deposited pellets from the transect. If no pellets are encountered after 2 visits, the transect will be discontinued. The pellets will be analyzed by a genetics laboratory at UC Davis to determine the individual identities and gender of deer to create of a 4-period detection history for each individual.

The camera data will be used to estimate local abundance (deer per station) by means of an N-mixture model (Royle 2004). The pellet data will be used to estimate local abundance (deer per transect) by means of a closed, mark-recapture model (Kéry and Schaub 2011). We will also combine the data and attempt to estimate local abundance by means of an integrated population model (Kéry and Schaub 2011). We will use gender- and season-specific information on deer movement and home range size to scale-up local abundance to an estimate of density and population size for the study area. This ancillary data will be provided by GPS collars to be deployed on does and buck in the study area. 20 does and 20 buck will be collared. The results will be used in Monte Carlo simulations (Metropolis and Ulam 1949) and power analysis (Purcell et al. 2005) to determine the precision of baseline abundance estimates and ability to detect population trends over 20 years. These simulations will also identify the optimal mix of sample size allocation among camera traps and fecal DNA transects.

Products

Quarterly reports will be prepared and submitted starting October 2015

A final report will be prepared in the last quarter of 2018.

Final study results will be submitted for journal publication.

Collaborators

Dr. Brett Furnas will lead the project. He will model the data with the assistance of Russ Landers. Russ Landers will lead crews in the field and oversee data collection/quality. Stuart Itoga will lead the capture effort with assistance from Conrad Jones and John Kraus. We will collaborate with Dr. Justin Brashares from UC Berkely on genetic analysis of the pellet samples. Scientific Aides will conduct the field surveys and review camera trap images.

Budget Detail

	Year 1	Year 2	Year 3	Year 4
Sci Aids	$55,000.00	$55,000.00	$55,000.00	**$165,000.00**
Collars	$100,000.00			**$100,000.00**
Supplies	$20,000.00	$20,000.00	$20,000.00	**$60,000.00**
Equipment	$20,000.00			**$20,000.00**
Total	**$195,000.00**	**$75,000.00**	**$75,000.00**	**$345,000.00**

References

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Figure 1. Survey sites for camera traps and fecal DNA transects in Marin County