Proposal Format: Large Mammal Advisory Committee

North Central Region (R2)

ESTIMATION OF ABUNDANCE OF THE PACIFIC DEER HERD USING FECAL DNA

Project Leader: Terri Weist

Executive Summary

Obtaining data necessary to monitor deer populations in forested environments is difficult. Aerial surveys of mule deer in the D zones of the North Central Region have proven ineffective in observing deer through heavily forested canopies. Population estimates for migratory deer in these zones are non-existent.

We propose to utilize non-invasive DNA techniques to obtain rigorous estimates of abundance and density with moderate precision for the migratory Pacific Deer Herd and assess the feasibility of implementing DNA-based monitoring of this deer herd in the future.

This project will culminate both in population estimates and a cost-effective protocol that can be applied to future censuses of this and other deer herds throughout the state of California.

Introduction

Management of deer in California requires knowledge of population parameters in order to effectively determine hunting quotas, season dates and direct activities that will ensure population viability of our deer herds.

Estimating populations of mule deer in densely vegetated environments has been problematic. Aerial surveys to ascertain population estimates of mule deer in densely vegetated coniferous forest are not practical due to poor visibility through canopies. Moreover, because aerial surveys are typically conducted in the fall and spring when deer are on their winter ranges, surveying deer from the air is limited due to the presence of houses, restricting the area that can be effectively surveyed from the air when deer in the D zones are on winter range habitats. Given these limitations, helicopter survey methodology is not warranted in heavily forested regions.

Road surveys are also unreliable in forested environments since surveys are limited to accessible roads (Brinkman et al. 2011). Road surveys rarely provide unbiased estimates, nor do they provide a representative sample of habitats, and are therefore statistically less reliable (Garton et al. 2004). Road surveys also are limited by visibility issues and access is often limited due to weather related road conditions or ownership.

Population indices derived from pellet counts have been used to monitor trends in deer populations. However, this method is confounded by weather related variations, unknown defecation rates and the variable detectability of pellets in different habitats (Brinkman et al. 2011). Therefore, estimates derived from pellet counts tend to result in imprecise and biased estimates.

In principle, mark-recapture approaches are the most reliable and accurate way to estimate population abundance (Lukacs and Burnham 2005). However, physically marking and re-capturing or re-sighting deer is prohibitively expensive. Consequently,

non-invasive DNA-based mark-recapture techniques are the only feasible way to conduct such surveys and are necessary to establish robust population estimates for deer within the D zones. In particular, DNA from deer fecal pellets would be used. This method has been successfully used to estimate population density of ungulates and black bears (Brinkman et al. 2011, Harris et al. 2010, and Bellemain et al. 2005).

Objective

1) Estimate abundance of the PDH using deer fecal DNA
2) To provide a cost-effective protocol that can be applied as a practical and efficient way of obtaining population information in migratory deer herds throughout the State.

Study Area

The Pacific Deer Herd (PDH) is located on the western slope of the Sierra Nevada in Central California. The migratory PDH occupies approximately 914 km^2 of public and private lands in El Dorado and southern portion of Placer Counties (Fig. 1). This herd was selected due to the small herd boundary size and proximity to UC Davis, where the DNA analysis would most likely be conducted.

The summer range of approximately 531 km^2 consists primarily of Ponderosa pine (*Pinus ponderosa*), red fir (*Abies magnifica*), lodgepole pine (*P. contorta*) and white bark pine (*P. albicaulis*). Shrub species consist of huckleberry oak (*Quercus vaccinifolia*), snowberry (*Symphoricarpus albus*), sagebrush (*Artemisia tridentata*) and chinquapin (*Castanopsis sempervirens*). Meadows provide important grasses and forbs during fawning season.

Within the summer range of the PDH, elevations range from 4800 feet to nearly 9,900 feet at Pyramid Peak.

Methods

In order to make sure we are sampling only migratory deer, fecal pellets will be collected on the summer range of the PDH. In order to obtain samples from throughout the entire summer range of the PDH, the area will be subdivided into three sampling areas consisting of approximately 177 km^2 each: the north, central and southern areas. From each of the three areas, at least one 30 km^2 sampling unit will be randomly selected. Within each 30 km^2 sampling unit, belt transects will be established according to Brinkman et al. 2011. If possible, a grid-like transect array will be employed to utilize likelihood-based estimators of density (Lukacs and Burnham 2005; Brinkman et al. 2011).

We propose to visit each transect four to six times per season for two years. Each belt transect will be resampled after ten days to ensure to ensure pellets would provide usable DNA. This two-level sampling approach with it's primary sampling occasion (annual sampling) and secondary sampling occasion (i.e., multiple visits within a short time interval) is a robust design for capture-recapture studies (Lukacs and Burnham 2005),

Summary of sampling protocol based upon Brinkman et al. 2011.

Sampling design:

(1) Choose random points in major habitat types
(2) From each random point, follow a predefined compass bearing until a deer trail is encountered.
(3) Follow deer trail until intersecting with another and continue on whichever trail is closest to the predefined bearing (i.e., go as close to a series of parallel transects as is possible while staying on deer trail).
(4) Mark trails with flagging to ensure repeatability within and across seasons
(5) They made sure that each habitat type was transected approximately in proportion to its composition in the study area
(6) Each adjacent (parallel) transect was separated by at least 500 m (because this was the radius of an average deer home range in their study area, i.e., 0.78 km^2)
(7) 4-6 pellets per pellet group were collected and the rest were removed from the transect
(8) Each transect was sampled 4-6 times per 2-month season, depending on snow-melt in a given year and location; ideally, transects were sampled once every 10 days
(9) Only obviously fresh pellets were collected during the first annual run of a transect and all others cleared.

Collection protocol

(1) Collect pellets within the 2-m wide transect, but will clear from 4-m wide.
(2) Record date, time, and GPS waypoint and WHR habitat type of each collected sample (4-6 pellets from each pile; others cleared)
(3) Put the 4-6 pellets in a conical with 95% ethanol
(4) Extract DNA within 6 months of collection

Laboratory methods (see Brinkmann et al. 2010; used multiple tubes approach)

Data analysis

Brinkman et al. (2010) used Huggins closed models (Huggins 1991) in Program MARK (White 2008) to estimate population size. Akaike's Information Criterion may be used to determine best approximating model among the suite of candidate modes.

GIS will be used to quantify habitat in relation to transects, individual deer location as assigned from fecal DNA and deer density and abundance estimates.

We will separate genotypes into sexes and calculate estimates separately. This could be done before and after hunting seasons and combined with change-in-ratio estimators to validate the method as well if harvests are known.

Proposed Time Frame

This project will address the cost-benefit analysis of using fecal DNA to provide accurate and precise estimates of deer abundance within migratory deer herds. Laboratory and statistical analyses will be conducted by contracting entity (preferably a PhD or masters' student at UC Davis under the direction of Dr. Ben Sacks). Start of project is dependent

upon a smooth contractual process. We anticipate grid and transect establishment will start once access to study area is allowed, probably early May 2013.

YEAR 1 (2012-13)	YEAR 2(2013-14)	YEAR 3 (2014-15)
Study design development	redesign if necessary	
Establish sampling units	Collect samples (yr2)	Lab analysis
Establish belt transect locations	First progress rept due	Final Report due

Annual progress reports will be submitted 12 months following the start date of the project. This report will contain data summaries and will address project impediments and other issues.

The final report will be submitted the California Department of Fish and Game Resource Assessment Program and to the North Central regional office by July 1,2014.

LMAC committee recommends initiating a RFP process to choose contracting individual. Results of this project will be published by the contracting individual/UC institution in the appropriate peer-reviewed journal.

Data will be delivered to the Wildlife and Habitat Data Analysis Branch by and contain the following:

Final report containing (Funding Option 1):

- Data including maps with sample locations, numbers of individuals based upon genotypes, habitats, etc)
- Results (size estimates and confidence intervals)
- Conclusions regarding feasibility of regular monitoring, sample size and efforts required, power analyses related to trend detection, field protocols for regular monitoring and
- Estimated costs for annual abundance estimates.
- Publication in peer reviewed journal

Collaborators

DFG Project Lead: Terri Weist

Personnel Requirements and Funding from CDFG

Regional personnel may be used to assist in data collection. Most data will be collected by DFG volunteers and UC Davis participants.

CDFG funding sources

Funding will be provided by the large mammal project funds

Budget Estimation

Budget estimation for UC Davis personnel, laboratory costs and field work are shown in Table 1. If RFP system is initiated, amounts listed could be lower depending upon contracting entity.

Table1. Budget outline for UC Davis graduate student, Dr. Sacks and all other related costs to conduct DFG DNA pilot study for the Pacific Deer Herd.

UC Davis	Year 1	Year 2/3
Personnel costs		
PI (3 mos per yr)	$27,000.00	$27,000.00
student researcher (summer)	$6,000.00	$6,000.00
	$33,000.00	**$33,000.00**
Operating expenses		
Field supplies	$3,000.00	$1,000.00
Lab costs (750/yr @ $25/sample)	$18,750.00	$18,750.00
Publication costs		$1,200.00
	$21,750.00	**$20,950.00**
Total Direct costs	$54,750.00	$53,950.00
Indirect costs (UCD overhead, 25%)	$13,687.50	$13,487.50
UCD Total Cost	$68,437.50	$67,437.50

CDFG Costs		
Scientific Aid @ 9 months (PhD student)	$25,200.00	$28,080.00
Scientific Aid @4 mo. Yr 1 & 3 mo yr2	$8,500.00	$8,500.00
Travel/mileage	$2,000.00	$2,000.00
Miscellaneous (field supplies/travel)	$500.00	$500.00
	$36,200.00	$39,980.00
Total UCD/CDFG	$104,637.50	$106,517.50
TOTAL PROJECT COST	**$211,155.00**	

* $11.58(+34.76% benefits) / hr in year 1 = $2705/mo

**$13.38/hr(+ 34.76%) = $3,120/mo in year 2 higher wages due to previous year's experience

Products:
Final report containing:

- Data including maps with sample locations, numbers of individuals based upon genotypes, habitats, etc)
- Results (size estimates and confidence intervals)
- Conclusions regarding feasibility of regular monitoring, sample size and efforts required, power analyses related to trend detection, field protocols for regular monitoring and
- Estimated costs for annual abundance estimates.
- Field protocols for regular monitoring
- Estimated costs for annual abundance estimates
- Publication in peer-reviewed journal

Literature Cited

Bellemain, E., J.E. Swenson, D. Tallmon, S. Brunberg and P. Taberlet. 2005. Estimating population size of elusive animals with DNA from hunter-collected feces: four methods for brown bears. Conservation Biology: 19 (1): 150-160

Brinkman, T. J., D.K. Person, M.K. Schwartz, K.L. Pilgrim, K.E. Colson and K. Hundertmark. 2010. Individual identification of Sitka black-tailed deer using DNA from fecal pellets. Conservation Genetics Resources 2:115-118.

Brinkman, T.J., D.K Person, F.S. Chapin III, W. Smith and K. J. Hundertmark. 2011. Estimating abundance of Sitka black-tailed deer using DNA from fecal pellets. Journal of Wildlife Management 75(1):232-242.

Garton, E.O., J.T. Ratti and J.H. Giudice. 2004. Research and experimental design. Chapter 3 in Braun, Clait (ed.). Techniques for Wildlife Investigations and Management. The Wildlife Society, Bethesda, MD.

Harris, R.B., J. Winnie Jr., S.J. Amish, A., Beja-Pereira, R. Godinho, V. Costa and G. Luikart. 2010. Argali abundance in the Afghan Pamir using capture-recapture modeling from fecal DNA. Journal of Wildlife Management 74(4): 668-667.

Huggins, R.M. 1991. Some practical aspects of a conditional likelihood approach to capture experiments. Biometrics 47:725-732.

Lukacs, P. and K.P. Burnham. 2005. Review of capture-recapture methods applicable to noninvasive genetic sampling. Molecular Ecology. 14:3909-3919.

White, G.C. 2008. Closed population estimation models and their extensions in program MARK. Environmental and Ecological Statistics. 15: 89-99.

Fig. 1. Location of the Pacific Deer Herd DNA Pilot Study Area in El Dorado County, CA