Abundance estimates of black-tailed deer using noninvasive sampling in a genetic capture-mark-recapture framework

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Introduction:

Estimates of population parameters derived from capture-mark-recapture (CMR) studies have been used to inform management recommendations for species across a wide range of taxa. Several recent studies have focused on the utility of molecular assays designed to amplify low-yield, non-invasively sampled DNA to be used within a CMR framework (Luikart et al. 2010). Here, we present preliminary estimates of abundance for a population of black-tailed deer (*Odocoileus hemionus columbianus*), in the Mendocino National Forest, California, using DNA derived from fecal pellets.

Mule deer (*O. hemionus*) and black-tailed deer have experienced significant population fluctuations during the past century (Unsworth et al. 1999). Efforts to elucidate the ecological factors contributing to these fluctuations have focused largely on the effects of habitat conditions and predation on population dynamics (e.g., via direct effects on population growth rates and mortality). However, the causes of observed fluctuations remain poorly understood (Forrester & Wittmer 2013). We are currently studying black-tailed deer in the Mendocino National Forest, one of California's prime hunting areas, with the explicit goal of quantifying the relative contributions of forage, predation as well as possible interactions on observed population dynamics and vital rates. Estimates of population size are essential for such analyses.

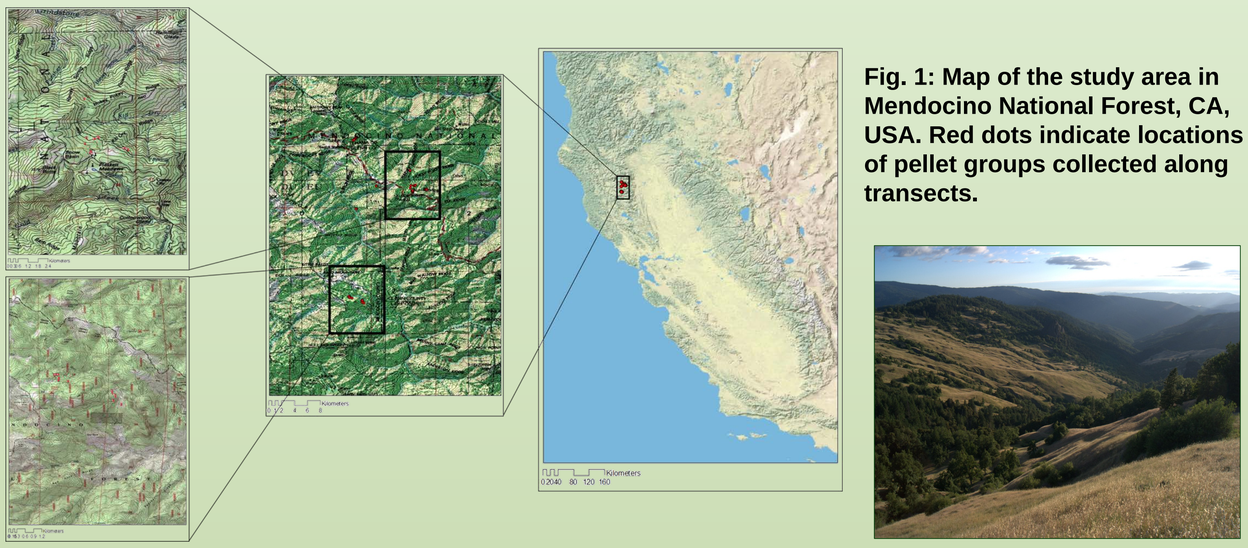
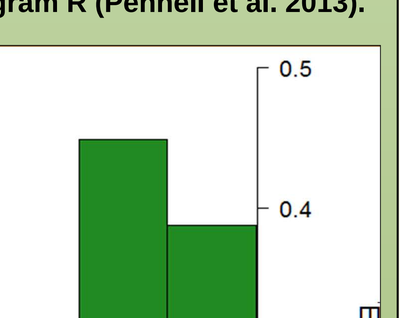


Fig. 1: Map of the study area in Mendocino National Forest, CA, USA. Red dots indicate locations of pellet groups collected along transects.



Methods:

- From July to September of 2011 and 2012, we collected deer fecal pellets along multiple approx. 1-km transects throughout a 450 km^2 portion of the Mendocino National Forest, CA (Fig. 1). Each transect was sampled 2-4 times.
- We extracted DNA from pellet groups and genotyped individuals at 11 loci using a multiplex polymerase chain reaction (PCR) assay developed for use in Columbian black-tailed deer (see Olegario et al. poster). We based consensus genotypes for each pellet group on 3 replicate PCRs.
- We assigned genotypes to individuals using exclusion based on locus matches in Program CERVUS (Kalinowski et al. 2007) and calculated the unbiased probability of identity (PI) and PI for siblings (Psib) in Program GIMLET (Valière 2002).
- Once all pellet groups have been extracted, our abundance estimates will be based on encounter histories built using sequential transect runs as discrete re-survey events to be analyzed in Program Mark. In the present study, we used unique and duplicated ("recaptured") samples to estimate abundance for each of 6 transects using a single-sample, equal capture method in the *Capwire* package in Program R (Pennell et al. 2013).

Fig. 2: Frequencies of 0 to 10 locus matches between pairwise comparisons of genotype profiles. Bars indicate observed frequencies for all 8320 pairwise comparisons (130 pellet group genotypes; brown bars) and among 49 pairwise comparisons of only resampled genotypes (22 individuals; green bars). Lines indicate the expected frequencies for two randomly sampled individuals (PI) or siblings (Psib) having identical genotypes. The dotted blue line indicates the individual assignment threshold.

Table 1: Transect ID, number of individuals (M = males, F = females, U = unknown), number of pellet groups, and abundance estimates (N-hat) from a single-sample, equal capture model. Upper and lower confidence limits (CL) refer to a 95% confidence interval.

Transect	*Year*	*No. Individuals (M/F/U)*	*No. pellet samples*	*N-hat*	*Lower CL*	*Upper CL*
CH12-3	2012	(0/13/0)	17	28	13	62
CH12-5	2012	(3/6/0)	13	15	9	35
PM12-5	2012	(3/7/0)	13	22	10	74
PT-CS11-1A	2011	(3/10/1)	21	23	14	45
PT-PM11-5A	2011	(3/1/1)	8	7	5	25
PT-PM11-7A	2011	(2/7/2)	14	26	13	86

Results and Discussion:

- We assembled consensus genotypes for 130 pellet samples from 6 transects (1-2 runs).
- Because of the high polymorphic information content (mean PIC = 0.69 ± 0.16) for our loci, distinct individuals rarely matched at more 50% of loci (Fig. 2).
- Conservatively, we considered 2 genotypes matching at ≥7 loci to reflect replicate samples from the same individual.
- Of the so-defined replicate sample pairs, 84% matched at 9 or more loci, indicating very low error in consensus genotypes (Fig. 2).
- The 130 pellet group genotypes were assigned to 98 unique individuals using a 7-locus match threshold.
- We selected the 3 most well-sampled transects ($N_{transect} \geq 8$ pellet samples; $N_{total} = 86$ pellet samples) to estimate abundance. Estimates and their 95% confidence intervals are given in Table 1.
- Abundance estimates using the 7-locus assignment threshold were more precise than 8-, 9-, or 10-locus thresholds (data not shown).
- Based on how well the data conform to theoretical predictions (Fig. 2), it appears our multiplex assay was well-suited to estimate abundance in a genetic CMR framework.

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