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DNA-BASED MARK-RECAPTURE OF WILD DEER: USING FAWNS TO CAPTURE THEIR MOTHERS

Graham Nugent\textsuperscript{1}, Jackie Whitford\textsuperscript{1}, Mary McEwan\textsuperscript{2}
\textsuperscript{1} Landcare Research, PO Box 69, Lincoln, 8152, New Zealand
\textsuperscript{2} AgResearch, Invermay Agricultural Centre, Private Bag 50034, Mosgiel, New Zealand
nugentg@landcareresearch.co.nz

INTRODUCTION

A lack of affordable techniques for accurately estimating the density of wild animals has long been a major constraint in wildlife management. An important breakthrough has been the use of DNA fingerprinting in conjunction with mark-recapture (MR) methods of density estimation (Taberlet et al. 1997; Mowat and Strowbeck 2000). Provided the DNA fingerprint from each individual is unique and can be recognised on two or more occasions, mark-recapture methods can be used to estimate the absolute numbers of animals present. The main challenge is often to find ways to obtain DNA cheaply from the population. To date, most interest has centred on using hair or faeces, because use of such ‘non-invasive’ sources of DNA avoids the cost of capturing the animal. In pest management, however, a high proportion of the population is often killed annually, providing a potentially low cost ‘recapture’ option for animals ‘marked’ by previous or simultaneous recovery of DNA from hair or faeces. In New Zealand, this approach has already been applied to brushtail possums (\textit{Trichosurus vulpecula}) and stoats (\textit{Mustela erminea}) (Nugent et al. 2003; Byrom et al. 2004).

In our previous attempt to estimate absolute densities of wild deer, however, we were unable to obtain DNA of sufficient quality to reliably identify individual deer from faeces or shed hair. We therefore explored the practicality of using parentage assessment based on a sample of killed animals, an approach first applied to estimating numbers of painted turtles (\textit{Chrysemus picta}) in Mississippi (Pearse et al. 2001).

The deer killed during control usually include both adults and their offspring, with the offspring effectively representing recaptures of their parents’ genotypes. The number of adult females can therefore be estimated (using the formula for a modified Lincoln-Petersen Index; from Pollock et al. 1990):

\[
N_{af} = \left[ \frac{(n_{af} + 1)(n_{f} + 1)}{n_{m} + 1} \right] - 1
\]

95\% CI = 1.96 * \left[ \frac{(n_{af} + 1)(n_{f} + 1)(n_{af} - n_{m})(n_{f} - n_{m})}{(n_{m} + 1)^2} \right](n_{m} + 2)

where \(N_{af}\) = estimated number of adult females present during a particular breeding season, \(n_{af}\) = the number of adult females present in that breeding season shot in subsequent years, \(n_{f}\) = the number of fawns born in that breeding season shot in subsequent years, and \(n_{m}\) = the number of fawn-dam matches in the shot sample. In this paper, we assess the practicality and utility of this approach as a tool for estimating key population parameters of regularly harvested species such as deer.

METHODS

The wild red deer (\textit{Cervus elaphus scoticus}) of the 51 800 ha Murchison Mountains, Fiordland, New Zealand have been heavily controlled for over 40 years, with an estimated 424 deer remaining in early 2002 (0.8 deer/km\textsuperscript{2} overall, 1.3 deer/km\textsuperscript{2} of forest; Fraser and
Nugent 2003). This total includes new and unborn fawns, and was obtained using population reconstruction methods.

In 2003/04 we collected hair samples and the jawbone from most of the deer shot in the area. Females at least 2 y old in late 2002 (the fawning season) were classed as potential mothers, whilst those that had been born then were classed as their potential offspring.

DNA was extracted from the hairs using alkaline treatment, and amplified by PCR using up to 14 microsatellite markers, with the products run on an ABI3730 DNA Analyzer. Genotypes were analysed using GeneMapper™ Software Version 3.5. Mother-offspring pairs within this sample were then identified using AgResearch’s proprietary Pedigree Analysis Software. Where both members of a pair had been shot at the same place on the same day, the pair was deleted from the mark-recapture analysis because marking and recapture were not independent events. The total number of adult females present in late 2002 was then estimated using the modified Lincoln-Petersen index above.

RESULTS

The sample
A total of 118 deer were collected over the 1 July 2003 – 30 June 2004 period, with 8 or more DNA markers (genetic loci) identified in 93 of these. These 93 deer included 18 adult females (potential mothers) and 30 deer <18 months (potential offspring) (Fig. 1).

Parentage assignment and density estimation
Seven mother-offspring pairs were identified. Of these, three shot together were deleted from the MR analysis, leaving a total of 15 potential mothers, 27 potential offspring, and four mother-offspring pairs. From equation 1, we estimate there were 89 ± 64 (95%CL) adult females present in late 2002. Adding back in the three adult female deleted from the analysis give a total of 92. Using an unmodified Lincoln-Petersen index gives an estimate of 104.

The average distance between the kill locations of all possible adult–subadult pairs was 10.6 km compared with an average of just 0.9 km for the seven mother-offspring pair identified (actual distances were 0.0; 0.0; 0.0; 1.3; 1.3, 1.7, and 2.3; Figs. 1 and 2).

Fraser and Nugent (2003) estimated the breeding population size in late 2002 was 304 deer, and that the long-run average annual productivity was 34%, indicating that about 100 fawns would have been born then. Because the population is much reduced, about 95% of adult females are likely to have produced young (Challies 1985), so population reconstruction suggests that about 110 adult females were present, which is within 20% of the DNA-based estimates above.
Fig. 1. Kill locations for 18 female deer >2 years of age in December 2002 (filled squares for those matched to an offspring, unfilled squares for those not matched), and 30 of their potential offspring from the 2002/03 fawning season (filled large circles for those matched to mothers, unfilled large circles for unmatched offspring. The large circles for unmatched offspring are likely to encompass the location of their surviving mother.

Fig. 2. Frequency distribution of the distances between all possible pairings of potential mothers and offspring, showing separately the distances between the seven matched pairs (filled bars) and the unmatched pairs (unfilled bars).
DISCUSSION

This trial indicates that offspring can successfully be used to recapture their parents, and that the resulting estimate of adult female numbers (albeit imprecise) matches an estimate derived from population reconstruction. Here we have estimating adult female density simply to demonstrate the technique, but the same logic can be used to estimate numbers of adult males, and, in conjunction with demographic data, the numbers in other age-sex classes. The necessary genotyping techniques and software are increasingly available to managers as ‘black box’ technologies. Like any other density estimation tool, however, practical utility will depend on accuracy (freedom from bias), precision, and cost.

Accuracy: One peculiarity of the approach used here is that adults are often ‘recaptured’ before they themselves are ‘tagged’. Offspring are effectively tagged at conception, but as they cannot be independently sampled until they have left their mother’s care, the estimate of adult female numbers is, effectively, the number of adult females present after fawns are weaned. This will be biased if the mortality rate of females that do not raise fawns to independence differs from that for those that do. However, the number of non-reproductive females is low (<10%) in deer so this is unlikely to have a major effect on accuracy for this species.

In contrast, fawns can be obtained independently of their fathers immediately after conception (i.e. fathers can legitimately recaptured via foetuses obtained from shot females), so an MR estimate for males would, effectively, be an estimate of the number of potentially reproductive males present during the rut preceding the fawning season of interest. Because reproductive success amongst male deer is usually heavily skewed in favour of a few fully mature males, there is far greater potential for bias due to differential mortality between ‘tagged’ fathers and reproductively unsuccessful males.

Bias could also arise from errors in identification and parent-offspring matching. In this trial, no two deer sampled had the same set of markers, so there was no bias through duplication of tags. Parentage assignment creates a higher risk of matching errors, but in this study no offspring were assigned two mothers, suggesting the risk was low.

Failure to detect some alleles (allelic drop out) can also result in failure to identify a real match between parent and offspring, or to wrongly assign kinship between unrelated deer. These potential biases can be objectively assessed (McKelvey and Schwartz, 2004), or can be overcome by repeating analyses (Paetkau 2004). In this study, the short distances between mother-offspring pairs (Fig. 2) suggests the matches are correct.

Precision: One third of the breeding population was surveyed in this trial but only 4 useful mother-offspring matches were obtained. However, continued collection of deer in 2004/05 will increase the proportion of the population surveyed, especially the proportion ‘recaptured’. We expect a 2-year sample of c. 30 adult females and 50 offspring, with about 15 matches. This would give a similar estimate of c. 100 adult females but improve precision (95%CL) from 60 to 11 deer.

Cost: In this study, the cost per hair sample genotyped was about $NZ30, including parentage assignment. An extra $3000 was required to recover samples from helicopter-shot deer, while ground-shot material was (effectively) free. The average cost per sample was therefore c. $NZ55/sample, 12% of $NZ460 spent to kill each deer.
**Summary**: Both demographic and genetic measures suggest there were close to 100 adult females present in late 2002. Although the equivalent of one third of the breeding population is killed annually (Fraser and Nugent 2003), only about 20% of the adult female population (the reproductive engine of the population) is removed. Thus, although intergenerational mark-recapture as tested here does not directly produce an estimate of total population size, it does permit direct estimation of the minimum annual kill needed to reduce the population. It also identifies where the mothers of unmatched offspring are likely to be, so that control effort can be targeted at them.

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