

‘DEER IMPROVEMENT’ – GENETIC SELECTION IN A RECENTLY DOMESTICATED LIVESTOCK SPECIES.

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SUMMARY

‘Deer Improvement’ is a commercial red deer breeding program based in the South Island of New Zealand. The breeding program utilises progeny testing, AI, MOET, foetal aging, DNA parentage testing, computer tomography (CT) and ultrasound carcass scanning, to maximise genetic progress towards the objective of improving the profitability of venison production. Annual genetic trends (based on the industry DEERSelect breeding values) of +0.8 kg/yr weaning weight, +1.1kg/yr yearling weight, +0.6kg/yr carcass weight and -0.01 days/yr conception date have been realised and ‘Deer Improvement’ has bred 14 of the top 20 stags on the ‘DEERSelect’ replacement index (July 2013 across herd evaluation). This paper discusses the structure of the breeding program and estimates genetic parameters for growth and eye muscle area traits.

INTRODUCTION

First farmed in New Zealand in 1969, there are currently ~1.1 million farmed deer in New Zealand from which ~23 thousand tonnes of venison (~\$200 million) and 434 tonnes of deer velvet (soft antler, ~\$26 million) was exported in the 2010-11 financial year (DINZ 2011). With the short history of deer domestication, farming and breeding deer has its challenges. Firstly, there is little prior knowledge/research on the species that can be utilised; secondly, deer exhibit marked seasonality in growth with little or no growth during winter and in reproduction; and thirdly, they retain a lot of wild behaviours that can adversely affect production and/or farmer safety. The ‘Deer Improvement’ breeding program began in 2004 with the intention of breeding superior venison producing red deer for distribution to the industry both on the hoof and via artificial breeding. Due to the relatively low value of the velvet exports, no emphasis has been placed upon selection for these traits. The objective of this paper is to profile the ‘Deer Improvement’ breeding program, thus illustrating the difficulties encountered in the genetic improvement of this recently domesticated livestock species and how these difficulties were overcome.

MATERIALS AND METHODS

The ‘Deer Improvement’ breeding program started with the purchase of 20 stags in 2004 and 15 in 2005 from a range of bloodlines. These stags were selected on the basis of within herd growth breeding values and, as a consequence, were predominantly of the recently imported Eastern European subtype which is larger/faster growing than the English subtypes that were originally captured from the wild for farming purposes in NZ. The selected stags were then progeny tested (1000 AI over 4 farms) and the top 2% of the resulting yearling stags and 6% of the yearling hinds were selected to form a nucleus herd at Deer Improvement’s farm at Balfour (Southland). Currently, the farm has approximately 1000 hinds, of which the top 3% are used in an MOET program, the remaining 1st and 2nd fawners (2 & 3 year old hinds) are naturally mated and the mixed age older hinds are mated via a single round of artificial insemination (AI) and back up natural matings. The natural mating of the 1st and 2nd fawners allows the recording of conception date and avoids the lower AI conception rates that occur in these hind age groups. By selecting on conception date, the reproductive seasonality of red deer can be altered to allow more time for fawns to reach target weights before the venison price premiums expire in late spring and the next

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cohort of fawns are born (Archer and Amer 2009). This is currently the only reproductive trait for which breeding values are estimated in deer.

Physically matching red deer fawns to their mothers and accurately determining birth dates is difficult due to the 'wild' origins of the species. Hinds typically hide their new born offspring (Morris and Archer 2007) and human interaction at this time adversely affects fawn survival (Asher and Pearce 2002). As a consequence, the parentage of each live fawn is established via DNA parent matching (GeneMark, LIC, Hamilton, NZ) in conjunction with mating, foetal age and mob information. Each fawn was DNA sampled at approximately 3 months of age. Originally the parent matching utilised microsatellite markers, but these were upgraded to a SNP panel for the 2010 born and subsequent cohorts (for more detail, see Gudex *et al.* 2013). Knowledge of birth dates is required for the accurate evaluation of growth (Amer *et al.* 1999) and is determined from the date of artificial breeding and/or foetal ages determined by ultrasonic pregnancy scanning, plus the gestation length of red deer (232 days). Prior to foetal aging, the conception date of naturally born fawns was determined by rotating stag teams between mobs of hinds so that each possible mating could only have occurred in a specific 2 week period. Unfortunately, this process adversely affected conception rates and stags are difficult to handle during the mating season.

In addition to conception date, weights (up to 8 are recorded during the first year), lean meat yield, hind fertility, conformation and behaviour traits are also recorded/observed. The collection of lean meat measurements started in 2007 and involves yearling stags that have been identified as potential sires undergoing a computed tomography (CT) scan prior to reaching 100 kg live weight (limit of scanner) and since 2010, all fawns undergoing ultrasound eye muscle scanning in October. The ultrasound scans cannot be carried out before the CT scanning as the winter coat of deer is comprised of hollow hair which interferes with the ultrasound waves (Ward *et al.* 2010). Fertility is assessed through ultrasound pregnancy scanning and both conformation and behaviour are observed subjectively by the farm manager. To date, no objective measures of deer behaviour have been found that adequately describe temperament with sufficient variation and heritability to be utilised in a breed program (Archer *et al.* 2009).

Breeding values are estimated primarily by the national deer genetic evaluation system – DEERSelect (Archer 2005, Archer and Amer 2009), though a separate growth breeding value is also estimated internally. The internal breeding values are estimated from all weights collected prior to 1 year of age using a bespoke random regression program (only direct genetic effects fitted - D. Johnson *unpublished* 2006). These are used to assist the selection of 16 month old stags in mid to late February for semen collection before a DEERSelect evaluation including the latest fawn cohort and their weaning weights is available. The genetic parameters for growth up to 1 year of age and for eye muscle area (ultrasound) were estimated via a multivariate animal model (no maternal effects) fitted in ASReML (Gilmour *et al.* 2009). The model included dam age, age at measurement, contemporary group (mob & birth year) and sex as fixed effects and covariates. Live weight at the time of measurement was also included as a covariate for the eye muscle area.

Avoiding inbreeding and maximising genetic diversity is a challenge due to the small number of stags that comprised the founder population of the Eastern European subtype in NZ and also the extensive use of AI and MOET. Currently, multiple lines are maintained to allow crossing where necessary and outcrosses are actively sought and progeny tested. The average herd inbreeding coefficients published in this paper were calculated using the pedigree viewer software (Kinghorn 2011) and the mate selection function of this software was used for the first time in 2013.

RESULTS AND DISCUSSION

The age of the semen donor and farm were found to influence the conception rate to AI. On the Balfour farm in 2012, the average conception rate achieved using semen obtained from yearling stags was 49%, compared with the 77% obtained using semen from older stags. Variation

in AI conception rate between farms was observed by Deer Improvement's commercial AI service in 2012 to be between 63 and 83%. The flushing of hinds for embryo transfer revealed a hind age effect, with maiden hinds producing an average of 6 embryos per flush and older hinds (3 or 4 year old) an average of 12. Of the 247 embryos implanted in 2012, 70% were identified as being alive after tagging and DNA matching. The 2010 fawn cohort had parentage assigned using both the then new (in 2011) SNP marker panel and the existing microsatellite marker panel. The SNP panel was able to resolve both parents for 92% of the fawns and the microsatellite panel 68%. Utilising mating / mob / foetal age data allowed a further 2% to be resolved by the SNP panel and 4% by the microsatellite panel (Gudex *et al.* 2013). With 90 to 95% of fawns now being identified to their dams, it is possible to cull hinds that do not have progeny matched to them knowing that it is unlikely that the hind actually reared a fawn but the DNA failed to match them.

Table 1. Fawn traits recorded by 'Deer Improvement' & their heritability (\pm standard error)

Trait(s)	Units	First recorded	Number of animals recorded	Phenotypic standard deviation	Heritability
Weaning Weight	kg	2004	10700	7.58	0.392 \pm 0.025
Autumn Weight	kg	2004	9258	8.24	0.396 \pm 0.025
Spring Weight	kg	2004	8245	9.43	0.308 \pm 0.023
Yearling Weight	kg	2007	515	n/a - too few records	
Ultrasound Eye Muscle Scan*	mm & cm ³	2009	1227	3.07	0.246 \pm 0.061
Computer Tomography Scan	kg, mm & cm ²	2007	59	n/a - too few records	

* genetic parameters estimated from eye muscle area (cm³), other measurements recorded include eye muscle depth and width (both mm).

Since 2004, 'Deer Improvement' has collected over 90000 progeny, weight, foetal age and lean meat records from approximately 13500 animals on 7 farms (6 progeny test and 1 breeding farm). No culling is carried out prior to the collection of the spring weight and although DEERSelect estimates breeding values for yearling weight, spring weights are submitted as they are within the age range permissible for yearling weight and the timing allows the weights to be included in October DEERSelect across herd evaluation. This evaluation is crucial for the business as the breeding values are used in each year's sale catalogue. 'Deer Improvement' also considers that spring weight is a better breeding objective than yearling weight given that there are venison price premiums available in the spring, feed is more abundant and the new cohort of fawns has not yet been born (Archer and Amer 2009). Genetic parameters for and between some of the traits recorded in the fawns are displayed in tables 1 and 2. It is important to note that these genetic parameters are estimated only from 'Deer Improvement' data and that the estimates used by DEERSelect (not publically available for comparison) are obtained separately from a larger and more diverse dataset.

Table 2. Genetic (below diagonal) and phenotypic (above diagonal) correlations (\pm standard error) between the fawn traits recorded by 'Deer Improvement'

Weight	Wean	Autumn	Spring	EMA
Weaning		0.918 \pm 0.002	0.783 \pm 0.005	0.512 \pm 0.023
Autumn	0.984 \pm 0.004		0.843 \pm 0.004	0.507 \pm 0.107
Spring	0.906 \pm 0.015	0.924 \pm 0.012		0.443 \pm 0.027
EMA	0.573 \pm 0.105	0.605 \pm 0.107	0.444 \pm 0.126	

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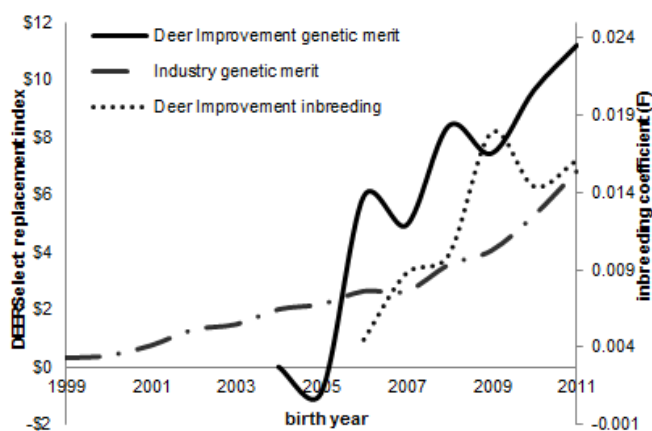


Figure 1. The genetic trend for the DEERSelect Replacement index for ‘Deer Improvement’ & across the whole industry. The inbreeding trend for ‘Deer Improvement’ is also displayed.

Since ‘Deer Improvement’ began in 2004, its’ genetic improvement in the DEERSelect replacement index has been over twice that of the industry average (\$1.60 vs \$0.69 - figure 1). While most of the extra gain was achieved during the initial screening and selection step (2004 to 2006), the genetic trend after 2006 has remained ahead of the industry average (\$1.05 vs. \$0.84 per year) but the difference is less pronounced. This gain is reflected in the July 2013 DEERSelect across herd evaluation sire list where 14 of the top 20 stags ranked on the replacement index were bred by ‘Deer Improvement’. Underpinning the increase in the index, weaning weights have risen by 0.8 kg per year, yearling weight up by 1.1kg per year (with ‘Deer Improvement’ 15 out of the top 20 sires), carcass weight up by 0.6kg per year (16 out of the top 20 sires) and conception date down by 0.01 days per year (9 out of the top 20 sires). The benefit to commercial farmers from this is that the increased growth and earlier conception date will make it easier to target finishing in the early spring where price premiums exist, there is greater feed availability and before the next cohort of fawns are born (Archer and Amer 2009). Balancing the genetic gains made has been a small increase in inbreeding within the herd, though it is impossible to determine how much of this increase is correlated with selection and how much is due to the more accurate and deeper pedigrees now available for the younger animals.

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