

**THE ALLIANCE CENTRAL PROGENY TEST (CPT): AN EVALUATION OF SHEEP MEAT GENETICS IN NEW ZEALAND**

**A.W. Campbell<sup>1</sup>, N.B. Jopson<sup>2</sup>, N. J. McLean<sup>1</sup>, K. Knowler<sup>1</sup>, M. Behrent<sup>3</sup>, T. Wilson<sup>3</sup>, G. Cruickshank<sup>4</sup>, C.M. Logan<sup>5</sup>, P.D. Muir<sup>6</sup>, and J.C. McEwan<sup>1</sup>**

<sup>1</sup>AgResearch, Invermay Agricultural Centre, Private Bag 50034, Mosgiel, New Zealand

<sup>2</sup>Abacus Biotech Limited, PO Box 5585, Dunedin, New Zealand

<sup>3</sup>Alliance Group Limited, 51 Don St, Invercargill, New Zealand

<sup>4</sup>Sheep Improvement Limited, PO Box 12146, Ahuriri, Napier, New Zealand (current address Genequest Limited, RD 12, Havelock North, New Zealand)

<sup>5</sup>Lincoln University, PO Box 84, Lincoln University, New Zealand

<sup>6</sup>On-Farm Research Ltd, PO Box 1142, Hastings, New Zealand

**SUMMARY**

The Alliance Central Progeny Test (CPT) was established in 2001 with the aims of improving the carcass dollar value of sires under the Alliance grading system and establishing genetic links among sire referencing schemes. Over the past two seasons, 52 sires from both terminal and dual purpose breeds have been evaluated for meat genetics at the AgResearch Woodlands farm and in 2003 the Lincoln University Ashley Dene farm. All progeny were slaughtered through two Alliance plants in slaughters at monthly intervals at a threshold liveweight of 34kg. Carcass measurements included cut yield (measured by both ViaScan grading and commercial primal cut bone-outs) eye muscle area, GR, meat pH, meat and fat colour and days to reach an 18kg carcass weight. These measurements were used to calculate three key indices; days to kill, meat value and a combined meat and growth index. Results showed significant variation among sires for all key traits and that no single ram or breed dominated the top of the indices or breeding values. Public availability of findings has resulted in increased interest from commercial farmers in using performance recorded data for ram selection.

**Keywords:** *Ovis aries*, progeny test, meat evaluation, breeding values

**INTRODUCTION**

Central progeny test (CPT) schemes have been running in other countries for many years (Fogarty *et al.* 2002; Bibé *et al.* 2002). In New Zealand, the standard form of genetic evaluation has been across-flock analysis within a breed or breed group prior to the Alliance CPT. A number of these groups have been operating for over 30 years. However, genetic links between sire reference groups within a breed, or across breeds have been poor or non-existent. In 2001, the Alliance CPT was established with the twofold aim of providing information to improve the value of carcasses under the current and future Alliance grading systems, and to provide across-breed genetic linkages so that ram breeders have better information to select rams to meet their own breeding objectives.

**MATERIALS AND METHODS**

As at the end of 2004, two full cycles of slaughter progeny evaluations have been completed. For the first cycle, all animals were grazed at AgResearch's Woodland Research Farm (WDL), while the second cycle included animals at Lincoln University's Ashley Dene Pastoral Systems Research Farm (AD). Over the two cycles, a total of 52 sires and 1009 progeny have been evaluated for meat and

growth traits, comprising 32 terminal sire and 20 dual purpose sires from 18 breeds. There were four link sires across years and three link sires across the two sites for the second cycle. Rams were nominated by various breeding groups either for artificial insemination (AI) or for natural mating. The ewe flock comprised either Coopworth ewes (WDL and AD) with a small number of  $\frac{1}{4}$  East Friesian x Coopworth ewes (18% of ewes at WDL)

**Farm management.** All ewes were synchronised using CIDRs, and approximately half were mated using AI. The remainder were naturally single sire mated over a period of one week. Sufficient ewes were allocated to each sire to achieve a minimum of 20 lambs (accuracy of selection of 0.79 for a trait with a heritability of 0.30) based on expected success rates at each of the sites. A total of 46 of the 52 sires had at least 20 progeny evaluated (range 13 to 59).

Single bearing ewes were separated from twin and triplet bearing ewes prior to lambing. At WDL the smallest lambs in a triplet set were mothered onto single bearing ewes, while at AD triplets were not separated. At AD ram lambs were kept entire, while at WDL ram lambs were made into cryptorchids. Liveweights of all lambs were recorded at birth and docking. Lambs were weaned in early to mid December at 12-14 weeks of age. Lambs were drafted for slaughter at monthly intervals with the first draft at weaning, allowing for a maximum of four drafts. A liveweight target of at least 34 kg was set to draft lambs, with all remaining lambs going for slaughter at the last draft.

**Slaughter procedure.** Lambs were processed over the same period for each slaughter (commencing at 9 am). On the day of slaughter, data were collected for yield grades (ViaScan and the Meat Board National Grading system), hot carcass weight, GR on both sides of the carcass and a visual carcass conformation score. ViaScan was used to predict weights of lean in the hindleg, loin and shoulder. The following day (24 hours post slaughter) carcass pH and fat colour were measured in the chiller prior to boning out. In the boning room, measurements included: cold carcass weight, eye muscle area (EMA) and eye muscle colour (after allowing 30 minutes for the cut surface to bloom).

**Data analysis.** BLUP breeding values were estimated across breeds for the sires using a sire model, as the CPT sires were assumed to be unrelated. The variance components used were estimated from the CPT data itself. Components were estimated using an animal model applying a Restricted Maximum Likelihood procedure with ASREML (Gilmour *et al.* 1999). The direct genetic effects were fitted as a random effect in all models. Breed was not fitted as there were insufficient sires in each breed to be considered representative. The maternal genetic effects were fitted as a random effect for weaning weight (the direct and maternal genetic effects were assumed to be uncorrelated). Weaning weight was fitted in a model including terms for age of dam, birth rearing rank and sex and birth day deviation as a covariate. Weight of lean in the three primal cuts and other carcass linear or area measurements were analysed in a model that included sex and slaughter mob as fixed effects and cold carcass weight as a covariate. Meat quality measures (e.g. pH, meat and fat colour) were analysed fitting sex and slaughter mob as fixed effects. Differences between sites and years were handled by scaling the raw values so that the variances were equalised. EBVs were estimated for weaning weight, carcass weight, dressing percent, days to slaughter, eye muscle area, GR, ViaScan shoulder, loin and hindleg lean weight, meat pH, meat colour and fat colour. Economic indices were determined for meat value (the sum of ViaScan shoulder, hindleg and loin EBV weighted at 1:2:4),

days to slaughter (economic value -\$0.15/day), and a combined meat and growth index weighted 1:1.22 for the meat and growth indices, respectively. Genetic and phenotypic correlations between traits were estimated, but additional sires are needed to improve the initial estimates.

## RESULTS

A summary of trait data is presented in Table 1. The average liveweight at weaning for slaughter progeny across years and sites was 31.4 kg. Carcass measurements were adjusted to an average carcass weight of 18.0kg, which required an average of 129 days to achieve.

**Table 1. A summary of trait data collected from the Alliance Central Progeny test progeny**

Trait	Mean	SD	CV%	$h^2$
<i>Live animal measures</i>				
Weaning weight(kg)	31.4	4.4	14.0	0.31 ± 0.08
<i>Carcass measurements</i>				
DTS <sup>1</sup> (days)	129	2.6	2.0	0.44 ± 0.08
Carcass weight (kg)	18.0	1.5	8.3	0.23 ± 0.10
Dressing percent <sup>1</sup>	45.0	1.7	3.8	0.49 ± 0.08
EMA <sup>1</sup> (cm <sup>2</sup> )	12.0	1.4	11.7	0.65 ± 0.08
GR <sup>1</sup> (mm)	7.3	2.9	39.7	0.40 ± 0.12
Shoulder lean <sup>1,2</sup> (kg)	3.22	0.24	7.5	0.45 ± 0.06
Loin lean <sup>1,2</sup> (kg)	2.26	0.18	8.0	0.27 ± 0.05
Hindleg lean <sup>1,2</sup> (kg)	3.76	0.27	7.2	0.41 ± 0.05
<i>Meat measurements<sup>3</sup></i>				
Meat pH (pH)	5.60	0.08	1.4	0.34 ± 0.07
Meat Colour (a*)	20.0	1.3	6.5	0.49 ± 0.08
Fat Colour (b*)	11.5	2.1	18.3	0.55 ± 0.08

DTS = days to slaughter., EMA = eye muscle area <sup>1</sup>Traits adjusted to an 18.0 kg carcass; <sup>2</sup>As determined by ViaScan grading; <sup>3</sup> Collected 24 hours post slaughter, with meat colour allowed 30 minutes to bloom.

Of all of the traits, weaning weight, EMA, GR and fat colour were by far the most variable (CV% of 14.0, 11.7, 39.7 and 18.3%, respectively). Only minimal variation (<2%) was observed in DTS and meat pH. The heritabilities estimated for the data were mostly moderate with only loin lean being less than 0.20. Dressing percent, EMA, meat colour and fat colour all had high heritability estimates (>0.45), with EMA in particular being very high at 0.65.

## DISCUSSION

In general, the heritabilities calculated from the data are somewhat higher than published estimates for comparable traits (Waldron *et al.* 1992; Fogarty *et al.* 2003). This was expected as the number of sires evaluated is still relatively low and estimates are likely to be biased upwards by between breed genetic variance. An effect of the high heritability estimates will be that the spread in breeding values would also be inflated, but this will not have changed the rankings between sires. EMA in particular was very much greater than the value of 0.31 reported by Waldron *et al.* (1992), although

similar to the 0.59 reported by Bidé *et al.* (2002). The most likely explanation is the confounding of breed with sire in the analysis for a trait that is key to terminal sire selection, and often not in the selection objective for dual purpose breeds. Interestingly, the heritability for EMA was markedly greater than for loin lean which was not found by Waldron *et al.* (1992), possibly because of the likely presence of a major gene for EMA which the grading equipment may not be fully recognising.

Examination of the breeding values revealed that there was considerable variation amongst sires, and that no one sire or breed dominated across all traits or indices. In presenting the results to industry and farmer groups, the importance of selecting rams appropriate to a farming environment and breeding objective was emphasised.

The Alliance CPT has now moved into a stage of maternal evaluation (mating 2004 and mating 2005) where ewe lambs produced from dual purpose sires have been retained. Standard maternal measurements relating to reproduction, wool growth and lamb survival will be collected as well as faecal egg count, first oestrus and gestation length. Carcass meat evaluation will be continued for all terminal sire progeny and the male progeny from dual purpose sires as part of the same programme.

#### **SUMMARY**

The programme has had several outcomes: the first being that the detailed recording of carcass traits in processing plants, including the results from ViaScan for individual cuts has highlighted that any existing NZ evaluation system needs to address the value of cuts rather than carcass based indices. Secondly, sire referencing groups and breeds are now becoming better linked genetically, thereby allowing national across breed evaluations to be undertaken. There have also been sire reference groups developed in breeds where little sire referencing has been done in the past. Finally, results for the top performing rams are publicly available which has led to an increase in interest from commercial farmers using information from performance recording systems to aid their ram selection decisions.

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