

## CONTRIBUTION OF CT SCANNING TO GENETIC IMPROVEMENT IN A TERMINAL SIRE SHEEP BREEDING PROGRAMME

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### INTRODUCTION

Use of computed tomography (CT) scanning provides a non-invasive means of measuring carcass compositional data in live animals (Young *et al.*, 1987). In sheep, incorporation of CT measurements with ultrasonic fat and muscle dimensions into selection indexes improved predicted rates of genetic gain in carcass lean and fat compared with indexes using liveweight and ultrasonic measurements alone (Simm and Dingwall, 1989; Jopson *et al.*, 1995).

The present paper compares the realised genetic trends in a terminal sire sheep breeding programme using selection indexes incorporating either liveweight and ultrasonically scanned fat depth and *longissimus dorsi* (LD) muscle dimensions, or additionally including CT scanned measurements.

### MATERIALS AND METHODS

The Landcorp Lamb Supreme terminal sire breeding programme operates as two genetically linked nucleus flocks, providing terminal sires to the specialist slaughter lamb sector of Landcorp's 500,000 commercial ewe population (Nicoll *et al.*, 1992; Nicoll *et al.*, 1997). Nucleus flock replacements of both sexes have been selected since 1990 on a Lean Growth Index (LGI) incorporating economically weighted breeding values (BVs) for the weights of lean meat and fat in the carcass, based on ultrasonic measures of fat depth at the 12<sup>th</sup> rib and LD depth and width at the same site. For nucleus animals born from 1995 onwards, a subset of ram lambs selected on ultrasound results (15% per year), were scanned at the *INNERVISION* CT facility using the reference site approach described by Young *et al.* (1996) to obtain weights of carcass lean and fat, and LD area. The four reference sites comprised of images through thoracic vertebra 7, lumbar vertebrae 1 and 4, and the caudal tip of the ischium with the hind legs held so as to include the femur-tibia articulation in the image.

Data were scaled within flock/sex/year to a constant mean so that phenotypic variation was similar for all groups. An across-flock/sex/year multi-trait model was used, accounting for the fixed effects of birth-rearing rank, age of dam and birth date, and random individual additive genetic effects (PEST; Groeneveld and Kovac, 1992). Eight predictor traits were included in the BV estimation (Table 1). Genetic parameter estimates were similar to those of Jopson *et al.* (1995), which were adapted from Waldron *et al.* (1992).

BVs were estimated for weights of lean meat (LEAN) and fat (FAT) in a standard 14.6 kg carcass, as well as for *LD* area (EMA) and liveweight at 8 months of age (LW8). LEAN and FAT were combined in the LGI as:  $LGI (\phi) = 600(LEAN) - 500(FAT)$ .

**Table 1. Predictor traits in breeding value estimation and number of records analysed to estimate genetic trends for birth years 1991 to 1999 inclusive**

| Predictor traits   | Number of records |
|--|-------------------|
| Weaning weight (kg)  | 18,367            |
| Liveweight at 8 months (kg)  | 14,628            |
| “C” ultrasonic fat depth at 8 months (mm)                                    | 12,747            |
| Ultrasonic <i>longissimus dorsi</i> depth at 8 months (mm)                   | 12,746            |
| Ultrasonic <i>longissimus dorsi</i> width at 8 months (mm)                   | 11,073            |
| CT weight of lean at 8 months (kg) <sup>A</sup>                              | 448               |
| CT weight of fat at 8 months (kg) <sup>A</sup>                               | 448               |
| CT <i>longissimus dorsi</i> area at 8 months (cm <sup>2</sup> ) <sup>A</sup> | 448               |

<sup>A</sup> CT measurements commenced in the 1995 birth year.

Mean BVs were calculated for each birth year from 1991 to 1999, and regressed on year to estimate annual rates of genetic gain when using liveweights and ultrasonic records as predictor traits in the LGI (1991-95; LW+US), and additionally incorporating CT records (1995-99; LW+US+CT). For the LGI and each trait BV, differences in the regression coefficients were used to compare the genetic trends resulting from the two sets of predictor traits.

## RESULTS AND DISCUSSION

Regression coefficients were positive ( $P < 0.05$ ) for LGI, LEAN, EMA and LW8 in both sets of predictor traits (Table 2). The coefficient for FAT was positive and not significant in the LW+US predictor set, but was negative for the LW+US+CT set ( $P < 0.05$ ).

**Table 2. Regression coefficients of mean breeding value on year using predictor traits of liveweights, ultrasound and CT scanning (LW+US+CT), or liveweights and ultrasound scanning (LW+US)**

| Breeding value         | Regression coefficients (/year) |              |            |
|------------------------|---------------------------------|--------------|------------|
|                        | LW+US+CT                        | LW+US        | Difference |
| LGI ( $\phi$ )         | 169.5±17.5 **                   | 100.7±26.9 * | 68.8 *     |
| LEAN (g)               | 226.7±18.2 **                   | 185.0±36.7 * | 41.7 NS    |
| FAT (g)                | -66.9±14.8 *                    | 20.7±17.6 NS | -87.6 ***  |
| EMA (cm <sup>2</sup> ) | 0.20±0.02 **                    | 0.21±0.03 ** | -0.01 NS   |
| LW8 (kg)               | 0.42±0.04 **                    | 0.46±0.11 *  | -0.04 NS   |

Differences between the regression coefficients for the LW+US+CT and LW+US sets of predictor traits indicated that incorporation of CT data enhanced the rate of genetic improvement in mean economic merit (LGI;  $P < 0.01$ ), mean genetic merit for FAT ( $P < 0.001$ ),

and only marginally for LEAN ( $P < 0.13$ ; Table 2). No differences were observed for EMA and LW8.

During the period under study, the mean selection intensity and generation interval of the Landcorp Lamb Supreme breeding programme was 1.65 units and 2.22 years respectively. Applying these values and the LGI described previously, to the data of Jopson *et al.* (1995; Table 2), enabled the differences in predicted genetic improvement between the LW+US+CT and LW+US predictor sets to be calculated: 94.7¢ (LGI), 89.3g (LEAN), -82.0g (FAT), 0.13cm<sup>2</sup> (EMA) and 0.00kg (LW8). These predicted differences were generally larger than the differences realised in the present study (Table 2) for LGI, LEAN and EMA, but similar for FAT and LW8. The estimates from Jopson *et al.* (1995) were based on the assumption that all animals were CT scanned, rather than the two-stage selection process used here (*i. e.*, 15% of ram lambs scanned). The difference between the two predictor sets would be expected to diminish somewhat under two-stage selection, although the magnitude of the reduction would not be expected to be large, given the estimated differences reported in Jopson *et al.* (1997), where two-stage selection was included in their simulation.

Extrapolation of the LW+US predictor set of regression equations from 1995 to 1999 indicated that incorporating CT measurements in the predictor traits over five years resulted in an accumulated benefit in mean economic merit of over NZ\$3 (Table 3). This resulted from an increase in LEAN and a comparatively large reduction in FAT. CT scanning had no influence on EMA and appeared to reduce the improvement in LW8.

The increased rate of genetic gain in LGI from including CT scanned data, has to be balanced against the additional costs of CT scanning. Jopson *et al.* (1997) reported a net economic benefit from including CT scanning in a simulated large-scale terminal sire sheep breeding programme. Under the assumptions used by those authors, the present results fall within the likely range of values predicted and would have achieved an internal rate of return in excess of 20%.

**Table 3. Predicted breeding value differences in birth year 1999 between using predictor traits of liveweights, ultrasound and CT scanning (LW+US+CT), and liveweights and ultrasound scanning (LW+US)**

| Breeding value         | LW+US+CT | LW+US | Difference |
|------------------------|----------|-------|------------|
| LGI (¢)                | 1007     | 690   | 317        |
| LEAN (g)               | 1540     | 1354  | 186        |
| FAT (g)                | -155     | 245   | -400       |
| EMA (cm <sup>2</sup> ) | 1.5      | 1.5   | 0.0        |
| LW8 (kg)               | 3.4      | 3.7   | -0.3       |

## CONCLUSIONS

Incorporating CT measurements into predictor sets for breeding value estimation in the Landcorp Lamb Supreme terminal sire sheep breeding programme resulted in improved genetic gain in Lean Growth Index and weight of fat in the carcass. However, rates of improvement were only marginally increased for weight of carcass lean meat, and were not increased for *LD* area and liveweight at 8 months of age. From a practical point of view, routine use of CT scanning over time can enhance the mean genetic merit for profit-earning ability in lamb production enterprises in New Zealand. This is of particular relevance in large-scaled, well-integrated breeding and production operations.

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