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## Genetic parameters for liveweight and live animal ultra-sound fat and eye muscle dimensions in a synthetic terminal sire breed

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### ABSTRACT

During 1993-97, approximately 7000 lambs were weighed at weaning (WW), re-weighted (LW) and ultrasonically scanned for subcutaneous fat depth (FD) and eye muscle dimensions (depth (MD) and width (MW)) at 6 months of age. Animals belonged to Landcorp's 'Lamb Supreme' terminal sire breeding programme, derived in 1989-91 from mainly Romney ewes mated to Romney, Wiltshire, Coopworth, Texel and Poll Dorset sires selected for fast growth and leanness. Records representing the selection criteria were analysed by univariate and multivariate animal-model REML methods able to take account of the effects of selection on variance components.

Heritabilities were higher for LW ( $0.33 \pm 0.03$ ) than WW ( $0.28 \pm 0.03$ ) and litter contributions (as a proportion of phenotypic variance) lower ( $0.29 \pm 0.02$  and  $0.44 \pm 0.02$ , respectively). Heritability estimates for all traits were similar in both sexes except for MW, which was higher in females ( $0.34 \pm 0.05$ ) than males ( $0.23 \pm 0.05$ ). Averaged across sexes, estimates were: FD ( $0.30 \pm 0.03$ ), MW ( $0.29 \pm 0.04$ ) and MD ( $0.33 \pm 0.03$ ), litter contributions being lower for FD ( $0.13 \pm 0.02$ ) than MW ( $0.22 \pm 0.01$ ) or MD ( $0.19 \pm 0.02$ ). MD was closely related genetically with MW ( $0.97 \pm 0.01$ ), but less closely associated with LW ( $0.44 \pm 0.06$ ) than was MW ( $0.57 \pm 0.05$ ). Both muscle traits showed similar genetic correlations with FD ( $0.48 \pm 0.07$  for MW;  $0.43 \pm 0.07$  for MD).

Parameter estimates indicated positive genetic trends for LW (regression of estimated breeding values on year of birth) more than two-fold higher than those previously published, and with little concomitant increase in FD.

**Keywords:** genetic parameters; lamb growth; ultrasound; fat and eye muscle.

### INTRODUCTION

Landcorp Farming Ltd manages in excess of 0.6(m) breeding ewes on more than 100 properties. More than 0.3(m) lambs are slaughtered annually. It is estimated that approximately 30% of these ewes could be mated to special-purpose terminal sires selected for improved meat production, the remaining being required to breed flock replacements (Nicoll *et al.* 1997). To respond to this opportunity, a terminal sire breeding programme was established in 1989 (Nicoll *et al.* 1992). Over 3 consecutive seasons intensively liveweight-screened (<1%) ewe hoggets (mainly Romney) were mated to Romney, Wiltshire, Coopworth, Texel and Poll Dorset sires selected for growth and leanness. The resulting progeny, regardless of breed ancestry, were used to establish the synthetic terminal sire-breeding scheme (Landcorp Lamb Supreme), comprising two flocks maintained in different pastoral environments. Both flocks were subsequently selected for an index of lean growth based on liveweight at 6 months of age and ultrasonic fat and eye muscle dimensions taken at the same time, as described by Nicoll *et al.* (1997). Genetic linkages between the two flocks were maintained by the use of common sires both within and across years. These allowed the two flocks to be analysed as a single breeding population to provide estimates of the heritabilities and genetic correlations of liveweight and ultrasound tissue dimensions, of relevance to the genetic improvement of carcass growth and composition through selection based on live animal indicators.

### MATERIALS AND METHODS

#### Data

Approximately 9 500 lambs (both flocks) had weaning weight records (taken at approximately 10 weeks) over the years 1992 to 1996. Due to deaths and some early culling for a variety of reasons, fewer lambs (approximately 7000 or 75%) were re-weighted at 6 months of age. Most (approximately 6500), were at the same time also measured, using B-mode ultrasound equipment, for muscle depth (MD) and width (MW), and fat depth over the eye muscle (FD) at the last thoracic rib, all measurements being taken by the same operator. Record numbers by trait are presented in Table 1.

#### Statistical analysis

Data were analysed by univariate and multivariate mixed-model REML methods fitting an animal model using ASREML (Gilmore 1997). Fixed effects associated with birth rank, age of dam, birthday and a contemporary group representing flock x year subclasses (absorbed), were included in the model, the corresponding measurements on males and female being regarded as different traits in most cases. Sex was included as part of the contemporary group definition for the more conventional analyses in which corresponding measurements on males and females were regarded as the same biological trait.

## RESULTS

### Univariate analyses

Variance components estimated by univariate analyses gave rise to the genetic and phenotypic parameters summarised in Table 1.

Direct heritability estimates ( $h^2_d$ ) were similar (0.2 to 0.3) for all traits with no consistent difference between estimates for rams versus ewes. The proportionate contribution to total phenotypic variation of maternal genetic effects ( $h^2_m$ ) and permanent environmental effects on progeny born in different litters from the same dam ( $p_e^2$ ), were small (<0.07). Environmental variation common to litter-

mates ( $c^2$ ) averaged only a little less than  $h^2_d$  but was more variable (0 to 0.40), being highest for WW (0.4), moderate for LW (0.23), lowest for FD and MD, and of similar average magnitude for all traits in rams and ewes.

Univariate direct heritabilities estimated in a model ignoring random effects contributing to  $h^2_m$  and  $p_e^2$  gave similar conclusions on the relative sizes of estimates of  $h^2_d$  and  $c^2$  for the five traits measured on each sex, the estimates of both these ratios being on average higher than those presented in Table 1 by approximately 0.05. Similar conclusions were reached from multivariate analyses ignoring the relatively small contributions from maternal genetic and permanent environmental terms.

**TABLE 1:** Estimates of phenotypic and genetic parameters by sex (F,M) for liveweight and ultrasonic dimensions, from univariate analyses of variance components.

		WW	LW	FD	MW	MD	
Direct heri. ( $h^2_d$ )	F		0.21±04	0.29±.05	0.21±.05	0.23±.05	0.28±.06
	M		0.27±.05	0.24±.06	0.30±.07	0.19±.05	0.24±.06
Matn. heri. ( $h^2_m$ )	F		0.04±.02	0.02±.02	0.06±.03	0.07±.04	0.03±.03
	M		0.03±.02	0.01±.02	0.01±.03	0±.03	0.01±.02
Perm.envir. ( $p_e^2$ )	F		0.03±.03	0.05±.03	0.03±.03	0±.04	0.05±.03
	M		0±.03	0.07±.03	0±.03	0.05±.04	0.07±.04
Litter envir. ( $c^2$ )	F		0.39±.03	0.28±.03	0.16±.05	0.16±.05	0.11±.05
	M		0.41±.03	0.18±.05	0±.06	0.16±.06	0.13±.06
Phen. variance	F		11.4	14.5	0.873	24.6	5.40
	M		18.3	25.7	0.880	23.8	6.17
Mean	F		23.9	35.9	3.23	58.7	26.7
	M		25.9	41.8	3.26	63.6	28.6
n	F		4961	3965	3801	3801	3800
	M		4486	2981	2703	2723	2723

WW = weaning weight; LW = liveweight at scanning; FD = fat depth (corresponding to carcass measurement C); MW = eye muscle width (carcass measurement A); MD = eye muscle depth (carcass measurement B).

**TABLE 2:** Estimates of phenotypic\* and genetic (below diagonal) correlations, heritabilities ( $h^2_d$ ) and common environmental litter effects ( $c^2$ ), from fitting animal and litter components separately for each sex in multivariate runs including WW and LW

		WW	LW	FD	MW	MD	$\sigma_p$	$h^2_d$	$c^2$
Female	WW	-	0.73	0.39	0.49	0.44	14.4	0.27	0.44
	LW	0.85	-	0.50	0.60	0.59	15.3	0.35	0.33
	FD	0.34	0.44	-	0.41	0.42	0.942	0.30	0.22
	MW	0.46	0.55	0.37	-	0.82	27.3	0.34	0.21
	MD	0.36	0.49	0.42	0.97	-	5.95	0.35	0.20
			±.04	±.09	±.10	±.02		±.04	±.04
Male	WW	-	0.70	0.34	0.47	0.43	18.4	0.29	0.43
	LW	0.90	-	0.45	0.58	0.57	25.6	0.30	0.24
	FD	0.47	0.61	-	0.36	0.35	0.924	0.33	0.05
	MW	0.60	0.58	0.58	-	0.82	25.9	0.23	0.20
	MD	0.36	0.39	0.44	0.97	-	6.76	0.30	0.18
			±.04	±.10	±.12	±.02		±.05	±.05
		±.11	±.11	±.13			±.06	±.05	

\* s.e. phenotypic correlations <.02

### Multivariate analyses

Results are presented in Table 2. Heritability estimates for the corresponding trait measured in each sex were essentially the same, females higher than males for LW and MD (by 0.05) and MW (by 0.11).

Very similar  $h^2_d$  and  $c^2$  estimates were obtained from multivariate and univariate runs of a model fitting only animals and litters as additional components to the random error term, suggesting little advantage from accommodating the effects of early selection using a multivariate approach to data analysis in this case.

### Genetic trends

Combined estimates across both sexes were used to derive average genetic trends across birth years. They were derived from four three-trait multivariate analyses, each including WW and LW. Weighted across the two flocks the average genetic trends in estimated breeding values (EBV) were  $0.76 \pm 0.010$  kg/yr for WW,  $1.00 \pm 0.012$  kg/yr for LW,  $0.49 \pm 0.0064$  mm/yr for MW,  $1.06 \pm 0.013$  mm/yr for MD and  $0.003 \pm 0.002$  (ns) mm/yr for FD. For all traits except FD, these average trends were significantly different for the two flocks; the flock with the lower initial average EBV (in 1992) showing the highest trend in each case. Thus, the flocks tended to become more similar genetically with time, presumably as a result of sire-linkages giving rise to progeny in both flocks from the 1994 birth year onwards.

## DISCUSSION

There was little increase in phenotypic variation in liveweight from weaning to scanning despite the 55% increase in average weight; phenotypic coefficients of variation decreased from 16% to 11%. Coefficients of variation were highest for FD (28%) and lowest for MD (9%) and MW (8%). Genetic parameters were within the range of, but had lower standard errors, than published estimates (Fogarty 1995; Clarke *et al.* 1997). Muscle width was less heritable than MD (by 0.05), most notably in males (by 0.11). Otherwise the direct heritabilities of scan dimensions were similar ( $\sim 0.3$ ), although pooled estimates across both sexes gave higher estimates for MW (0.36) and MD (0.40) than the averages of those reported in Table 2, but not for other traits. In contrast to the conclusions of Connington *et al.* (1995), small, but important, maternal contributions to scan dimensions were found.

Both muscle dimensions showed similar phenotypic correlations with LW (0.6) and with FD (0.4). Genetic correlations were similar to the corresponding phenotypic estimates, except for WW with LW (+0.16), MD with MW (+0.16) and LW with MD (-0.11). A high genetic correla-

tion was found between MD and MW, suggesting that the same genes are involved in the expression of both traits, and in contrast to the estimates for carcass data presented by Waldron *et al.* (1992). Both muscle dimensions showed similar genetic correlations with FD. Muscle depth was less related to LW than was MW, as found by Waldron *et al.* (1992), although their estimates (for carcass data) were lower.

The average estimated genetic trend for LW (1 kg/yr) using genetic parameter estimates from within the breeding programme was more than two-fold higher than that published by Nicoll *et al.* (1997) for these same flocks. As noted by these authors, this response was accompanied by an increase in estimated lean content, eye muscle cross-sectional area and fat content. Our results indicate that muscle depth was more responsive than muscle width and that fat depth tended to remain the same despite the liveweight response achieved. These results presumably relate to the indexing algorithm used to evaluate animals for selection, and the phenotypic and genetic parameters implicit in its derivation. Selection indices to reduce fat depth and estimated carcass fat content while improving carcass growth (and hence lean growth rate), have been discussed by Clarke *et al.* (1991 and 1997).

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