HERITABILITIES, GENETIC AND PHENOTYPIC CORRELATIONS FOR CARCASS TRAITS AND ULTRASONIC FAT DEPTH OF SHEEP

A.C. Parratt[1], C.M. Burt[1], G.L. Bennett[2], J.N. Clarke[1], A.H. Kirton[1] and A.L. Rae[3]

[1] Ruakura Animal Research Station, Private Bag, Hamilton, New Zealand

[2] Production Systems Research Unit, Roman L. Hruska U.S. Meat Animal Research Center, Clay Center, Nebraska 68933, U.S.A.

[3] Department of Animal Science, Massey University, Palmerston North, New Zealand

INTRODUCTION

Over the last 10 years there has been considerable interest in New Zealand and Australia in genetic manipulation of carcass composition of sheep to produce leaner, heavier carcasses. Selection responses are affected by accuracy of measurement of the selection criterion and its genetic relationship with carcass leanness or fat content. New Zealand research has in the past used the ether-extract fat, protein and water contents of the carcass as baseline measurements for most trial work. Although useful for biochemical and nutritional experiments, this method does not address the important questions of variation in tissue distribution and rates of deposition at various depots. These questions are important to producers, meat companies and scientists for planning marketing strategies, grading and genetic improvement programmes. In an attempt to answer these questions and in particular genetic relationships among carcass traits, a large carcass dissection trial was undertaken at Ruakura between 1982-1984 in conjunction with N.Z. Meat Producers Board and several breed societies.

MATERIALS AND METHODS

Over a two year period 1431 lamb carcasses representing 110 sire groups from four breeds were slaughtered at the Ruakura research abattoir. Prior to slaughter all individuals were weighed and fat depth was assessed ultrasonically using AIDD-NZ probe. Assessment was made at the carcass C location. After slaughter, carcasses were split along the mid-line, half of each carcass was subject to full butcher's knife dissection whilst the remaining half was completely minced and analysed chemically for protein, fat and water. One aspect of this research is reported here, namely; heritabilities, genetic and phenotypic correlations of carcass traits.

Heritabilities, genetic and phenotypic correlations were obtained by Henderson's Method 3. Data were corrected for age of dam, breed, sex, year, birth/rearing rank. Data were analysed with covariates of either age at slaughter or pre-slaughter weight.

RESULTS AND DISCUSSIONS

Estimates for traits of major importance are presented in Table 1. Heritabilities, genetic and phenotypic correlations between body weight and carcass fat depths are similar to other studies (Wolf et al. 1981), however estimates for ultrasonic fat depth (UFD) are lower than have been reported elsewhere (Bennett et al. 1983). Correlations and heritabilities for dissected tissues are similar to values from U.K. The favourable correlations between fat depth measurements and total carcass components are encouraging for selection programmes incorporating these traits in their objectives to decrease total fat and increase total lean, though present methods of assessing backfat depth in the live animal are of concern. Results presented here suggest that present selection programmes at Ruakura, utilising progeny test for carcass composition, will produce accurate and reliable responses in carcass composition. Associated studies have shown considerable operator variation over time and could explain lower estimates reported here.

Table 1 Heritabilities, genetic and phenotypic correlations[1] for body weight, carcass depths and total body components. Analyses at a constant age

	Weights		Fat depths			Dissected Tissue			Percentage		
Trait[2]	SLW	HCW	GR	CarC	UFD	TL	TF	TB	PCL	PCF	PCB
SLW	0.22	0.96	0.65	0.39	0.37	0.88	0.79	0.69	-0.31	0.49	-0.51
HCW	0.96	0.24	0.70	0.41	0.40	0.91	0.84	0.69	-0.34	0.54	-0.58
GR	0.53	0.60	0.19	0.54	0.42	0.55	0.79	0.29	-0.51	0.69	-0.68
CarC	0.47	0.45	0.75	0.23	0.55	0.30	0.53	0.18	-0.41	0.50	-0.40
UFD	0.59	0.53	0.52	1.12	0.09	0.33	0.45	0.24	-0.30	0.39	-0.31
TL	0.81	0.87	0.29	0.20	0.35	0.31	0.69	0.46	-0.03	0.37	-0.46
TF	0.71	0.68	0.73	0.83	0.65	0.30	0.25	0.47	-0.62	0.91	-0.70
TB	0.83	0.75	0.06	0.17	0.14	0.75	0.28	0.27	-0.20	0.19	-0.13
PCL	-0.14	-0.07	-0.42	-0.58	-0.26	0.39	-0.74	0.09	0.55	-0.71	0.29
PCF	0.71	0.26	0.57	0.81	0.52	-0.16	0.88	-0.16	-0.93	0.36	-0.64
PCB	-0.26	-0.41	-0.71	-0.53	-0.57	-0.27	-0.66	0.26	0.27	-0.61	0.25

[1] Genetic correlations below diagonal, phenotypic correlations above and heritabilities on the diagonal

[2] Slaughter Weight (SWT), Hot Carcass Weight (HCW), GR (GR), Carcass C (CarC), Ultrasonic fat depth (UFD), dissected total lean (TL), dissected total fat (TF), dissected bone (TB), percent lean (PCL), percent fat (PCF), and percent bone (PCB).

Results for dissected lean tissues are presented in more detail in Table 2. These results show high heritabilities for dissected lean tissue and that there is significant independence among tissue depots. Though selection for total components (TF, TL and TB) would result in favourable changes in body composition, these changes would not be uniform across all depots. This confirms previous concerns expressed by researchers, that compositional changes in tissue distribution should be monitored in long term selection programmes.

Table 2. Heritabilities, genetic and phenotypic correlations for dissected lean tissue. Analyses at constant carcass wt[1]

	FL	RL	LL	LeL	SHL	SKL	TL	INTF	SubF	TF	TB
FL	0.21	0.21	0.37	0.24	0.26	0.32	0.56	-0.16	-0.19	-0.21	0.27
RL	0.17	0.22	0.25	0.32	0.25	0.00	0.58	0.03	-0.05	-0.02	0.17
LL	0.58	0.74	0.27	0.31	0.27	0.23	0.55	-0.29	-0.29	-0.33	0.23
LeL	0.09	0.44	0.66	0.49	0.42	0.27	0.76	-0.39	-0.36	-0.42	0.27
SHL	0.45	0.57	0.68	0.72	0.50	0.18	0.67	-0.21	-0.36	-0.34	0.23
SKL	0.49	0.12	0.48	0.52	0.58	0.25	0.36	-0.34	-0.35	-0.40	0.36
TL	0.52	0.66	0.91	0.89	0.91	0.65	0.45	-0.29	-0.36	-0.38	0.42
INTF	-0.35	-0.52	-0.81	-0.56	-0.49	-0.37	-0.71	0.32	0.52	0.84	-0.25
SubF	-0.52	-0.57	-0.79	-0.59	-0.57	-0.50	-0.79	0.84	0.49	0.90	-0.27
TF	-0.46	-0.57	-0.83	-0.60	0.56	-0.46	-0.78	0.94	0.97	0.50	-0.30
TB	-0.15	0.15	0.57	0.14	0.17	0.45	0.27	-0.41	-0.44	-0.45	0.23

[1] Heritabilities on diagonal, genetic correlations below diagonal, phenotypic correlations above diagonal

Flap Lean (FL), Rack Lean (RL), Loin Lean (LL), Leg Lean (LeL), Shoulder Lean (ShL), Shank lean (SKL), Total Lean (TL), Intramuscular Fat (IntF), Subcutaneous Fat (SubF), Total fat (TF), Total Bone (TB).

ACKNOWLEDGEMENTS

The authors wish to express their appreciation of financial support of N.Z.M.P.B. and New Zealand sheep breed societies. Also, we are grateful for the long hours of dissection undertaken by the Ruakura Dissection Unit under the careful guidance of Grant Woods. Special thanks to M. Fraser (Wairakei), Department of Lands and Survey and the many helpers at Genetics, Ruakura.

REFERENCES

Bennett, G.L., Meyer, H.H., Bass, J.J., Clarke, J.N. and Rae, A.L. 1983. In "Summaries of papers given at Overfatness/Lean Meat Workshop" Lincoln College, June, 1983 : 11-12.

Wolf, B.T., Smith, C., King, J.W.B. and Nicholson, D. 1981. Anim. Prod. 32: 1-7.