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THE ESTIMATION OF GENETIC AND PHENOTYPIC
PARAMETERS FOR A SYNTHETIC LEAN MEAT
AND WOOL SHEEP BREED

A thesis presented in partial fulfilment
of the requirements for a degree of
Master of Agricultural Science at
Massey University.

BRUCE ROBERT SOUTHEY

1989

ABSTRACT

A study of the inheritance and interrelationships between wool, growth and carcass traits was carried out as part of the development of a large lean white-faced sire breed. Cross-bred progeny, from three sire breeds (Romney, Dorset, and Border Leicester) mated to Romney ewes, provided information on carcass fatness and composition, liveweight, ultra-sonic backfat depth, fleeceweight and objective measures of fleece characteristics. An overall total ~~a total~~ of 28 sires and 765 progeny were used to collect this information.

The analysis of half-sib records was carried out under an assumption of positive assortive mating on ultra-sonic backfat depth. It was considered that any bias, relative to random mating, was minimal due to incomplete assortment, dominance, epistasis and crossbreeding influences. It was assumed that the progeny were only half-sibs in relation to breed, and thus the between-breed component only estimated one-quarter of the between-breed variance. Further, the sires were nested within their respective breeds. The data corrected for the significant non-genetic effects before the variance and covariance components were estimated.

In general, the estimates of the Within-breed heritability for the wool and growth traits ranged from 0.1 to 0.6 and were similar to literature values. The carcass estimates were higher than literature values in most cases. The incorporation of the between-breed component resulted in the between-breed heritability being larger in magnitude.

This may have been due to non-additive genetic effects, such as heterosis, in the between-breed component. The ratio of the between-breed genetic variance to the total genetic variance indicated that there was large between-breed variation in liveweight and wool traits and small variation in the carcass traits.

The total genetic and total phenotypic correlations presented here suggest that selection for lean growth and wool production can be accomplished by the joint selection of liveweight and greasy fleeceweight. Expected correlated responses in the other traits would include: a) increase liveweight and fleeceweight at all ages, increase ultra-sonic fat depth, GR measurement, lean content, clean fleeceweight, staple length, mean fibre diameter, clean scoured yield, and b) decrease the carcass C measurement, decrease bone and fat contents, and loose wool bulk.

Selection against ultra-sonic backfat depth would result in leaner animals at a constant weight. But the moderately positive correlations with liveweight and fleeceweight would appear to negate the associated advantage of a reduction in carcass fatness.

ACKNOWLEDGEMENTS

My deepest gratitude is extended to my supervisors, Dr. H.T. Blair and Prof. A.L. Rae, for their considerable time, effort and support.

I am deeply indebted to Carol Burt for her excellent help. I am also indebted to Mr. J. Dobbie. Special thanks to Dr. A.C. Parratt, Dr C.A. Morris, and the other people at Ruakura who have helped. Also thanks must go to the farm staff of data collection and to the staff at the wool laboratories.

I also extend my thanks to the staff in the Department of Animal Science, particularly Prof. R.D. Anderson for their time, effort and help in various matters. And also to the postgraduates in Animal Science, especially Carlos Sosa, Meng Jiao Shi and John Rendel, for their friendship, help and other matters during my study. A special thanks go to my friends Murray, Jane, Cindy and the others for many things.

Finally, I extend a extremely special thankyou (to say the least) to my parents and family for their support, encouragement etc. in my studies.

(And to those I have forgotten TA.)

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CHAPTER ONE

INTRODUCTION

Although Captain Cook unsuccessfully introduced a pair of Merino sheep in 1772, it was another century later before sheep were permanently established New Zealand (Miller, 1950). Initially, wool was the main sheep product that was exported, until the development of refrigerated shipping in the 1880's (Miller, 1950). The effect on the New Zealand sheep industry was the development of the present day two-tier structure: On the hill country and poorer lands, the dual-purpose breeds (such as the Romney) are farmed mainly for wool production, with some meat production mainly from the cull male lambs. On the more productive lands, cull ewes are often crossed with terminal meat sire breeds (such as the Southdown) to produce first cross lambs for meat production. This type of structure has the important consequences of 1) breed complementarity, 2) cost spreading, 3) specialised parental breed improvement, 4) heterosis in the lamb progeny (Clarke, 1982).

The sheep breeding objectives for this structure have generally been based on a market price system where the weight of the product have a major influence. The introduction of objective measurement may provide price differentials within certain measurements that are economically advantageous. It is therefore necessary to have an understanding of the inheritance and interrelationships between these measurements in order to develop future breeding plans.

An important aspect of future sheep breeding plans is the potential breeding objective of dual meat and wool production. There are extremely few reports of this dual-production, yet there have been reports that have compared sire breeds on the basis of meat and wool production. The present breeds available in NZ show a wide range of performance, but when meat and wool production are combined, this variation is greatly reduced (Clarke and Meyer, 1982). This variation is further reduced when the body weight differences are taken into account (Clarke and Meyer, 1982). From experimental results, it is apparent that first-cross individuals would offer economic advantages, though heterosis, (Clarke and Meyer, 1982; Clarke et al, 1982), but would require the inferior purebreds to maintain the system. One possible solution is to develop synthetic breeds that would retain some superiority over the purebreds.

This study provides information on the inheritance and inter-relationships of liveweight, fleeceweight, objective measurement wool quality characteristics, carcass dimension and quality characteristics and the ultra-sonic measurement of back fatness in a cross-bred population.

CHAPTER TWO

LITERATURE REVIEW

2.1 WOOL PRODUCTION

Sheep breeds can be classified into three broad selection groups based on the type of wool produced: the fine wool apparel breeds, eg the Merino; the general purpose wool breeds, eg the Romney; and the speciality carpet wool breeds, eg the Drysdale (NZSAP, 1974). Each of these groups will have particular breeding objectives and associated selection criteria. Of particular importance in the New Zealand wool industry is the general purpose breeds, mainly the Romney and it's crosses, whose wool is identified as the 'Romcross' wools. The Romcross wool has been described by Elliott (1985) as typically having a fibre diameter in the range of 33 to 37 microns, being essentially free from medullation, kemp and pigmented fibres, have a white and bright colour, and tends to show some lustre. In addition, this wool has a reputation of high processing efficiency and in blends to improve yarn strength due to good fibre length and good soundness (Elliott, 1985).

Many studies (eg NZSAP, 1974; Clarke and Rae, 1976 and 1977; Rae, 1982; Morris et al, 1982; McPherson, 1982; Wickham and McPherson, 1985) have highlighted the importance of increasing fleeceweight as a breeding objective, and using greasy fleeceweight as an selection criterion. While there are differences attributed to birth rank, sex and age at measurement (Table 2.1), the population

estimates of the heritability of fleeceweight (Table 2.2) are generally around 0.3 to 0.4. These estimates indicate that fleeceweight would respond favourably to selection. However while the experimental results of selection experiments tend to confirm this, the estimates of the realised heritability of fleeceweight are often slightly smaller than in the base population (McGuirk et al, 1986). It has been suggested that in these experiments, the selection differential has been overestimated (Blair, 1986; James, 1986).

McPherson (1982) and Wickham and McPherson (1985) have reviewed the importance of wool quality traits in potential breeding objectives and as selection criteria in the New Zealand Romney. It was concluded that on the basis on the available information, there was no need to select for any wool quality traits. However this may change under the introduction of the 'sale by description' system based on objective measurement (Simpson, 1986). The main objective measures that are under consideration for the New Zealand system are:- yield, staple and fibre length, clean scoured colour, fibre diameter, staple strength, loose wool bulk (Elliott, 1986). The inclusion of these and other measures in breeding plans will depend on the clear price differentials within each of the measures (Stanton, 1987).

Table 2.1: Estimates of the Effects of Birth Rank and
Regression on Age for Fleeceweight in the
New Zealand Romney.

Trait ¹	Birth rank ² (s-t)	Regression on age	Reference
lfwt	0.27	0.02	Hight and Jury (1971)
lfwt	0.26	-0.10	Tait (1983)
hfw	0.66	0.02	Lundie (1971)
hfw	0.14	0.02	Hight and Jury (1971)
hfw	0.10	0.01	Baker <u>et al</u> (1974)
hfw	0.02	-0.01	Tait (1983)

1)lfwt=lamb fleeceweight; hfw=hogget greasy fleeceweight,

2)s=single; t=twin.

Table 2.2: Estimates of Heritability of Fleeceweight
and Wool Quality Traits in the NZ Romney

a) Hogget Fleeceweight

Estimate	Reference
0.32	Rae (1958)
0.23	Lundie (1971)
0.29	Baker <u>et al</u> (1974)
0.57	Baker <u>et al</u> (1974)
0.38-0.61	Chopra (1978)
0.3	Tait (1983)
0.74	McEwan <u>et al</u> (1984)
0.25-0.56	Newman (1988)

b) Clean Fleeceweight

Estimate	Reference
0.23-0.36	Blair (1981)
0.29-0.53	Newman (1988)

c) Staple length

Estimate	Reference
0.48	Rae (1958)
0.54-0.63	Chopra (1978)
0.09-0.33	Blair (1981)
0.37	Tait (1983)
0.34-0.57	Newman (1988)

(cont.)

Table 2.2 (Cont.)

d)Mean Fibre Diameter

Estimate	Reference
0.34-0.87	Chopra (1978)
0.21-0.64	Blair (1981)
0.26-0.62	Newman (1988)

e)Yield

Estimate	Reference
0.19-0.53	Chopra (1978)
0.04-0.40	Blair (1981)
0.19-0.34	Newman (1988)

f)Tristimulus Y-Z value (COLOUR)

Estimate	Reference
0.13	Bigham <u>et al</u> (1983)

g)Loose Wool Bulk

Estimate	Reference
0.41	Bigham <u>et al</u> (1983)
0.50	Sumner <u>et al</u> (1989)

Table 2.3: The Genetic (g) and Phenotypic (p) Correlations
of Fleeceweight and Wool Quality Traits in the
NZ Romney

a)The Results of Bigham et al (1983)

Traits ¹	gfwt		bulk		colour	
	g	p	g	p	g	p
cfwt	0.95	0.91	-0.23	-0.23	0.30	0.22
yield	-0.25	-0.09	-0.83	-0.49	-0.55	-0.01
stlen	0.32	0.29	-0.67	-0.50	0.36	0.17
mfd	0.55	0.41	-0.13	0.01	0.53	0.14
bulk	-0.06	-0.03	---	---	-0.04	-0.11
colour	0.49	0.23	---	---	---	---

b)Other Experimental Results

Traits		g	p	
lfwt	hfwt	0.59	0.32	Tait (1983)
	stlen	0.35	0.08	Tait (1983)
hfwt	cfwt	1.00	0.94	Blair (1981)
	cfwt	0.97	---	Newman (1988)
	yield	0.14	---	Chopra (1978)
	yield	0.36	0.13	Blair (1981)
	yield	0.48	---	Newman (1988)
	stlen	0.58	---	Chopra (1978)
	stlen	0.58	0.49	Blair (1981)
	stlen	0.74	0.37	Tait (1983)
	stlen	0.78	---	Newman (1988)

(cont.)

Table 2.3 (Cont.)

	mfd	0.81	---	Chopra (1978)
	mfd	0.82	0.50	Blair (1981)
	mfd	0.71	---	Newman (1988)
cfwt	stlen	0.85	0.53	Blair (1981)
	stlen	0.70	---	Newman (1988)
	yield	0.42	0.45	Blair (1981)
	yield	0.65	---	Newman (1988)
	mfd	0.82	0.52	Blair (1981)
	mfd	0.94	---	Newman (1988)
yield	mfd	0.33	---	Chopra (1978)
	mfd	0.27	0.21	Blair (1981)
	mfd	0.45	---	Newman (1988)
	stlen	0.03	---	Chopra (1978)
	stlen	---	0.29	Blair (1981)
	stlen	0.46	---	Newman (1988)
stlen	mfd	0.41	---	Chopra (1978)
	mfd	0.79	0.37	Blair (1981)
	mfd	0.46	---	Newman (1988)

1)gfwf=hogget greasy fleeceweight, cfwt=hogget clean fleeceweight

yield=clean scoured yield, stlen= staple length

mfd= mean fibre diameter, bulk= loose wool bulk

colour= clean wool colour (Trimstimulus Y-Z value)

There are two wool quality traits, clean colour of wool and loose wool bulk, that may be of future importance to the wool industry and hence, their evaluation in breeding objectives for wool production. Since the tristimulus values for scoured wool represent the best colour of a lot of wool, any dyeing or other chemical treatments (with the exception of bleaching) would lead to lower tristimulus values (Elliott, 1986). This means that unless the wool is bleached, then the tristimulus values cannot be increased above their 'base' colour, and which could present difficulties to certain dye colours, such as pastel shades (Elliott, 1986). However, with the introduction of objective measurement for yellowness, it is necessary to be able to determine whether or not the cause is genetic, and therefore selectable. The present measurement system, and also environmental influences, involve the degrading effects of wet processes involving heat, such as steaming and overdrying. These result in an increase in yellowness and have generally been appreciated by the industry (Elliott, 1986). In addition, there is an apparently wide genetic variation in the susceptibility of fleeces to discolouration. Wilkinson and Aitken (1985) reported that the resistant fleeces designated by a predictive test, were always lower in fleece yellowness than the susceptible fleeces under different conditions used to promote discolouration.

The practical importance of the bulkness of wool has been discussed for many years (Simpson, 1986), and has been associated with many desirable properties in the final product (Elliott, 1986). Elliott (1984) reported that price premiums for subjectively assessed bulk in Perendale wools was not large nor consistent. It was suggested

that there was the possibility of specialist lines to take advantage of any price premiums that may occasionally occur. While there is little information on bulk, Binnie and Elliott (1986) concluded that bulk would respond rapidly to direct selection, particularly if there is a major gene present as indicated by Bigham et al (1985). But the results of Sumner et al (1989) could not confirm this major gene hypothesis.

The limited evidence available on inheritance of the various objective measurements of the wool characteristics (Table 2.2) suggest that these are at least moderately heritable and respond to selection in a similar manner to fleeceweight (Davis and McGuirk, 1987). This maybe offset by desirable correlations observed between fleeceweight and certain objective measures. Bigham et al (1983) reported that the correlations obtained (Table 2.3) indicated that selection for increased fleeceweight in the Romney, would result in the correlated increases of staple length, yield, mean fibre diameter, colour yellowness, and a correlated decrease in loose wool bulk. In experimental results for increased fleeceweight, the realised relationships have generally agreed with the expectations, though the actual magnitude has varied (Turner et al, 1970; Mortimer, 1987; Davis and McGuirk, 1987).

2.2 GROWTH AND MEAT PRODUCTION

2.2.1 Growth and the Carcass

The increase in liveweight of an animal follows a distinct pattern from the earliest embryonic stage to a genetically determined mature size (Taylor, 1982). This is indicated by the estimates of heritability of liveweight (Table 2.4), and also the high correlations between liveweight at different ages (Table 2.5). The majority of heritability estimates for early liveweight are low and are usually attributed to the importance of maternal effects, especially in milk production, and to competition between littermates (Baker et al, 1979). The estimates generally increase as the animal grows older, since performance becomes more dependent on the genotype and less dependant on the maternal environment. The effect of the maternal environment is also evident in the estimates of the effects of birth rank and age at measurement in liveweight (Table 2.6).

There is limited evidence on the inheritance and interrelationships of the carcass dimensions and tissues. In general, the estimates of heritability (Table 2.7) for measures of carcass dimensions and carcass tissues are low to moderate, and low estimates for the carcass quality traits (Botkin et al, 1969; Wolf et al, 1981). The correlations in Table 2.8 reported by Wolf et al (1981) and Parratt et al (1987a) probably reflect the growth of the body as a whole, and the relative growth of the fat, lean and bone tissues to slaughter.

Table 2.4:Heritability Estimates of Liveweight and
Ultra-sonic Backfat Depth at Different
Ages in the Romney or Romney Derived Breeds

Time	Estimate	Reference
Weaning	0.30	Ch'ang and Rae (1970)
	0.35	Lundie (1971)
	0.18	Baker <u>et al</u> (1974)
	0.02	Baker <u>et al</u> (1974)
	0.13	Baker <u>et al</u> 1979)
	0.10	Baker <u>et al</u> 1979)
	0.10	Tait (1983)
	0.15	McEwan <u>et al</u> (1984)
	0.04-0.22	Newman (1988)
Febuary	0.22	Baker <u>et al</u> (1974)
	0.27	Baker <u>et al</u> (1979)
March	0.34	McEwan <u>et al</u> (1984)
Apirl	0.26	Baker <u>et al</u> (1979)
May	0.46	Baker <u>et al</u> (1979)
July	0.38	Baker <u>et al</u> (1979)
October	0.29	Baker <u>et al</u> (1979)
November	0.51	Ch'ang and Rae (1970)
	0.22	Baker <u>et al</u> (1974)
	0.21-0.72	Chopra (1978)
	0.15	Tait (1983)
	0.49	McEwan <u>et al</u> (1984)
	0.05-0.46	Newman (1988)

(cont.)

Table 2.4 (Cont.)

Ultra-sonic Backfat Depth

Time	Estimate	Reference
April	0.17	Beatson (1987)
July	0.34	Beatson (1987)
October	0.16	Beatson (1987)
May	0.23	McEwan <u>et al</u> (1984)
November	0.45	McEwan <u>et al</u> (1984)
Index P	0.28	McEwan <u>et al</u> (1984)
Index G	0.24	McEwan <u>et al</u> (1984)

Table 2.5: Estimates of Genetic (g) and Phenotypic (p)
Correlations Between Liveweight Traits in
the NZ Romney

Trait ¹		Correlation		Reference
		g	p	
wwt	Feb	0.78	0.69	Baker <u>et al</u> (1979)
	Apr	0.80	0.80	Tait (1983)
	Jun	0.38	0.68	Tait (1983)
	Jul	0.74	0.57	Baker <u>et al</u> (1979)
	Jug	0.49	0.71	Tait (1983)
	Oct	0.77	0.49	Baker <u>et al</u> (1979)
	Nov	0.74	0.52	Blair (1981)
	Nov	0.45	0.57	Tait (1983)
Feb	Jul	0.87	0.72	Baker <u>et al</u> (1979)
	Oct	0.87	0.60	Baker <u>et al</u> (1979)
Apr	Jun	0.86	0.83	Tait (1983)
	Aug	0.91	0.85	Tait (1983)
	Nov	0.84	0.68	Tait (1983)
Jun	Aug	0.97	0.86	Tait (1983)
	Nov	0.84	0.69	Tait (1983)
Jul	Oct	0.97	0.83	Baker <u>et al</u> (1979)
Aug	Nov	0.84	0.74	Tait (1983)

1) wwt=weaning weight; Feb=February weight;

Apr=April weight; Jun=June weight;

Jul=July weight; Aug=August weight;

Oct=October weight; Nov=November weight.

Table 2.6: Some Estimates of Nongenetic
Effects for the NZ Romney

a)Weaning Weight

Birth Rank ¹	Sex ²	Reg. ³	Reference
4.20	----	0.16	Wewala (1984)
3.7-4.7	1.6-22.9	0.12-0.21	Jury <u>et al</u> (1979)
4.23-4.63	2.19-2.98	0.17-0.28	Ch'ang and Rae (1961)
3.77	1.54	0.16	Newman <u>et al</u> (1983)
4.2	1.9	0.12	Baker <u>et al</u> (1974)
3.45	1.68 [^]	0.27	Hight and Jury (1971)
3.59	1.68	-0.21 - -0.12	Tait (1983)
9.72	----	0.37	Lundie (1971)

b)Liveweight at different months

Month	Birth rank ¹	Reg. ³	Reference
Febuary	3.10	0.13	Baker <u>et al</u> (1974)
April	2.24	-0.13	Tait (1983)
June	1.75	-0.13	Tait (1983)
July	2.10	0.01	Baker <u>et al</u> (1974)
August	1.74	-0.12	Tait (1983)
November	1.05	-0.10	Tait (1983)
November	2.10	0.01	Baker <u>et al</u> (1974)

1)Single-twin;

2)Ram-ewe, expect for [^] where wether-ewe

3)Regresion on age.

Table 2.7: Some Estimates of Heritability
of Carcass Traits

Carcass Weight	0.02	Bowman <u>et al</u> (1968)
	0.11	Bowman and Hendy (1972)
	0.33	Botkin <u>et al</u> (1969)
	0.11	Thorsteinsson and Bjornssen (1982)
	0.03	Mohamed (1976)
	0.24	Parratt <u>et al</u> (1987a)
Carcass length	0.50	Botkin <u>et al</u> (1969)
	0.45	Bouix <u>et al</u> (1982)
	0.31	Bouix <u>et al</u> (1982)
	0.45	Bouix <u>et al</u> (1982)
	0.59	Thorsteinsson and Bjornssen (1982)
	0.79	Cotterill and Roberts (1976)
	0.34	Mohamed (1976)
Tissue GR	0.19	Parratt <u>et al</u> (1987a)
Carcass C	0.40	Bowman and Hendy (1972)
	0.31	Bouix <u>et al</u> (1982)
	0.34	Bouix <u>et al</u> (1982)
	0.14	Bouix <u>et al</u> (1982)
	0.26	Bradford and Surlock (1972)
	0.32	Thorsteinsson and Bjornssen (1982)
	0.23	Parratt <u>et al</u> (1987a)
	0.51	Botkin <u>et al</u> (1969)
	0.37	Cotterill and Roberts (1976)
	0.21	Wolf <u>et al</u> (1981)
	0.31	Mohamed (1976)

(cont.)

Table 2.7 (Cont.)

Total Tissue Weight:

Lean	0.39	Botkin <u>et al</u> (1969)
	0.31	Parratt <u>et al</u> (1987a)
Bone	0.28	Botkin <u>et al</u> (1969)
	0.27	Parratt <u>et al</u> (1987a)
Total Fat	0.44	Botkin <u>et al</u> (1969)
	0.37	Wolf <u>et al</u> (1981)
	0.25	Parratt <u>et al</u> (1987a)
Subcutaneous fat	0.36	Wolf <u>et al</u> (1981)
Intermuscular fat	0.37	Wolf <u>et al</u> (1981)

Percentage Tissue:

Fat	0.54	Botkin <u>et al</u> (1969)
	0.54	Johnson <u>et al</u> (1968)
	0.36	Parratt <u>et al</u> (1987a)
	0.17	Munson (1966)
Bone	0.23	Botkin <u>et al</u> (1969)
	0.16	Wolf <u>et al</u> (1981)
	0.25	Parratt <u>et al</u> (1987a)
	0.64	Munson (1966)
Lean	0.40	Botkin <u>et al</u> (1969)
	0.41	Wolf <u>et al</u> (1981)
	0.55	Parratt <u>et al</u> (1987a)
	0.17	Munson (1966)

Table 2.8: The Estimates of Genetic and Phenotypic

Correlations¹ Parratt et al (1987a),
and, Wolf et al (1981).

a) Parratt et al (1987a)

Trait ²	slw	hcw	gr	c	ufd	tl	tf	tb	pcl	pcf	pcb
slw	---	0.96	0.65	0.39	0.37	0.88	0.79	0.69	-0.31	0.49	-0.51
hcw	0.96	--	0.70	0.41	0.40	0.91	0.84	0.69	-0.34	0.54	-0.58
gr	0.53	0.60	---	0.54	0.42	0.55	0.79	0.29	-0.51	0.69	-0.68
c	0.47	0.45	0.75	--	0.55	0.30	0.53	0.18	-0.41	0.50	-0.40
ufd	0.59	0.53	0.52	1.12	--	0.33	0.45	0.24	-0.30	0.39	-0.31
tl	0.81	0.87	0.29	0.20	0.35	--	0.69	0.46	-0.03	0.37	-0.46
tf	0.71	0.68	0.73	0.83	0.65	0.30	--	0.47	-0.62	0.91	-0.70
tb	0.83	0.75	0.06	0.17	0.14	0.75	0.28	--	-0.20	0.19	-0.13
pcl	-0.14	-0.07	-0.42	-0.58	-0.26	0.39	-0.74	0.09	--	-0.71	0.29
pcf	0.71	0.26	0.57	0.81	0.52	-0.16	0.88	-0.16	-0.93	---	-0.64
pcb	-0.26	-0.41	-0.71	-0.53	-0.57	-0.27	-0.66	0.26	0.27	-0.61	---

Table 2.8 (Cont.)b) Wolf et al (1981)

Trait ³	pcl	pcb	ptf	psf	pif	c
pl	---	0.67	-0.98	-0.98	-0.75	-0.80
pb	0.41	---	-0.82	-0.31	-0.77	-0.14
ptf	-0.93	-0.71	---	0.92	0.83	0.74
psf	-0.83	-0.64	0.91	---	0.57	0.80
pif	-0.77	-0.47	0.79	0.50	---	0.50
c	-0.61	-0.50	0.68	0.69	0.43	---

1) genetic below diagonal, phenotypic above,

2) slw=pre-slaughter liveweight, hcw=hot carcass weight, ufd=ultra-sonic
c

fat depth, tl= total lean weight, tf=total fat weight, tb=total bone weight, pcl=percent lean, pcf=percent fat, pcb=percent bone.

3) pcl=percent lean, pcb=percent bone, ptf=percent total fat, psf=percent subcutaneous fat, pif=percent intermuscular fat.

For a given breed and sex, the growth of the lean and bone tissues follow an almost predictable pattern (Berg, 1982). Since both of these tissues have lower growth rate than the body as a whole, they decline in proportion as the animal grows older, although some studies have reported an almost constant muscle growth relative to liveweight (Butterfield, 1988). The fat tissue has a higher growth rate than the body as a whole and is the most variable tissue with greatest influence of the composition of the carcass (Berg, 1982; Butterfield, 1988). With consumer resistance to fatness, it is necessary to examine the fat depots of importance, where there is variation and breed differences

Over 60% of the total body fat can be found in the carcass depots and this is almost divided evenly between intermuscular and subcutaneous fat depots (Butterfield, 1988). There is apparently little variation in the actual distribution of fat between these two depots (Thompson et al, 1979; Kempster, 1980). However, there is a large difference in partitioning of fat tissue between these carcass fat depots and non-carcass fat depots (Wood et al, 1980; Butler-Hogg, 1984; Butterfield et al, 1985).

There have been various reports, briefly summarised by Thompson (1985), of breed differences in total and percent fat when compared at the same weight. When these breed differences are expressed in terms of mature size, the breed differences are removed at the same proportion of mature size (McClelland et al, 1976). This is assuming that the growth of the carcass components are the same in both breeds (Butterfield, 1988). Fat distribution between the carcass fat depots appears to follow a closely defined path, such that at equal fat

depot weights, breed differences are small (Kempster, 1980). However, fat partitioning between the carcass and noncarcass depots shows more variation and suggests that substantial differences have occurred in the evolution and selection of domestic breeds (Kempster, 1980). While comparisons at an equal degree of maturity reduces the differences, there may be between breed differences at equal maturity due to genetic variation and variation in fatness and hormone levels (Butterfield, 1988). Wood (1982) suggested that the breed differences in the partitioning of fat may be due to differences in the intrinsic metabolism between subcutaneous and abdominal fat tissues.

2.2.2 Selection Indices For Leanness.

Morris et al (1982) derived and evaluated selection indices for breeding objectives for the various sheep breed selection groups. For the dual-purpose wool breeds the ewe progeny could be either kept as replacements or used as dams in the production of cross-bred lambs for slaughter. But the distinction between these objectives were considered to be small in terms of the genetic changes in practice. It was considered that the major objectives, in decreasing importance, were the number of lambs weaned, fleeceweight and weaning weight. In the terminal sire breeds, the main selection trait was liveweight at sale. However, the importance of carcass quality and wool-pull returns were unknown, due to the limited evidence available.

Without considering economic values, Bennett and Clarke (1984) calculated theoretical responses for lean growth rate (LGR), and fat percent adjusted for weight (APF). The incorporation of fat depth

measurement reduced fatness and increased carcass weight, but there was little improvement over selecting on liveweight alone. Frazer (1982) suggested that the average lamb carcass exported in 1982 (13.5kg carcass weight and about 24% fat) should be increased to 15kg carcass weight with no more than 24% fat. This would be most rapidly achieved by selection against APF. The quickest method was progeny testing on the ribfat depth, 8.5 years. In comparison, selection based on the sire's own ultra-sonic fat depth would take 12 years.

Rae (1984) investigated the potential implementation of a breeding program to bring about the desired changes in weight and leanness in lamb meat. Selection indices were constructed using corrected Autumn liveweight and fat depth measured by the ultra-sonic probe (UFD). The indices were then used to predict an objective function based on the relative economic values of 140 for carcass weight and -42 for the GR measurement. Under the necessary assumptions, the annual genetic change was calculated at a constant age for each index. Compared to selection based solely on liveweight, the full index would result in slightly smaller increases in GR and percent chemical fat. In order to restrict the change in GR to zero, a relative economic value of -55 for GR would be required. Selection against UFD corrected for liveweight (based on the phenotypic relationship) would reduce fatness at the same age. If UFD was omitted from the index, the overall gain would be reduced by at least 15% in most of the indices calculated. The ultra-sonic fat depth may also eliminate the need to slaughter progeny for carcass assessment. The additional gain over slaughtering no progeny from slaughtering 5, 10 and 15 progeny out of 20, was 6%, 10% and 14%, respectively. Depending

on the accuracy of the genetic parameter estimates, there would appear to be little advantage in slaughtering progeny.

Economic selection indices for lean meat production in terminal sire breeds were developed under New Zealand conditions by Simm (1986) and Simm et al (1987) and under British conditions by Parratt and Simm (1987). These selection indices were compared to an aggregate breeding value (ABV) of carcass lean weight and total carcass fat weight. Using British data, Parratt and Simm (1987) constructed indices involving birth weight, growth rate, and either X-ray computer tomography (CT) or ultra-sonic fat depth (UFD). The correlations between the ABV and the index of birth weight and growth rate with either CT or UFD were 0.4 and 0.38, respectively. There was very little difference using both birth weight and growth rate (0.38), or growth rate alone (0.37). With New Zealand data, Simm (1986) and Simm et al (1987) constructed an index using liveweight, UFD, and ultra-sonic muscle depth (UMD). The correlation of the full index and the ABV was 0.23. This dropped to 0.18, 0.15 and 0.07, when UMD, UFD, and UMD and UFD, were omitted, respectively. The reductions in this index were much larger than for the British indices, probably due to the relatively strong economic penalty for overfat carcasses in New Zealand.

2.2.3 Direct Selection for leanness

At Massey University, Southdown ewes were screened from various sources to form divergent selection lines for weight-adjusted ultra-sonic backfat depth. It was apparent that there was a tendency

for the animals selected for fatness to be shorter in body length and body height than the lean line animals, at a constant weight (Purchas et al, 1981; Purchas et al, 1982). After 8 years of selection, Solis (1988) reported a difference of 1.7mm and 2.0mm between lines for the rams and ewes respectively. The estimates of heritability were low to moderate, with the daughter-dam regression method being higher than the parental half-sib method. The lean line was found to be significantly longer in body length (Solis, 1988) and carcass length (Kadim, 1988). The correlated responses on birth weight and growth rate were generally small with no consistent effects. Unpublished results have suggested no effect on wool production. From an analysis of carcass information, Kadim (1988) reported that at a constant carcass side weight, the lean line contained significantly more muscle and bone and less fat than the fat line. But there no differences in the actual weight distribution and the placement of muscle, fat and bone components. While there was no difference in the actual fat distribution between the various fat depots, at a constant carcass side weight, the fat line had more subcutaneous fat, more intra-muscular fat, and less intermuscular fat than the lean line. This has resulted in a greater change in the fat depth C than at any other depots.

Fennessy et al (1982) reported the setting up of divergently selected Coopworth lines for high or low ultra-sonic backfat depth. But due to a number of reasons, it was considered that this initial selection was ineffective. Further details on the lines were given by Fennessy et al (1987). Fennessy et al (1982) screened rams from the two lines and these were mated to Perendale ewes to provide carcass information on the male progeny. Of the carcass fat measures, only

carcass C and the fat depth at the shoulder region were significantly different and no differences in carcass GR or total chemical fat were found. Fennessy et al, (1987) reported that there had been significant responses after five years of selection. The results suggested that when compared to the control, the progeny from lean rams were leaner with greater eye-muscle area at the same carcass weight. While the lean line lambs had higher birth weights than the fat line and the subsequent growth rates were similar between lines.

Bennett et al (1983a) reported the results of Suffolk and Southdown rams selected on the basis of weight-adjusted ultra-sonic fat depth, crossed over Perendale ewes. Overall, there was a difference in the carcass C measurement and a smaller, probably nonsignificant, difference in the GR measurement.

2.3 THE RELATIONSHIP BETWEEN WOOL, MEAT AND GROWTH TRAITS

2.3.1 The Relationship Between Growth And Wool Traits.

In the New Zealand Romney, the genetic and phenotypic correlations between liveweight and wool traits (Table 2.9) indicate that there is an low to moderate relationship. In experimental work, Johnson (1981) and Johnson and Dobbie (1987) have shown that Romney animals selected for hogget greasy fleeceweight had significant positive correlated responses in weaning weight, lamb fleeceweight, hogget body weight, clean staple length and mean fibre diameter. Selection for hogget body weight led to increases in weaning weight and hogget fleeceweight, with smaller positive changes in the other fleece

traits. Blair (1981) observed that selection for increased fleeceweight in Romneys caused increases in clean fleeceweight, staple length, mean fibre diameter, clean scoured yield, weaning weight and hogget liveweight, relative to the controls.

In selection experiments for high clean wool weight in Australian Merinos, the correlated responses in body weight ranged from zero to positive and in experiments for low wool production, body weight decreased (Turner, 1972; Davis and McGuirk, 1987). But in experiments for high body weight, there has been no correlated response in fleeceweight, yet in low body weight selection, wool weight decreased (Turner, 1972; Davis and McGuirk, 1987).

Heydenrych et al (1984) reported that in South African Merinos that selection for clean fleeceweight had increased body weight at all ages from 42 days to 18 months, compared to the controls. However, the magnitude of the response had varied between the years reported.

Table 2.9: Some Estimates of the Genetic (g) and
Phenotypic (p) Correlations of Liveweight
and Wool Traits in the NZ Romney

Liveweight Traits ¹		g	p	
weaning	lfwt	0.81	0.65	Tait (1983)
	hfwt	0.39	0.25	Baker <u>et al</u> (1979)
	hfwt	0.13	0.35	Blair (1981)
	hfwt	0.48	0.26	Tait (1983)
	cfwt	0.27	0.32	Blair (1981)
	yield	---	0.01	Blair (1981)
	stlen	0.55	0.03	Blair (1981)
	stlen	0.02	-0.02	Tait (1983)
	mfd	-0.09	0.17	Blair (1981)
February	hfwt	0.37	0.38	Baker <u>et al</u> (1979)
April	lfwt	0.26	0.46	Tait (1983)
	hfwt	0.70	0.44	Tait (1983)
	stlen	0.18	0.12	Tait (1983)
June	lfwt	0.26	0.46	Tait (1983)
	hfwt	0.70	0.44	Tait (1983)
	stlen	0.18	0.17	Tait (1983)
July	hfwt	0.40	0.52	Baker <u>et al</u> (1979)
August	lfwt	0.28	0.48	Tait (1983)
	hfwt	0.60	0.48	Tait (1983)
	stlen	0.07	0.15	Tait (1983)
October	hfwt	0.41	0.44	Baker <u>et al</u> (1979)
(cont.)				

Table 2.9 (Cont.)

November	lfwt	0.32	0.35	Tait (1983)
	hfw	0.11	---	Chopra (1978)
	hfw	0.64	0.47	Blair (1981)
	hfw	0.54	0.47	Tait (1983)
	hfw	0.11	---	Newman (1988)
	cfwt	0.74	0.41	Blair (1981)
	cfwt	-0.02	---	Newman (1988)
	yield	0.06	---	Chopra 1978
	yield	---	-0.03	Blair (1981)
	yield	0.31	---	Newman (1988)
	stlen	0.50	---	Chopra 1978
	stlen	0.77	0.18	Blair (1981)
	stlen	0.45	0.18	Tait (1983)
	stlen	-0.08	---	Newman (1988)
	mfd	0.02	---	Chopra (1978)
	mfd	0.21	0.21	Blair (1981)
	mfd	-0.12	---	Newman (1988)

1)lfwt=lamb fleeceweight; hfw=hogget fleeceweight;

cfwt=clean hogget fleeceweight;

stlen=staple length; mfd=mean fibre diameter.

2.3.2 The Relationship Between Wool And Carcass Traits.

In the USA, Johnson et al (1968) reported the heritability estimates and correlations of meat and wool traits in purebred Rambouillet, Columbia and Corriedale lambs at a 50kg liveweight. The genetic correlations were generally moderate to highly negative between the carcass traits and either clean fleeceweight or staple length. More comprehensive results shown in Table 2.10 were presented by Botkin et al (1971). Average daily gain, weaning weight and carcass weight all showed negative genetic correlations with fleeceweight and there appears to be a low negative phenotypic correlation between meat and wool. The ultra-sonic backfat depth showed little association with any of the other live traits. The relationship between greasy fleeceweight and the UFD was slightly positive, but clean fleeceweight, staple length and weaning weight were negatively correlated. Both fleeceweight and staple length were negatively correlated with carcass weight, carcass length and fat depth. Fleeceweight was also lowly and negatively correlated to bone weight, but staple length was low and positively correlated to bone weight. Fat weight was low to moderately and positively correlated to fleeceweight, but staple length and fat weight were negatively correlated.

Table 2.10:The Genetic Correlations Between Fleeceweight,
Liveweight and Carcass Traits From
Botkin et al (1971).

Traits ¹	gfw	cfw	stlen	wwt	ufd
cfw	0.77	--	---	---	---
stlen	0.38	0.87	---	---	---
wwt	-0.23	-0.24	-0.18	---	---
ufd	0.08	-0.13	-0.11	-0.12	---
ccwgt	-0.67	-0.67	-0.19	-0.17	0.22
clen	-0.50	-0.41	-0.12	0.21	-0.30
c	-0.04	-0.29	-0.25	-0.25	0.69
fwgt	0.47	0.11	0.07	-0.45	0.43
bwgt	-0.33	-0.12	0.15	-0.39	-0.56

1)gfw=greasy fleeceweight; cfw=clean fleeceweight;

stlen=staple length; wwt=weaning weight;

ufd=ultra-sonic backfat depth; ccwgt=carcass weight;

clen=carcass length; c=carcass c; fwgt=total fat weight;

bwgt=total bone weight.

McEwan et al (1984) examined the correlated effects of selection for increased production on ultra-sonic backfat depth in Romney ewe lambs from 5 self-contained selection lines. The lines were for number of lambs born, 100-day weight, hogget fleeceweight, a production index of the previous traits, and a control, and selection had been undertaken for 9 years. The realised genetic correlations suggested that selection for the number of lambs born greatly reduced fatness, and probably accounted for the moderate negative relationship between fatness and the production index. Selection for increased hogget fleeceweight had little or no influence on fatness, but at a constant age, the selection line animals tended to be slightly fatter than their controls. Animals selected for 100-day weight were heavier and fatter at constant age, but leaner at a particular weight.

The parental half-sib estimates of the genetic and phenotypic correlations calculated by McEwan et al (1984) for UFD with liveweight and hogget fleeceweight are shown in Table 2.11. Age adjusted UFD had a low to moderate positive relationship with liveweight. The genetic correlation between the age adjusted-UFD and hogget fleeceweight was negative, but the phenotypic correlation was positive. The UFD adjusted for the phenotypic relationship between UFD and liveweight (Index P) had moderately negative genetic correlations with liveweight and fleeceweight and negligible phenotypic correlations. When UFD was adjusted for the genetic relationship between UFD and liveweight (Index G), the correlations that were obtained were variable. With liveweight there was lowly negative genetic, but lowly positive phenotypic correlations, hogget fleeceweight was moderately negative for the genetic but negligible for the phenotypic correlations.

Table 2.11: The Genetic (g) and Phenotypic (p) Correlations
of Ultra-sonic Backfat Depth with Liveweight and
Fleeceweight From McEwan et al (1984)

Trait ⁴	May UFD ¹		Index P ²		Index G ³	
	g	p	g	p	g	p
wwt	0.17	0.27	-0.44	-0.05	-0.16	0.11
Mar	0.30	0.37	-0.34	-0.03	-0.04	0.18
May	0.33	0.44	-0.30	0.00	0.00	0.23
Nov	0.17	0.30	-0.43	-0.09	-0.16	0.10
hfwt	-0.35	0.17	-0.68	-0.09	-0.55	0.04
index p	0.80	0.90	--	---	---	---
index g	0.94	0.97	0.95	0.97	---	---
ufd n	0.97	0.52	0.79	0.36	0.90	0.45

1)May UFD= May ultra-sonic backfat depth at a constant age

2)Index P= May ultra-sonic backfat depth corrected for the
phenotypic correlation between liveweight and UFD

3)Index P= May ultra-sonic backfat depth corrected for the
genetic correlation between liveweight and UFD

4)wwt=weaning weight; March=March liveweight; May=May

liveweight Nov=November liveweight;

hfwt=hogget fleeceweight;

ufd n=November ultra-sonic backfat depth.

Parratt et al (1987b) investigated the correlated changes in ultra-sonic backfat depth in Romney ewe lambs from various selection lines and their respective controls, for body weight, fleeceweight, dam's fertility and an index of fertility and body weight. The deviations were presented from the contemporary controls and showed a wide variation even among lines of the same selection criteria. The lines for high hogget body weight were both heavier and fatter at the same age, but at a constant weight there was a trend for the high lines to be leaner than the controls. Selection for high hogget fleeceweight at a constant age resulted in heavier animals, but at a constant weight they were lighter than their controls. The high fleeceweight animals were leaner at a constant weight, but were fatter at a constant age at the 14-month UFD scan.

2.3.3 Selection For High And Low Weaning Weight

Wood et al (1980) reported that at any given weight genetically large animals tend to be less fat. From the various between breed studies, an increase in mature weight would be expected to result in leaner animals at a given weight (Thompson, 1985). The selection for high and low weaning weight in Australian Merinos has led to increased and decreased weaning weight in each line, in subsequent generations (Pattie, 1965a) and also at other ages including maturity (Pattie, 1965b; Pattie and Williams, 1966 and 1967; Thompson et al, 1985a).

Thompson et al (1985a) reported that the high and low weaning weight Merino lines had similar growth efficiency, although there was a

tendency for the high line to be higher in gross food conversion at the same weight than the low line. But there was no difference at the same age. Thompson et al (1985b) reported that there was no difference between lines in the maturity coefficients for protein and muscle. Fat was found to be late maturing in the low line relative to high line, whereas bone was early maturing in the low line relative to the high line. At the same body weight, the different maturing rates for fat resulted in a crossover between the strains in the proportion of fat in the body, at around 20 kg liveweight. At the heavier body weights, the high line had a lower proportion of fat than the control, which was lower than the low line. The higher levels of fat in the high line at the earlier ages was suggested by Thompson et al (1985b) to be due to the greater milk production of the high line dams (Pattie, 1965b). The effect of greater milk production would be to increase the milk intake of the lambs, and increase the amount of body fat in the lamb (Black, 1974).

There have been significant correlated changes in fleeceweight in these Merino lines selected for high and low weaning weight (Pattie, 1965b; Pattie and Williams, 1967; Davis, 1987). There have been confusing and conflicting reports of the associated changes in the various components of fleeceweight, but it is apparent that the main significant deviation has been in surface area. Davis (1987) explained an observed 10% correlated response in greasy fleeceweight, over the controls after 10 generations of selection, as an 30% increase in skin surface area, which resulted in a 10% increase in the skin area for wool production. The changes in the other wool traits have been variable and generally negligible, and were considered

as responses to the change in fleeceweight (Davis, 1987).

2.4 POSITIVE ASSORTATIVE MATING

2.4.1 Basic Theory

The previous genetic and phenotypic parameters have, in general, been estimated under the assumption of random mating. However, it is possible that the population is under either of two types of non-random mating, inbreeding and assortative mating (Falconer, 1981). Inbreeding is when the mated individuals are related to each other by descent. With assortative mating the individuals tend to mate preferentially with respect to their phenotypes, and can be either positive or negative.

When animals are selected and mated on the basis of the similarity of their phenotypic resemblance for a particular trait, this is termed positive assortative mating. This is in contrast to negative assortative mating, where the individuals are selected and mated on their dissimilarities in their phenotypes. Since the positively mated individuals have similar phenotypes, it would be expected that the genotypes would be somewhat similar and therefore have similar consequences as inbreeding (Crow and Felsenstein, 1968).

When a trait is controlled by a single locus, then the effects of positive assortment are essentially the same as inbreeding, in that it results in the proportion of heterozygotes being halved in each generation (Jennings, 1916; Wentworth and Remick, 1916). The

effect of positive assortment on traits that are inherited in a multifactoral fashion was formulated in the classic papers of Fisher (1918) and Wright (1921a), who used two different approaches. Similar conclusions were reached, in that under the assumption of negligible dominance and no selection, positive assortative mating increased the variability in the population. This was due to an increase in the additive genetic variance (which was in accordance with the assumptions that were made) and would therefore lead to a greater selection response than with random mating. Dominance and other factors, such as incomplete assortment and epistasis, will tend to reduce the effectiveness of this type of mating.

The consequence of an excess of consanguineous mating would result in an increase of the average homozygosity and, also an increase in the total population variance. Positive assortment would have either or some combination of these consequences (Crow and Felsenstein, 1968). This variance enhancing effect of inbreeding and positive assortment was illustrated by Crow and Felsenstein (1968) with a trait influenced by two loci, A and B, without dominance. Let the subscripts 1 add one unit to the phenotype and subscript 0 add nothing. The two extremes of the phenotype are then $A_1A_1B_1B_1$ and $A_0A_0B_0B_0$, and the intermediate phenotypes are $A_1A_1B_0B_0$, $A_1A_0B_1B_0$, and $A_0A_0B_0B_0$. The effect of inbreeding will increase the frequency of all of the four homozygotes, $A_1A_1B_1B_1$, $A_0A_0B_1B_1$, $A_1A_1B_0B_0$, and $A_0A_0B_0B_0$. This would double the variance if the original population is changed from random mating proportions to complete homozygosity.

With positive assortment, the population would approach a

state where only the extreme homozygotes, $A_1A_1B_1B_1$ and $A_0A_0B_0B_0$, would remain. The rate of increase in the homozygosity is less than inbreeding because inbreeding causes a positive correlation only between the homologous genes, whereas positive assortment also induces an positive correlation between non-homologous genes (Crow and Kimura, 1970). Thus, the long term effect would be to distribute a unimodal population under random mating to a bimodal population (Wright, 1921b). This clearly causes a much greater enhancement of the variance. This is in contrast to negative assortative mating, which keeps the population around a single mean (Wright, 1921b). Using the example, negative assortment results in the heterozygote, $A_1A_0B_1B_0$, and therefore less variation. In either case of assortative mating, the resumption of random mating would quickly result in the disappearance of these effects, unless any accompanying selection has resulted in any permanent change of the gene frequencies (Wright, 1921b).

The above example also illustrates the differences between inbreeding and assortative mating. Inbreeding affects all segregating loci and would tend to fix all the four homozygotes, as the individuals mated would be more likely to have the same genes (Lush 1945). Whereas, positive assortment only affects the loci associated with the trait used for positive assortative mating and would tend to fix only the two extreme homozygotes as the individuals would tend to have similar characteristics, irrespective of their relationship (Lush, 1945). These differences between random and non-random mating was illustrated by Breeze (1956) in Nicotiana. Breeze (1956) reported that positive assortment had significantly greater genetic variation than random mating, but in no case was the genetic variation as great as

under selfing. While there is a greater response of positive assortative mating over random mating, McBride and Robertson (1963) found that the rate of increase in inbreeding tended to be slightly, but not significantly, higher in assortative mating than random mating.

2.4.2 Experimental Results

Various experimental results in Nicotiana (Breeze, 1956); Drosophila melanogaster (McBride and Robertson, 1963); Tribolium castenum (Wilson et al, 1965; Mwenga et al, 1984); Computer simulation (Baker, 1973; De Lange, 1974; Fernando et al, 1984; Garcia and Toro, 1985; Kemp et al, 1986), have generally agreed with the above theory. In general, positive assortative mating resulted in a greater variance and selection response in the trait which was used for positive assortative mating than under random mating. In many cases, the difference between positive assortative mating and random mating was not found to be significantly different. From these experimental studies, it is apparent for positive assortative mating to be efficient than random mating, a high heritability and a high phenotypic correlation between parents as to generate a high genetic correlation, a large number of loci, a low intensity of selection would be required. Complex genetic control systems, such as dominance and linkage, would reduce the effectiveness.

Gianola (1982) reported that positive assortment could have a large influence on the magnitude of the genetic correlation between two characters. Under mating rules to change the genetic parameters so to

increase the response to selection, Fernando and Gianola (1984) reported that the sign could be changed with positive assortment. Kemp et al (1986) observed in simulated study that only the additive variance of the trait under positive assortative mating was significantly increased, but the absolute values of the covariances and the correlations were not significantly increased. Fernando et al (1984) and Mwenga et al (1984) both reported that there were no significant correlated responses from positive assortative mating.

The effect of truncation selection on positive assortative mating was investigated by Baker (1973) with genes of equal effects and frequencies. Truncation selection generated negative correlations between genes both within the same loci and at different loci, reduced the maximum correlation between the parents, and therefore, tended to reduce the effectiveness of assortative mating. Baker (1973) concluded that positive assortment could increase the response by 1 to 10%, with greater responses depending mainly on a high heritability and a low selection intensity. However, while in agreement with the general result, Smith and Hammond (1987a) criticized this mainly because by assuming that the selection response is proportional to the genotypic standard deviation, Baker (1973) had underestimated the response. Smith and Hammond (1987b) reported that while being generally correct, Baker slightly under-valued the responses obtained.

Tallis and Leppard compared the joint effects of selection and positive assortative mating on a single polygenic character (Tallis and Leppard, 1987) and on multiple polygenic characters (Tallis and Leppard, 1988). With a single character, Tallis and Leppard (1987)

reported that the generation by generation gains were greatest under straight assortative mating. But the total progress was greatest when positive assortative mating and selection were combined at generation zero. The introduction of a second character, using a selection index with positive assortative mating, resulted in an considerable increase over the expected gain of a single character selection, even if only one of the characters was of economic merit (Tallis and Leppard, 1988). Smith and Hammond (1987b) had found that under index selection, assortative mating can increase the selection response in the progeny compared to the selection on progeny phenotype.

The effects of positive assortative mating on one trait in the estimation of cattle breeding values using computer simulation was examined by Kemp and Wilton (1987). In the assortatively mated trait, the mean product moment correlation between the estimated breeding value and the true breeding value was increased. This was due to increases in the mean additive genetic variance, mean variance of the estimated breeding value, and in the covariance between the true and the estimated breeding values.

CHAPTER THREE

MATERIALS AND METHODS

3.1 THE DATA

3.1.1 Background

A cooperative lean lamb breed development programme between the Ministry of Agriculture and Fisheries (MAF^{Tech}), the Department of Land and Surveys (Landcorp) and Massey University was established in 1982 at Landcorp's Wiremu block in Taranaki. The initial objective was to develop a sire breed whose crossbred progeny (from mating with dual-purpose dam breeds) would have a high lean growth rate with reasonable production of non-pigmented wool and adequate reproductive performance.

In order to meet these requirements, methods of assessing lean meat production were required. This involved research on the inheritance and interrelationships between growth, carcass traits and the ultra-sonic probe. Industry sires from 4 breeds (Romney, Border Leicester, Poll Dorset and Coopworth) were mated to Romney ewes in 1982 and 1983. Over the two year period, 1431 male and female lamb progeny were slaughtered and the carcass composition was determined by chemical and dissection methods. Prior to slaughter, the lambs were weighed and the backfat depth ultra-sonically assessed at the carcass C site. The genetic and phenotypic parameters of these traits have been reported by Parratt et al (1987a).

The research was then extended to investigate the inheritance and the relationships between growth, wool and reproduction. Three groups of industry sires (most of which were repeated from the earlier study) were selected on the basis of a predicted growth rate of lean tissue (the lean growth rate index of Purchas et al 1985), and either high or low weight adjusted backfat. These sires were then mated to Romney ewes, in 1984 and 1985, and the progeny were assessed for growth, wool, and reproductive traits.

3.1.2 The Data Used In This Analysis

The growth and wool data used were recorded from ewe progeny, born in 1984 and 1985, of sires that were from three breeds (Romney, Border Leicester and Poll Dorset). These sires had been selected for either high or low weight-adjusted ultra-sonic backfat depth. The dams used were from the Romney flock at Landcorp's Wiremu property. Unfortunately, only the low line sired progeny were available from 1984. From earlier matings of these sires, the growth and wool traits were linked to the carcass traits. The separation of the data set into the meat and wool sub-components, with the number of sires and the total progeny per sire breed for each sub-component is given in Table 3.1.

Table 3.1:Details of the number of sires and
total progeny per sire breed
and source of data

Sire Breed	Romney		Dorset		B.Leic	
Source of data ¹	M	W	M	W	M	W
Number of sires	13	15	6	4	5	4
Number of hoggets	193	252	101	78	67	74

1)M=Meat data; W=wool data.

The information recorded on the progeny is given in chronological order. On all the progeny at birth: ewe identity (hence sire identity and dam age), lamb identification, day of birth, sex, birth rank, rearing rank, and lambing paddock were recorded. In November, approximately 7 weeks after the mean birth date, all the lambs were weighed and then were weaned.

The carcass traits analysed in this study were those of major importance from Parratt et al (1987a), with the inclusion of carcass length. Prior to slaughter, the animals were weighed and their backfat was ultra-sonically assessed at the carcass C site using a AIDD-NZ probe. After slaughter, hot carcass weight, carcass length and the fat depths GR and carcass C were measured. The carcass was then halved for carcass composition by chemical and dissection analysis for total and percentage weights of bone, lean, inter-muscular fat and subcutaneous fat.

The ewes in the growth and wool study were weighed in January, February, and August. The ultra-sonic backfat depth was recorded at the same time as the August liveweight. Lamb fleeceweight was measured in February and hogget greasy fleeceweight in October. At the hogget shearing, mid-side samples were taken for additional analysis.

Mid-side wool samples were stored until analysis was undertaken at Whatawhata Hill Country Research Station and Massey University in January 1988. Prior to any wool metrology measurements, the samples were conditioned at 20°C and 65% relative humidity for 48

hours. From the conditioned sample an approximately 20g sub-sample was removed (with the actual weight being recorded) for further analysis. At the same time, staple length was measured on two randomly drawn staples and the average length was recorded; care was taken to avoid stretching the staples during the measurement. If these two staples were widely different, a third was drawn and the average of all three was taken.

Each 20g sub-sample was lightly hand-carded before being placed in a wash bag for scouring. The samples were scoured using three twin tub hovermatic washing machines. All machines were filled with warm water and were topped up when necessary. The first machine had 60mls of detergent added initially, with a further 20mls was added after every 16 samples. The second machine had 40mls at the outset, while the third was used as a rinse. The samples were washed in groups of four for 3 to 4 minutes in each machine, before being spun briefly (less than 30 seconds) to remove the excess water. The samples were then transferred to the next machine. After rinsing, the samples were teased out and dried in an oven for 3 to 4 minutes at approximately 100°C; care was taken to avoid overdrying. After drying, the samples were conditioned for 48 hours before being weighed. This allowed the calculation of percentage clean scoured yield as:

$$\text{YIELD} = \text{clean sample weight} \times 100 / \text{greasy sample weight}.$$

Clean fleeceweight was then calculated as:

$$\text{CFWT} = \text{greasy fleeceweight} \times \text{YIELD} / 100.$$

The scoured samples were hand carded and a 10g carded sample was weighed off. This 10g sample was used to measure loose wool bulk

using the WRONZ Bulkometer. Loose wool bulk is defined as the volume occupied by a fixed mass of wool under a fixed force per unit area (Bigham et al, 1984a). This is slightly different to the Australian system of resistance to compression. Resistance to compression is defined as the force per unit area required to compress a fixed mass of wool into a fixed volume (Teasdale, 1987). For wool there is an loose relationship between bulk and resistance to compression, but it is generally considered that bulk is better for New Zealand wools and resistance to compression for merino type wools (Teasdale, 1987). The procedure used to measure bulk was an automated version of that described by Bigham et al (1984a):

- 1) load the 10g sample into the cylinder of the bulkometer,
- 2) load the sample to a pressure of 30 gf/cm² for 30 seconds,
- 3) remove the load and allow 30 sec for recovery,
- 4) load the sample to 30 gf/cm² for 30 sec,
- 5) remove the load and allow 30 sec for recovery,
- 6) load the sample to 10 gf/cm² for 30 sec,
- 7) the load was then removed and the height of the wool
was measured, and
- 8) then the loose wool bulk was calculated automatically.

The yellow colour of scoured wool can be a major concern in future colouring of the final product (Elliott, 1986). The scoured colour of wool can be described objectively by measuring the Commission Internationale de l'Eclairance (1971) tristimulus values X, Y, and Z. The Y-Z value was considered by Edmunds (1977) as a good indicator of yellowness of a scoured wool sample. The tristimulus values Y and Z were measured on the 10g sample in an Instrumental Colour Systems

Digital colorimeter (Bigham et al, 1984b).

The 10g samples were then transferred to Massey University and the mean fibre diameter was measured using the airflow technique (van Luijke, 1984). A 3g sample was obtained and packed into a chamber. The associated reduction in air pressure was then recorded. The sample was then repacked and a further reading was taken. The mean fibre diameter was then calculated from the average reduction in air pressure.

The list of traits analysed and the abbreviations used are shown in Table 3.2.

Table 3.2:The list of traits and their abbrevations

a)Recorded in the Wool Component:

Weaning Weight	WWT
January Weight	JWT
Febuary Weight	FWT
August Weight	AWT
Backfat UFD	UFD
AWT adjusted UFD	AUFD
Lamb fleeceweight	LFWT
Hogget Greasy fleeceweight	HFWT
Hogget Clean fleeceweight	CFWT
Clean Scoured Yield	YIELD
Staple length	STLEN
Loose Wool Bulk	BULK
Mean Fibre Diameter	MFD
Scoured colour	COLOUR

(cont.)

Table 3.2 (Cont.)

b)Recorded in the Meat Component:

Meat Weaning Weight	MWWT
Pre-slaughter liveweight	PLWT
Pre-slaughter UFD	PUFD
PLWT adjusted UFD	PAUFD
Hot Carcass Weight	HCWT
Carcass Length	CLEN
Carcass GR	GR
Carcass C	C
Total Subcutaneous Fat	TSF
Percent Subcut. Fat	PCSF
Total Intermus. Fat	TIF
Percent Intermus. Fat	PCIF
Total Lean	TLEAN
Percent Lean	PCLEAN
Total Bone	TBONE
Percent Bone	PCBONE

3.2 STATISTICAL PROCEDURE

3.2.1 Background

3.2.1.1 Assortative Mating

The animals used in this study were from sires that had been selected on the basis of either high or low ultra-sonic backfat scan. This meant the information recorded was more correctly obtained under the assumption of positive assortative mating rather than random mating. Therefore, a positive assortative mating analysis was considered to be a more appropriate than a random mating analysis, to account for the phenotypic correlation that was induced between the mates. Therefore, depending on the heritability of the trait concerned, a genetic correlation would be induced between mates, and this would result in an increase in the variation between families from that obtained by random mating (Wright, 1952). Thus, any estimates of variance and covariance components would be bias to the generally expected components obtained under random mating.

Reeve (1953) derived the relationship between parameters estimated under either positive assortment, selection to increase the variance, or both, and the equivalent parameters estimated under random mating. With regression on the mid-parent value, the estimates of the variance and covariance components would not be biased. However, Wright (1952) had previously criticised this result on the basis that assortative mating must induce correlations between non-additive genetic effects and therefore, introduce unpredictable bias. Reeve (1961) replied by showing that the bias would be negligible provided

that all individual gene substitution effects were small compared to the phenotypic standard deviation of the character. More recently, Gimelfarb (1985) reported that the result of Reeve (1961) pertained only to the model of Fisher (1918), as used by Reeve (1953), and that while reducing the sampling variance, assortative mating could also bias the estimated mid-parent regression value.

With half-sib analysis, the bias in the parameters obtained under positive assortment, relative to random mating, would be due to the closer within family relationships and to greater between family relationships, in a similar manner to inbreeding (Reeve, 1953).

From path analysis methodology, Reeve (1953) derived the following formulae to correct for this bias:

$$(3.1) \ h_w^2 = \frac{-1 + [1 + 4LG_w(1 - \frac{1}{2}G_w)]^{\frac{1}{2}}}{2L(1 - \frac{1}{2}G_w)}$$

$$(3.2) \ r_g = \frac{Gwt}{[1 + Lh_w^2(1 - Gwt^2)]^{\frac{1}{2}}}$$

$$(3.3) \ h_t^2 = \frac{Gt}{1 + Lh_w^2r_g^2(1 - \frac{1}{2}Gt)}$$

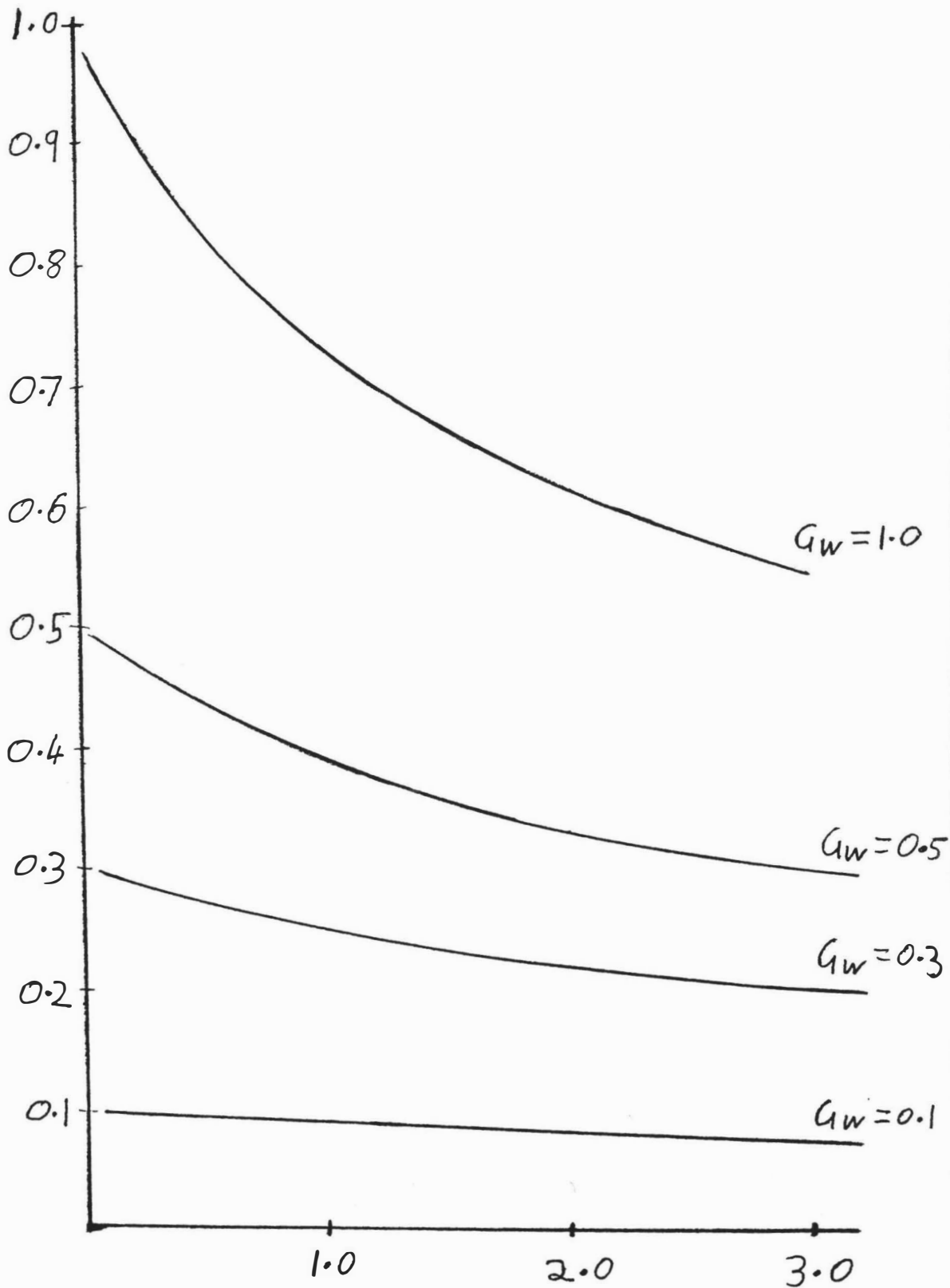
Where G_w , and h_w^2 = the uncorrected and corrected
heritabilities of trait w,
respectively,

Gwt and r_g = the uncorrected and corrected genetic
correlation between the traits w and t,

Gt and h_t^2 = the uncorrected and corrected
heritabilities of trait t, and,

L = change in the mid-parent variance
of trait w.

Figure 3.1: The effect of the change in the Mid-parent Variance (L) on the Heritability (h_w^2) of an Positively Assortatively Mated Trait.



Change In Mid-Parent Variance (L).

The effect of equation (3.1) on different heritability estimates is shown in Figure 3.1. It should be noted that due to the nature of Equation (3.1) that the corrected heritability (h_w^2) can never equal the original heritability (Gw) (i.e L cannot be zero). Reeve (1953) noted that the formulae were of the same form whether the parents were assortatively mated or selected so as to increase the phenotypic variance of one character under the assumption of additive gene effects. Further, the relationship depended only on the mid-parent variance and the values Hw and Rwt . The effect on the mid-parent variance by the degree of assortative mating (M) and selection to change the variance (K) is given by the relationship $(1+L)=(1+K)*(1+M)$, where K and M relate to the ratio of the selected parent variance to the base population variance (Reeve, 1953). Prout (1958) simplified the formulae of Reeve (1953) after it was observed that Reeve's assumption for half-sib analysis, that the environmental conditions under which the progeny were raised to be the same as the parents' environment, was unnecessary.

3.2.1.2 Between-Breed Parameters

Dickerson (1969 and 1973) presented models of the genetic components in a crossbreeding situation, where each component was defined as a mean deviation in offspring performance from the average performance for the purebreds of a specified set of breeds. However, their estimation procedure was not discussed and this has resulted in other authors (e.g. Alenda et al, 1980; Robison et al, 1981; Cunningham and Magee, 1988) using regression techniques.

Taylor, in a series of papers (Taylor 1976a and 1976b; Taylor and Thiessen, 1984; Taylor and Hnizdo, 1987), described experimental designs for multi-breed comparisons and the estimation of multi-breed parameters. These multi-breed designs are characterized by the testing of a large number of breeds in limited facilities by using few sires per breed with few offspring per sire, to obtain a reasonable assessment of between-breed rankings. The use of these designs in multi-breed cattle comparisons have been reported by Thiessen et al (1984), Thiessen (1985), Thiessen et al (1985), and Taylor and Murray (1987). In a topcross Bos taurus cattle experiment, Cundiff et al (1986) provided slightly modified formulae of the multi-breed parameters of Taylor (1976a and 1976b) for a crossbreeding situation. Cundiff et al (1986) assumed that the differences between the cross-bred animals estimated only one-half of the genetic difference between the parental pure-bred animals. Such that the between-breed variance estimated only one-quarter of the additive genetic variance between-breeds, plus the non-additive genetic variance due to differential effects of the individual heterosis amongst the different

breeds in the crosses. It was further assumed that the differential effects of heterosis were small in relation to the within-breed additive effects.

3.2.2 The Analysis Procedure

A half-sib analysis was undertaken based on the procedures of Reeve (1953), Taylor (1976a) and Cundiff et al (1986). The knowledge of the classification of sires on ultra-sonic backfat depth was ignored and the sires were nested within their breed classification. Using the method of fitting constants (Searle, 1971), the data was corrected for the non-genetic effects and the mean square values of the random effects were then equated to their respective expected values (Table 3.3). The Statistical Analysis System (SAS, 1985) was used for the analysis.

Table 3.3: Coefficient Of the Expected Mean
Squares For the Wool Traits

Source	Between-Breed	Between-Sire	Residual
Between-Breed	104.98	18.49	1.00
Between-Sire	0.00	16.59	1.00
Residual	0.00	0.00	1.00

Initially, the data was examined to test for significant non-genetic effects and first-order interactions. In all cases, the first-order interactions were found to be non-significant and only the significant non-genetic effects (at a 5% critical level) were included in the model. The full linear model fitted to the data representing the wool traits was:

$$X_{ijkmn} = Y_i + A_j + R_k + L_m + DP_{ijkmn} + E_{ijkmn},$$

where X_{ijkmn} = an observation on the n th animal in
the i th year, from the j th dam age
class, of the k th birth rank,
born in the m th lambing paddock,

Y_i = the fixed effect of the i th year,

A_j = the fixed effect of the j th dam age,

R_k = the fixed effect of the k th birth rank,

L_m = the fixed effect of the m th lambing paddock,

P_{ijkmn} = the (coded) date of birth of the $ijkmn$ th
animal,

D = the coefficient of the regression of X_{ijkmn}
on P_{ijkmn} , and,

E_{ijkmn} = the random residual of the n th animal, the
residual effects were assumed to be
independently and identically distributed
with mean zero and variance E .

The trait ADUFD was adjusted for August liveweight before fitting the model. The model was modified to include the sex effects before fitting to the meat data. In addition, PAUFD was adjusted for

PLWT, and also CLEN and the other carcass traits were adjusted for the hot carcass weight before the model was fitted.

After adjusting for the above mentioned non-genetic effects, the estimates of the variance and the covariance components were obtained by fitting the following model and equating the mean squares to their expected values:

$$Z_{ijk} = B_i + S_{ij} + E_{ijk},$$

where Z_{ijk} = adjusted observation of the k th animal from
 j th sire in the i th sire breed,

B_i = the random effect of the i th sire breed, sire
 breed effects are assumed to be independently
 and identically distributed with mean zero and
 variance B ,

S_{ij} = the random effect of the j th sire from the i th
 sire breed, sire effects are assumed to be
 independently and identically distributed with
 mean zero and variance S , and

E_{ijk} = a random residual unique to the k th
 observation, residual effects are assumed to
 be independently and identically distributed
 with mean zero and variance E .

Furthermore, sire breed, sire and residual effects were assumed to be mutually independent.

For the ease of management, the traits were split into four

groups: the wool traits, the liveweight growth traits, the carcass dimension traits, and the carcass component traits. The variance and covariance components were then estimated within each group of traits. The covariance components between traits in different groups were estimated using the various combinations of two groups in each analysis. This procedure had the added advantage of minimising the effects of missing data and the unbalanced nature of this experiment. From a preliminary analysis, there was little difference in the magnitude of these components compared to analysing all the traits together.

3.2.3 The Estimation Of Heritability

The estimation of the heritability of a trait can be determined in two ways. It can be assumed that the variance components were obtained within a single breed, so that the within breed heritability was estimated as:

$$H_p = 4S/(S + E) ,$$

where H_p = the within-breed heritability,

S = the within-breed, between-sire variance component, and

E = the within-breed, within-sire variance component.

The approximate standard error of the heritability was given by

Swiger et al (1964) as

$$S.E(H_p) = 4 \sqrt{\frac{2(n.-1)(1-t)^2(1+(k_1-1)t)^2}{k_1^2(n.-S)(S-1)}}$$

where $n.$ = the total number of observations,

S = the number of sires,

t = the intraclass correlation,

= H_p

$$k_1 = \frac{1}{S-1} (n. - \sum n_i^2 / n.)$$

Alternatively, Cundiff et al (1986) assumed that the differences between sire breeds estimated one-half of the genetic difference that could be expected in a purebred. Thus, the between-breed variance estimated one-fourth of the additive direct genetic variance between sire breeds, plus the non-additive genetic variance due to differential effects of the individual heterosis amongst the different breeds in the crosses. It was also assumed that the variance due to differential effects of heterosis were small relative to the direct additive variance within a breed. In a population of first-cross animals, the expected value of the between breed mean square is one-quarter of the between breed variance. The definition of a first-cross animal in this case would be when the sire was of a different genetic source, whether in terms of breed or strain, than the dam.

Therefore, an estimate of the between-breed heritability is:

$$H_x = 4*(B + S) / (4*B + S + E) ,$$

where H_x = the between-breed heritability,

B = the between-breed variance component, and

S and E are defined as above.

The approximate standard error of this heritability was given by Becker (1984)

The approximate standard error of this heritability was given by Becker (1984):

$$S.E.(H_x) = \sqrt{(\text{var } H_x)}$$

$$\text{where var } H_x = 4 [\text{var } B + \text{var } S + 2\text{cov } (BS)] / (B + S + R)^2$$

$$\text{var } B = 2/k_3^2 \left[\frac{MS_B^2}{df_B+2} + \frac{MS_S^2}{df_S+2} \right]$$

$$\text{var } S = 2/k_1^2 \left[\frac{MS_S^2}{df_S+2} + \frac{MS_R^2}{df_R+2} \right]$$

$$\text{cov } (BS) = \frac{[\text{var } B - k_2^2 \text{var } S]}{k_1 k_3}$$

MS= Mean Square

$$k_1 = \frac{1}{m_b - 1'} (n. - \sum n_i^2 / n.)$$

$$k_3 = \frac{1}{\sum m_s - m_b'} (n. - \sum m_s^2 / n.)$$

m_b = number of breeds

m_s = number of sires per breed, and

$n.$ = total number of observations.

In addition to the standard heritability, multi-breed parameters can be estimated from the formulae provided by Taylor (1976b). Of particular importance is the ratio of between breed genetic to total genetic variance:

$$Hr = B/(S+B)$$

where Hr=ratio of between breed genetic variance

to the total genetic variance,

B, and S are as previously defined.

The standard error was given by Taylor (1976b).

$$S.E.(Hr) = \sqrt{(\text{var } Hr)}$$

$$\text{var } Hr = \frac{2}{(\rho_b + \rho_s)^4 (JK)^2} [X + Y + Z]$$

$$X = \frac{\rho_s^2 [1 + (K-1)\rho_s + (JK-1)\rho_b] 2}{I-1}$$

$$Y = \frac{[\rho_s + J\rho_b]^2 [1 + (K-1)\rho_s - \rho_b]^2}{I(J-1)'}$$

$$Z = \frac{[J\rho_b]^2 [1 - \rho_s - \rho_b]^2}{IJ(K-1)'}$$

$$\rho_b = B/(B+S+R)$$

$$\rho_s = S/(B+S+R)$$

I = number of breed, 3,

J = number of sires per breed, 8,

K = number of progeny per sire, 17.

3.2.4 The Estimation of the Correlations

Information in the literature on the theory of parameters in cross-bred populations or in the development of synthetic breeds was scarce. The sources of the information used were Taylor (1976a, b), Taylor and Hnizdo (1987), and Cundiff et al (1986). While the formulae for estimating various multi-breed parameters were given, their application or meaning was not adequately discussed.

The concept of breeds is based on the assumption that sires within the same breed have different genetic material than sires within another breed. Therefore, any analysis involving sires from different breeds would need to nest sires within their respective breeds. The decision to treat the breed and sires nested within breed as random effects was because they represented samples from the sheep population. Under a preliminary analysis it was observed that the residual covariance components were similar when breed was treated as either a fixed effect or a nested random effect.

By fitting breed and sire nested within breed as random effects, three estimates of covariance components could be obtained. Based on these components, Cundiff et al (1986) provided formulae to estimate a between-breed genetic correlation, a within-breed genetic correlation, a total genetic (the sum of the between-breed and between-sire variance and covariance components), and a within-breed phenotypic correlation. However, in the data set employed in this study, the between-breed correlation would have no valid meaning under a limited breed choice and incomplete reciprocal crossing. In

addition, to being strongly influenced by the number of breeds and observations per breed. The between-breed and the between-sire variance and covariance components could be combined to obtain a total genetic correlation, but would be biased due to non-additive genetic effects and would be strongly influenced by the magnitude of the between-breed component.

For the estimates of the within-breed correlations to be valid, it must be assumed that the genetic variation contained in the between-breed components is negligible in comparison to the between-sire variation. (Which may or may not be valid considering the range of estimates for H_r). The within-breed genetic and phenotypic correlations would be less biased by the between-breed effects since they would pertain only to the variation that is observed between the sires, partially corrected for breed differences.

The within-breed correlations were calculated within each of the two data sets to give the genetic and phenotypic correlations. Standard errors were not calculated because it was considered that the theory of standard errors for this type of analysis was inadequate.

The within-breed genetic correlation was calculated as:

$$R_g = (\text{CovS}) / \sqrt{(S)_i * (S)_j}$$

where R_g = the within-breed genetic correlation,

$(S)_i$ = the between-sire variance of the i th trait,

$(S)_j$ = the between-sire variance of the j th trait, and

$CovS$ = the between-sire covariance between the two traits.

The within-breed phenotypic correlation, R_p , was calculated as:

$$R_p = Cov (S+E) / (\text{sqr} [(S+E)_i * (S+E)_j])$$

where R_p = the within-breed phenotypic correlation,

$(S+E)_i$ = the total within-breed variance of the i th trait,

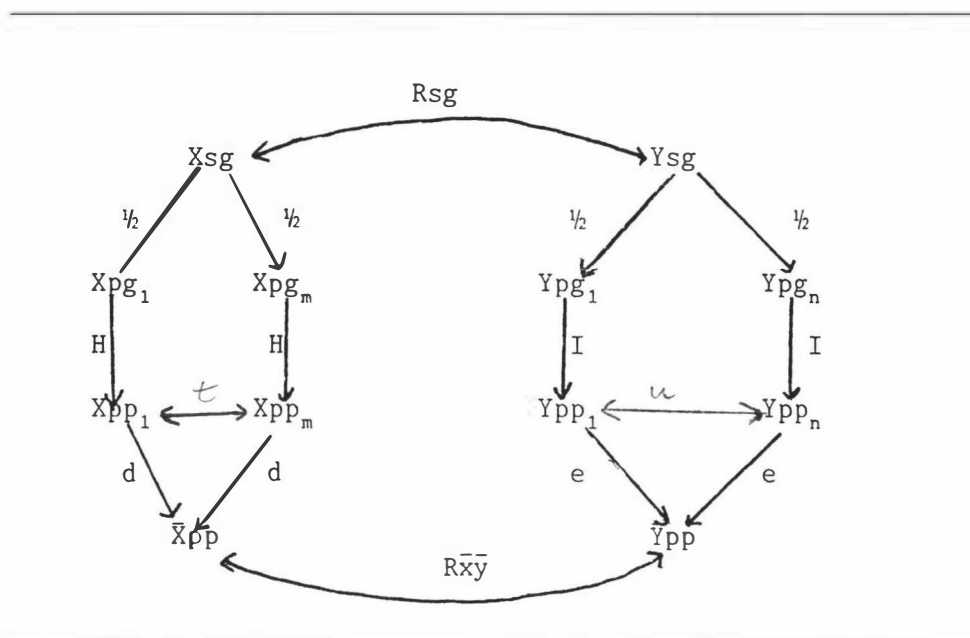
$(S+E)_j$ = the total within-breed variance of the j th trait,

and

$Cov (S+E)$ = the total within-breed covariance between the two traits.

The relationship between two traits recorded on two different individuals in different environments, but with the same sire is shown in Figure 3.2. The genetic correlation, R_{sg} , can then be solved by path analysis:

Figure 3.2: The Path Analysis Diagram of the Relationship Between the Two Data Sets



$$\begin{aligned}
 R_{\bar{x}\bar{y}} &= dH\frac{1}{2}R_{sg}\frac{1}{2}I + dH\frac{1}{2}R_{sg}\frac{1}{2}In(n-1)ue + dm(m-1)tH\frac{1}{2}R_{sg}\frac{1}{2}Ie \\
 &\quad + dm(m-1)tH\frac{1}{2}R_{sg}\frac{1}{2}In(n-1)ue \\
 &= \frac{1}{4}HIR_{sg}de[(1+m(m-1)t)(1+n(n-1)u)]
 \end{aligned}$$

but $\text{var}x = 1 = md^2 + m(m-1)d^2$
and hence $d = [1/(m(1+(m-1)t))]^{\frac{1}{2}}$
similarly,
 $e = [1/(n(1+(n-1)t))]^{\frac{1}{2}}$

Therefore,
 $R_{\bar{x}\bar{y}} = \frac{1}{4}HIR_{sg}[mn/(1+(m-1)t)(1+(n-1)u)]^{\frac{1}{2}}$

Rearranging to
 $R_{sg} = 4R_{\bar{x}\bar{y}}/[HI(mn/(1+(m-1)t)(1+(n-1)u))^{\frac{1}{2}}]$

where $R_{\bar{x}\bar{y}}$ = the correlation between the means x and y ,
 h = square root of the heritability of x ,
 i = square root of the heritability of y ,
 m = mean number of progeny per sire (17) for trait x ,
 n = mean number of progeny per sire (15) for trait y
 t = Intra-class correlation for trait x ,
 $= \frac{1}{4}H^2$,
 u = Intra-class correlation for trait y ,
 $= \frac{1}{4}I^2$.

The correlation between the means values of x and y was estimated using only the sires that had been repeated in both data sets. This meant that there were less sires involved than in the earlier analysis. The traits were corrected for the effects of breed and the non-genetic effects, and the mean value of each trait was calculated for each sire. The correlations between these mean values were then calculated for each pair of traits. The estimates of h and i were taken directly from Table 4.3, and therefore, are likely to be slightly different than if h and i had been calculated with the breeds treated as fixed effects. The values of the progeny per sire were mean values, but this is unlikely to effect the final result due to the large standard errors involved. The phenotypic correlation was not obtained due to the unknown relationship between the two data sets.

CHAPTER FOUR

RESULTS AND DISCUSSION

4.1 Least Square Means of the Progeny

The Romney sire breed least square means are shown in Table 4.1, with the Dorset (D) and Border Leicester (BL) breed means given relative to the Romney (R). The breed means provide an indication of the variation that is present in the population and the necessity to account for breed in any further analysis. While the BL and D progeny would contain an heterosis component, it's magnitude would not be identifiable due to incomplete reciprocal mating.

The BL-cross progeny were superior in fleeceweight and staple length compared with the R and D-cross progeny, with the R progeny superior to the D-cross progeny. There were significant breed differences in yield, mean fibre diameter and colour, but the actual differences were small. The differences in loose wool bulk were in agreement with Dunlop et al (1974) and Elliott (1986), where there was higher bulk in the Dorset than the Romney and Border Leicester sire breeds.

The liveweights within the wool data (weaning to 12 months of age) showed little difference, but there tended to be an advantage to the BL and D sired progeny.

Table 4.1: Least Square Romney Sire

Means and Standard Errors

TRAIT	ROMNEY (\pm Se)	BL	D
WWT(kg)	17.22 (\pm 0.21a)	97a	100a
JWT(kg)	23.83 (\pm 0.21a)	102a	106b
FWT(kg)	28.25 (\pm 0.21a)	102ab	104b
AWT(kg)	34.23 (\pm 0.21a)	109b	110b
UFD(mm)	2.85 (\pm 0.06a)	118b	106a
AUFD(mm)	2.83 (\pm 0.02a)	111b	113b
LFWT(kg)	1.30 (\pm 0.01a)	98a	85b
HFWT(kg)	2.82 (\pm 0.02a)	108b	92c
CFWT(kg)	2.43 (\pm 0.02a)	110b	93c
YIELD(%)	86.07 (\pm 0.23a)	102b	101ab
STLEN(cm)	11.10 (\pm 0.08a)	115b	88c
BULK(kg/cm ³)	21.57 (\pm 0.20a)	93b	118c
MFD(um)	35.24 (\pm 0.13a)	106b	103c
COLOUR	6.26 (\pm 0.09a)	92b	102a
MWWT(kg)	14.71 (\pm 0.36a)	122b	137c
PLWT(kg)	29.41 (\pm 0.43a)	109b	116c
PUFD(mm)	1.59 (\pm 0.07a)	156b	152b
PAUFD(mm)	1.85 (\pm 0.05a)	118b	131b
HCWT(kg)	13.60 (\pm 0.24a)	114b	125c
CLEN(cm)	92.99 (\pm 0.33a)	103b	105c
GR(mm)	6.17 (\pm 0.23a)	128b	151c
C(mm)	2.14 (\pm 0.07a)	126b	148c
(cont.)			

Table 4.1 (Cont.)

TSF(g)	601 ($\pm 22a$)	129b	152c
PCSF(%)	9.11 ($\pm 0.16a$)	113b	125c
TIF(g)	732 ($\pm 19a$)	120b	135c
PCIF(%)	11.29 ($\pm 0.08a$)	105b	110c
TLEAN(g)	3677 ($\pm 57a$)	112b	122c
PCLEAN(%)	57.67 ($\pm 0.10a$)	99b	98c
TBONE(g)	1124 ($\pm 12a$)	108b	115c
PCBONE(%)	17.76 ($\pm 0.11a$)	95a	92c

(BL and DOR breed means are given relative to the ROMNEY (100))

In contrast, the liveweights in the meat data (weaning and 6 months of age) showed that the BL and D sired progeny were superior to the R sired progeny. The R progeny had the lowest ultra-sonic backfat depths (UFD), but when the UFD's were adjusting to a common liveweight, the UFD in the BL sired progeny decreased and the D sired progeny increased. A possible reason is that a single phenotypic regression between liveweight and ultra-sonic scanning is not consistent between the breeds used.

The D sired progeny were heaviest in hot carcass weight with the R progeny being the lightest. These differences resulted in the breeds being significantly different for all the carcass traits. The BL and D sired progeny were also significantly fatter and contained greater bone and lean tissue weights compared to the R sired progeny. But, as a percentage of total tissue, the R progeny had significantly less fat, and significantly more lean and bone tissue, than the cross-bred progeny. While the percentage lean contents were significant, the actual difference was only 2% and would be consistent with the observation of constant lean or muscle growth relative to liveweight (Butterfield, 1988).

4.2 The Estimates of the Non-genetic Effects

The estimates of the significant non-genetic effects for the traits analysed are shown in Table 4.2. Lambing paddock was included in the linear model because earlier studies had found it to exert a significant effect on the early lamb performance (A.C. Parratt, pers.

comm.). In this study, lambing paddock was found to be significant for the traits WWT, JWT, FWT and MWWT. The age of dam was only found to be significant for WWT. Therefore, the effects of lambing paddock and age of dam were not included in Table 4.2.

In the wool traits where birth rank was significant, there was a slight superiority of singles over twins, and the estimates were also similar to the available literature estimates (Table 2.1). There was a greater advantage of singles over twins in liveweight and carcass weight traits, these were also similar to the literature (Table 2.6). But, the liveweight adjusted backfat depth showed that the twins were leaner than the singles at a constant weight. This was also evident in the carcass components, with the twins lower in fatness and greater in lean and bone tissue than the singles.

Table 4.2: Estimates of the Non-Genetic
Effects and Standard Errors

a)Wool Data Traits

TRAIT	COV ¹	YEAR (\pm SE) (84-85)	B.RANK (\pm SE) (s-t)	B.DAY (\pm SE)
WWT	-	-0.29 (\pm 0.41)	4.66 (\pm 0.29)	-0.09 (\pm 0.01)
JWT	-	-0.98 (\pm 0.32)	3.72 (\pm 0.34)	-0.10 (\pm 0.02)
FWT	-	-3.61 (\pm 0.35)	3.45 (\pm 0.37)	-0.09 (\pm 0.02)
AWT	-	-	2.37 (\pm 0.42)	-0.07 (\pm 0.02)
UFD	-	-0.87 (\pm 0.10)	-	-
AUFD	0.12 (\pm 0.01)	-0.99 (\pm 0.09)	-0.40 (\pm 0.11)	-
LFWT	-	-0.27 (\pm 0.02)	0.15 (\pm 0.03)	-0.01 (\pm 0.00)
HFWT	-	0.09 (\pm 0.04)	0.10 (\pm 0.01)	-0.01 (\pm 0.00)
CFWT	-	-	0.09 (\pm 0.04)	-0.01 (\pm 0.00)
YIELD	-	-2.54 (\pm 0.41)	-	-
BULK	-	3.19 (\pm 0.38)	-	-
COLOUR	-	-	0.32 (\pm 0.18)	-
(cont.)				

Table 4.2 (Cont.)

b) Meat Data Traits

TRAIT	COV ¹ (\pm SE)	YEAR (\pm SE) (83-82)	SEX (\pm SE) (m-f)	B.Rank (\pm SE) (s-t)	B.DAY (\pm SE)
MWWT	-	6.35 (\pm 0.33)	1.34 (\pm 0.31)	4.58 (\pm 0.34)	-0.12 (\pm 0.02)
PLWT	-	2.29 (\pm 0.47)	1.91 (\pm 0.47)	3.51 (\pm 0.51)	-0.15 (\pm 0.03)
PUFD	-	0.64 (\pm 0.09)	-	0.26 (\pm 0.10)	-0.02 (\pm 0.01)
PAUFD	0.12 (\pm 0.01)	0.38 (\pm 0.08)	-	-0.15 (\pm 0.08)	-
HCWT	-	1.62 (\pm 0.27)	1.05 (\pm 0.27)	2.02 (\pm 0.29)	-0.08 (\pm 0.02)
CLEN	1.26 (\pm 0.06)	1.97 (\pm 0.31)	-	-	-
GR	1.03 (\pm 0.05)	-0.40 (\pm 0.25)	-0.78 (\pm 0.24)	-0.99 (\pm 0.27)	-
C	0.35 (\pm 0.03)	-0.45 (\pm 0.13)	-0.26 (\pm 0.12)	-0.29 (\pm 0.14)	-
TSF	101 (\pm 3)	-57 (\pm 17)	-62 (\pm 17)	-51 (\pm 18)	-
PCSF	0.74 (\pm 0.04)	-	-0.82 (\pm 0.22)	-0.79 (\pm 0.25)	-
TIF	84 (\pm 3)	-61 (\pm 14)	-42 (\pm 13)	-46 (\pm 15)	-
PCIF	0.42 (\pm 0.04)	-0.49 (\pm 0.18)	-0.58 (\pm 0.18)	-0.74 (\pm 0.20)	-
TLEAN	236 (\pm 5)	-	-	-	-
PCLEAN	-0.62 (\pm 0.07)	2.22 (\pm 0.33)	0.82 (\pm 0.32)	0.86 (\pm 0.35)	-
TBONE	41 (\pm 3)	47 (\pm 15)	52 (\pm 14)	59 (\pm 15)	-
PCBONE	-0.60 (\pm 0.03)	1.15 (\pm 0.03)	0.84 (\pm 0.16)	0.90 (\pm 0.18)	-

1) covariate for AUFD is AWT, PAUFD is PLWT, and the carcass traits HCWT.

The superiority of males over females in liveweight, carcass weight and leanness was evident where the effect of sex was significant. This is generally consistent with comparisons of male and female carcass components (Butterfield, 1988). The apparent reason appears to be the differences in growth to maturity and that females appear to partition more fat to subcutaneous depots than the males (Butterfield, 1988).

The estimates of regression on the day of birth in the liveweight and wool traits were similar between this study and the literature (Tables 2.1 and 2.6). These estimates show that more production is obtained from older animals.

4.3 The Estimates of Heritability

The estimates of the between-breed and between-sire variance components of the traits analysed are presented in Table 4.3. Also presented in Table 4.3 are the estimates of the within-breed heritability (H_p), the between-breed heritability (H_x), and the ratio of the between-breed genetic variance to the total genetic variance (H_r).

It was not possible to estimate the change in the mid-parent variance and hence,, to correct the parameter estimates for the bias of assortative mating using the formulae of Reeve (1953). However, from Equation 3.1 and Figure 3.1, it can be observed that with any heritability estimates under about 0.3, the correction of the variance

components would be minimal. This would suggest that any bias due to positive assortative mating was negligible on the variance components compared to random mating. This is also supported by the similarity of the H_p estimates of the assortative mated trait, weight-adjusted ultra-sonic backfat depth, to the literature (eg Bradford and Surlock, 1972; Beatson, 1987; Parratt et al, 1987a). Any influence due to positive assortative mating in this analysis would have been confounded and reduced by the selection of only the sires, and also by the presence of dominance and epistatic effects. Various experimental studies (eg Breeze (1956), McBride and Robertson (1963), Wilson et al (1965), Mwenga et al (1984)) have reported non-significant differences between random mating and positive assortative mating.

The estimates of H_p for the wool traits were similar to the Romney estimates in the literature (Table 2.1). Although the estimates of BULK were lower than those reported by Bigham et al (1983) and Sumner et al (1989). The inclusion of the between-breed component raised the estimates, such that the estimates of H_x were generally greater than the literature. This was due to the high proportion of between-breed genetic variance apparent in the wool traits, except for COLOUR where there was negligible between-breed variation.

Table 4.3: Variance Components and the Estimates of
Heritability with Standard Errors

TRAIT	B.VAR	S.VAR	Hp (\pm SE)	Hx (\pm SE)	Hr (\pm SE)
WWT	0.01	0.13	0.10 (± 0.10)	0.11 (± 0.01)	0.07 (± 0.21)
JWT	0.95	0.46	0.27 (± 0.15)	0.54 (± 0.10)	0.67 (± 0.08)
FWT	1.83	0.56	0.29 (± 0.15)	0.64 (± 0.16)	0.77 (± 0.05)
AWT	4.71	0.73	0.29 (± 0.15)	0.76 (± 0.25)	0.87 (± 0.02)
UFD	0.16	0.08	0.38 (± 0.17)	0.65 (± 0.13)	0.67 (± 0.07)
AUFD	0.04	0.03	0.17 (± 0.12)	0.33 (± 0.04)	0.57 (± 0.13)
LFWT	0.01	0.001	0.10 (± 0.10)	0.54 (± 0.06)	0.91 (± 0.02)
HFWT	0.04	0.01	0.31 (± 0.15)	0.69 (± 0.18)	0.80 (± 0.04)
CFWT	0.03	0.01	0.36 (± 0.17)	0.70 (± 0.18)	0.75 (± 0.05)
YIELD	1.42	0.46	0.13 (± 0.11)	0.39 (± 0.06)	0.76 (± 0.07)
STLEN	1.49	0.28	0.60 (± 0.21)	0.90 (± 0.33)	0.84 (± 0.02)
BULK	5.01	0.33	0.13 (± 0.11)	0.71 (± 0.25)	0.94 (± 0.01)
MFD	1.35	0.28	0.25 (± 0.14)	0.66 (± 0.18)	0.83 (± 0.03)
COLOUR	0.00	0.30	0.55 (± 0.20)	0.55 (± 0.05)	0.00 (± 0.03)
MWWT	0.11	0.17	0.13 (± 0.16)	0.20 (± 0.01)	0.39 (± 0.20)
PLWT	0.52	1.55	0.44 (± 0.26)	0.51 (± 0.04)	0.25 (± 0.10)
PUFD	0.03	0.06	0.44 (± 0.26)	0.55 (± 0.05)	0.33 (± 0.11)
PAUFD	0.02	0.01	0.12 (± 0.16)	0.29 (± 0.03)	0.67 (± 0.12)
HCWT	0.37	0.64	0.55 (± 0.29)	0.66 (± 0.07)	0.37 (± 0.10)
CLEN	1.04	0.77	0.32 (± 0.28)	0.55 (± 0.09)	0.57 (± 0.09)
GR	0.09	0.80	0.73 (± 0.34)	0.75 (± 0.06)	0.10 (± 0.05)
C	0.24	0.06	0.24 (± 0.20)	0.61 (± 0.20)	0.80 (± 0.04)

(cont.)

Table 4.3 (Cont.)

TSF	1102	3931	0.77 (± 0.35)	0.81 (± 0.09)	0.22 (± 0.08)
PCSF	0.13	0.72	0.76 (± 0.35)	0.79 (± 0.07)	0.15 (± 0.07)
TIF	621	2179	0.68 (± 0.33)	0.74 (± 0.08)	0.22 (± 0.08)
PCIF	0.12	0.30	0.52 (± 0.28)	0.60 (± 0.07)	0.29 (± 0.10)
TLEAN	4114	13610	1.01 (± 0.40)	1.01 (± 0.14)	0.23 (± 0.08)
PCLEAN	1.36	1.65	0.96 (± 0.39)	0.99 (± 0.23)	0.45 (± 0.10)
TBONE	693	808	0.23 (± 0.19)	0.35 (± 0.04)	0.46 (± 0.13)
PCBONE	0.07	0.15	0.30 (± 0.22)	0.38 (± 0.04)	0.32 (± 0.12)

A similar trend between the heritability estimates was observed in the liveweight traits, with the H_p estimates being similar to the literature (Table 2.3). With the exception of weaning weight and PLWT, the estimates of H_r were generally greater than 0.6, and tended to result in the H_x estimates being larger in magnitude than the H_p estimates.

In contrast, the estimates of H_p in the carcass traits were generally greater than the literature (Table 2.5). In most cases the estimates of H_r in the carcass traits were under about 0.5 and thus the increase from H_p to H_x was small in magnitude.

The differences between the estimates of H_x and H_p can be explained by the presence of the between-breed component, as indicated by H_r . Since in addition to any between-breed additive genetic variance, the between-breed variance component would contain the differential effects of the individual heterosis amongst the different breeds involved (Cundiff et al, 1986). Such that in a crossbreeding situation, a high estimate of H_r may indirectly indicate the presence of heterosis. But, the more reliable conclusion is that there is a greater variability between the sire breeds than within each sire breed.

Due to the presence of any effects of heterosis, the estimates of H_x would overestimate the 'true' heritability observed in this population for any particular trait. Similarly, the H_p estimate would underestimate this heritability because the residual variance component, by definition, would contain $3/4$ of the between-breed

component. Whether or not this would bias the H_p estimate would depend on the validity of the assumption that H_p is an within-breed heritability. A possibly more reliable heritability estimate would be either the arithmetic mean or a weighted average of the H_p and H_x estimates. An weighted average could be the proportion of 'purebreds' (58% in the data used) multiplied by H_p plus the proportion of 'crossbreds' (42%) multiplied by H_x .

The relative differences in the source of the genetic variation is indicated by the ratio of the between-breed variance to the total genetic variance, (H_r). The estimates of H_r provide a wide range of values indicating that there are sometimes large between-breed genetic differences involved. These estimates would also relate to the additional likeness of members within the same breed (Cundiff et al, 1986). It would also tend to imply that there are different alleles or genes in the breeds investigated and that different selection pressure have been applied to these breeds.

By combining the estimates of H_r and H_p , it would be possible to develop multiple breed selection indices, like those proposed by Kinghorn (1984). Assuming that H_p is an valid estimate of the heritability, most of the traits would respond favourably to selection. H_r would provide an estimate of the total immediately 'selectable' genetic variation (Taylor and Thiessen, 1984), and therefore could be used to determine whether to select between breeds or within breeds. The high H_r estimates of the wool and liveweight traits indicate that selection should be between breeds, while selection should be within breed for the carcass traits. This would tend to hold unless

particular traits, eg loose wool bulk, are required or unfavourable correlations exist between the desirable traits.

The selection of individuals from this population would be based on their own performance and the magnitude of H_r . When the estimates of H_r are small, then there is apparently little between breed variation and selection would be based only on the sire's performance. However, where there are high estimates of H_r , such as the wool traits, then the sire breed needs to be taken into account. It would be insufficient just to take the breed with the 'best' breed mean because it would be unlikely to be best in all traits. Clarke and Meyer (1982) observed that the breeds of New Zealand represented a wide variation in performance, but this was greatly reduced when meat and wool production were combined. The 'average' breed would be inefficient because it would lack the extreme animals necessary for adequate genetic progress. Therefore, the selection of an individual would mainly be based on its relative performance followed by the benefits of breed. These benefits would be cross-breeding effects, possibility indicated by a high H_r estimate, and particular breed characteristics, such as loose wool bulk in the Dorset.

4.4 The Genetic And Phenotypic Correlations

The following genetic and phenotypic correlations provide information on the various relationships between wool, growth and carcass traits. Since only a small number of sires were used and also few observations per sire in the traits analysed, care is needed in their interpretation due to large standard errors.

4.4.1 Between the Liveweight and Carcass Traits

The correlations between the liveweights were moderate to highly positive (Table 4.4), and there was an apparent trend for the magnitude to decrease from young to old measures. While the literature estimates were similar (e.g Baker et al, 1979; Tait, 1983), no equivalent trend had been noted in these correlations. These high correlations would tend to suggest that selection at any age for liveweight would increase the liveweight measured at any other age. Further, an animal that is heavier than its contemporaries at a single age, would be heavier at other ages.

Table 4.4: The Genetic and Phenotypic Correlations¹ Between
the Liveweight Traits.

TRAIT	WWT	JWT	FWT	AWT	UFD	AUFD
WWT	----	1.01	0.85	0.74	0.17	-0.20
JWT	0.78	----	0.99	0.82	0.52	0.03
FWT	0.73	0.89	----	0.86	0.57	0.29
AWT	0.50	0.64	0.72	----	0.84	0.67
UFD	0.15	0.23	-0.02	0.40	----	0.95
AUFD	-0.06	-0.05	0.29	-0.05	0.94	----

1)Genetic correlations above the diagonal, Phenotypic below.

Table 4.5: The Genetic and Phenotypic Correlations¹ Between
the Carcass Dimension Traits

TRAIT	MWWT	PLWT	PUFD	PAUFD	HCWT	CLEN	GR	C
MWWT	----	0.81	0.52	0.12	0.72	-0.84	0.14	0.23
PLWT	0.62	----	0.98	0.90	0.99	-0.73	0.36	0.11
PUFD	0.29	0.61	----	0.99	1.01	-1.14	0.67	0.42
PAUFD	-0.11	0.00	0.78	----	1.13	-2.02	1.27	1.03
HCWT	0.60	0.95	0.65	0.09	----	-0.88	0.38	0.08
CLEN	0.08	0.09	-0.13	-0.22	0.01	----	-0.76	-0.57
GR	-0.19	-0.04	0.25	0.35	0.03	-0.38	----	1.01
C	-0.03	0.02	0.24	0.28	0.07	-0.18	0.51	----

1)Genetic correlations above the diagonal, Phenotypic below.

**Table 4.6: The Genetic and Phenotypic Correlations Between
the Carcass Dimension and Tissue Component Traits**

i)Genetic Correlations								
TRAIT	MWWT	PLWT	PUFD	PAUFD	HCWT	CLEN	GR	C
TSF	-0.02	0.19	0.42	0.83	0.15	-0.61	0.95	0.83
PCSF	0.17	0.40	0.65	1.12	0.38	-0.80	1.05	0.85
TIF	-0.55	-0.21	0.12	0.67	-0.13	-0.82	0.68	0.64
PCIF	-0.39	-0.18	0.17	0.80	-0.08	-0.94	0.72	0.72
TLEAN	-0.03	-0.15	-0.40	-0.85	-0.21	0.82	-1.03	-0.92
PCLEAN	0.15	-0.07	-0.30	-0.66	-0.07	0.68	-0.83	-0.68
TBONE	0.13	-0.10	-0.74	-2.05	-0.38	1.39	-1.01	-0.97
PCBONE	0.22	-0.03	-0.59	-1.69	-0.24	1.24	-0.73	-0.59
ii)Phenotypic Correlations								
TRAIT	MWWT	PLWT	PUFD	PAUFD	HCWT	CLEN	GR	C
TSF	-0.16	-0.03	0.23	0.31	0.04	-0.29	0.66	0.57
PCSF	-0.14	0.04	0.31	0.36	0.10	-0.31	0.66	0.56
TIF	-0.01	0.03	0.16	0.17	0.09	-0.20	0.46	0.36
PCIF	0.01	0.05	0.18	0.02	0.09	-0.21	0.44	0.38
TLEAN	0.01	-0.10	-0.25	-0.24	-0.11	0.18	-0.47	-0.47
PCLEAN	0.04	-0.05	-0.23	-0.07	-0.07	0.17	-0.53	-0.46
TBONE	0.16	0.06	-0.17	-0.26	0.01	0.34	-0.41	-0.33
PCBONE	0.18	0.02	-0.22	-0.31	-0.02	0.36	-0.44	-0.33

Table 4.7: The Genetic and Phenotypic Correlations¹ Between
the Carcass Tissue Component Traits.

TRAIT	TSF	PCSF	TIF	PCIF	TLEAN	PCLEAN	TBONE	PCBONE
TSF	----	0.95	0.89	0.96	-0.79	-0.96	-0.62	-0.62
PSCF	0.94	----	0.73	0.84	-0.88	-0.91	-0.74	-0.61
TIF	0.47	0.41	----	0.97	-0.49	-0.83	-0.52	-0.77
PCIF	0.41	0.45	0.93	----	-0.68	-0.92	-0.70	-0.81
TLEAN	-0.57	-0.67	-0.43	-0.58	----	0.85	0.72	0.34
PCLEAN	-0.77	-0.75	-0.71	-0.70	0.72	----	0.60	0.52
TBONE	-0.32	-0.44	-0.25	-0.41	0.47	0.08	----	0.80
PCBONE	-0.40	-0.51	-0.38	-0.49	0.28	0.16	0.90	----

1)Genetic correlations above the diagonal, Phenotypic below.

Table 4.8: The Genetic Correlations Between
the Liveweight and Carcass Traits.

TRAIT	WWT	JWT	FWT	AWT	UFD	AUFD
MWWT	0.41	0.44	0.14	-0.29	0.32	0.55
PLWT	0.28	0.18	0.14	-0.18	-0.06	-0.03
PUFD	0.67	0.73	0.49	0.08	0.23	0.29
PAUFD	0.74	0.90	0.56	0.05	0.72	0.76
HCWT	0.46	0.35	0.19	-0.04	0.09	0.10
CLEN	-0.53	-0.81	-0.41	-0.47	-1.06	1.24
GR	0.72	0.67	0.74	0.84	0.35	0.23
C	1.41	1.15	1.06	0.88	0.56	0.41
TSF	0.96	0.80	0.70	0.89	0.43	0.24
PCSF	0.75	0.71	0.68	0.83	0.40	0.29
TIF	0.67	0.49	0.28	0.77	0.67	0.63
PCIF	0.71	0.59	0.38	0.84	0.83	0.80
TLEAN	-0.87	-0.75	-0.67	-0.98	-0.49	-0.33
PCLEAN	-0.73	-0.63	-0.50	-0.79	-0.47	-0.35
TBONE	-0.84	-0.82	-0.57	-0.76	-1.00	-1.03
PCBONE	-0.37	-0.45	-0.22	-0.39	-0.89	-1.03

In the carcass data, the two liveweights were highly positively correlated with each other and also with HCWT (Table 4.5). The genetic correlations of the liveweights and HCWT with CLEN were highly negative, but the phenotypic correlations were negligible and positive. The difference between the genetic and phenotypic correlations could be attributed to the adjustment of CLEN by HCWT. A generally low to moderate genetic correlations were observed between the liveweights recorded in each data set (Table 4.8), except between AWT and the carcass liveweights. This indicates that there was different conditions operating within each data set. From the least square means, there were differences in the two weaning weight, and that the sire breeds were only significantly different for MWWT. This would tend to suggest that there is little relationship between animals born in different years from the same sire, ie that there is a large environmental influence on the expression of a genotype. This is especially so when the estimates of the heritability of weaning weight in the literature (eg Tait, 1983) and this analysis are generally between 0.1 and 0.2. Therefore, 80 to 90% of the variation in weaning weight is 'environmental', ie it cannot be attributed to additive genetic variance.

The total tissue weight showed high positive correlations to the percentage weight of the same tissue component (Table 4.7). The various carcass measurements of fatness: GR, C, TSF, PCSF, TIF, PCIF, were highly correlated with each other, and highly negatively correlated to the lean and bone contents (Tables 4.5, 4.6, 4.7). The correlation between lean and bone tissue was moderately positive (Table 4.7). The genetic and phenotypic correlations between the carcass

tissues were very similar to those reported by Wolf et al (1981). Whereas, only the genetic and phenotypic correlations between percent bone and percent total fat were similar between the studies of Wolf et al (1981) and Parratt et al (1987a). The correlations between the other carcass tissues components were different between those reported by Parratt et al (1987a) and either Wolf et al (1981) or this study. Similar genetic and phenotypic correlations between carcass C and percent tissue traits were reported by Wolf et al (1981), Parratt et al (1987a), and this study.

Liveweight, and also HCWT, were generally low to moderately positively correlated with the carcass measurements of fatness (Tables 4.5, 4.6, 4.8), but negatively correlated to the content of the lean and bone tissues. The growth data set liveweights were of a larger magnitude than the carcass data set liveweights. Carcass length was highly negative with carcass fat, but highly positively correlated to the lean and bone tissues (Table 4.6). This tends to be in agreement with the literature in sheep (eg Thorsteinssen and Bjornsson, 1982; Kadim, 1988), cattle (eg Good et al, 1961) and pigs (eg Fredeen and Mikami, 1986). In addition, Purser (1980) had reported that sheep selected for long cannon bone length were leaner at a constant weight than sheep selected for short cannon bone length. The growth data set liveweights were moderately to highly positively genetically correlated with the carcass measurements of fatness, but moderately to highly negatively correlated with the lean and bone contents (Table 4.8). When compared to the genetic correlations within the meat data, the correlations between growth and carcass traits were larger in magnitude and differed in sign with inter-muscular fat content.

Most of the correlations between the traits analysed by Parratt et al (1987a) and this study tended to be similar. But there was an apparent contradiction between the correlations of the total tissue weights and the percentage tissue with the other traits analysed by Parratt et al (1987a). While there are similarities in the source of data between this study and that of Parratt et al (1987a), there are substantial differences in the data sets used. In particular, Parratt et al (1987a) used about 4 times the number of progeny records and about 5 times the number of sires for their carcass study. Also, Parratt et al (1987a) used covariates of either age at slaughter or pre-slaughter liveweight. It is therefore probable that the differences in the estimates of the parameters can be primarily attributed to numbers, statistical technique and also due to some degree of assortative mating.

4.4.2 Between The Wool Traits

The genetic and phenotypic correlations of the wool traits are presented in Table 4.9. The relationship between HFWT and CFWT are almost unity and they have similar correlations with the other wool traits. Selection for increased fleeceweight would also increase staple length, mean fibre diameter, yield. The moderate to high correlations of these traits are consistent with the literature (Table 2.4) and can be explained in terms of larger fibres increasing the total fleece weight.

Table 4.9: The Genetic and Phenotypic Correlations¹ Between
the Wool Traits.

TRAIT	LFWT	HFWT	CFWT	YIELD	STLEN	BULK	MFD	COLOUR
LFWT	----	1.02	1.05	0.74	0.45	0.57	0.30	0.75
HFWT	0.52	----	0.99	0.56	0.72	-0.11	0.31	0.54
CFWT	0.51	0.95	----	0.67	0.69	-0.16	0.33	0.47
YIELD	0.12	0.11	0.40	----	0.29	-0.36	0.37	-0.12
STLEN	0.13	0.41	0.40	0.05	----	-0.61	0.34	-0.02
BULK	-0.03	-0.15	-0.18	-0.13	-0.52	----	0.23	0.86
MFD	0.21	0.37	0.39	0.17	0.34	-0.14	----	0.30
COLOUR	0.14	0.27	0.25	-0.002	-0.02	0.18	0.12	----

1) Genetic correlations above the diagonal, Phenotypic below.

The high positive genetic correlation between LFWT and HFWT would suggest that earlier selection for fleeceweight can be undertaken. But the moderate positive phenotypic correlation indicates that LFWT may be less accurate than HFWT in determining future wool production in an individuals lifetime. However, the relationship between LFWT and the wool traits in this study were similar to those between HFWT and the wool traits. With the exception of bulk, where the relationship of bulk and LFWT were moderately positive, and BULK and HFWT was low negative. The difference in this relationship could in part be explained, by the observation of Sumner et al (1989) of a moderate repeatability (0.5) between lamb bulk and hogget bulk.

COLOUR was moderately positively correlated with fleeceweight, BULK and MFD. The comparisons with Bigham et al (1983) tended to be variable. The moderate positive correlation between fleeceweight and colour, was consistent, as was to a lesser extent the relationship between MFD and colour. By selecting for increased fleeceweight, these correlations suggest that there would be a correlated increase in COLOUR, ie fleece yellowness. On a technical basis, this would cause some concern due to restricted wool dyeing performance. However, the limited evidence available suggests that this measurement of clean wool colour is not an inherited characteristic, and that selection should be against the incidence or suceptability to discolouring (Knight, 1989).

Loose wool bulk generally had a moderately negative relationship with HFWT, CFWT, YIELD and STLEN (Table 4.9). While there is very little information on bulk, these correlations are consistent

with Bigham et al (1983). From Australian work, similar results have been obtained with Resistance to Compression (R to C) and fleeceweight, yield and staple length (Mortimer, 1987). It is also consistent with the results of Dunlop et al (1974) where the short, fine, crimpy wools were found to have significantly more bulk than the long, coarse, less crimpy wools. The low positive genetic correlation and the low negative phenotypic correlation between BULK and MFD was similar to the correlations between fibre diameter and R to C reported by Watson et al (1977). Both BULK and R to C are influenced mainly by fibre diameter and crimp frequency, although the helical fibre shape in the Down type wools result in high values (Teasdale, 1987). This relationship would explain the observed low positive genetic correlation and the low negative phenotypic correlation between fibre diameter and bulk or R to C.

From the results presented earlier, most of the variation in bulk is between-breeds. Therefore, the within-breed heritability is low and the between-breed heritability is high. The negative correlations of BULK with the other wool traits would tend to support the concept of specialist lines. This would require sufficient price premium to offset the correlated reduction in fleeceweight and wool quality traits. However, there still needs to be more investigation into the inheritance of bulk and its relationship with other traits, particularly on the possibility of a major gene within certain breeds and also the effects of selection for increased fleeceweight in the high bulk Down breeds.

Until favourable price differentials are apparent within the

various objective measurements, greasy fleeceweight should remain the main wool selection criteria. From historical data, McPherson (1982) and Wickham and McPherson (1985) concluded that more selection emphasis was required on fleeceweight due to the economic and apparent favourable changes in wool quality traits. While there were some advantages in the selection of certain wool quality traits, it was thought that the potential gains involved were not worth the effort involved in their measurement. With the practice of second shearing there would also be some importance attached to staple length, as returns dropped when staple length was below about 75mm. It would still be necessary to be aware of potentially unfavourable correlated responses of increasing fibre diameter and yellowness and decreasing loose wool bulk.

4.4.3 The Correlations Between Liveweight and Fleeceweight

The relationship between fleeceweight and liveweight was variable and inconsistent between the genetic and phenotypic correlations (Table 4.10). This was particularly obvious in the correlations between LFWT and the liveweights. In general, the genetic and phenotypic correlations between hogget fleeceweight and liveweight

Table 4.10: The Genetic and Phenotypic Correlations Between
the Wool and Liveweight Traits.

i)Genetic Correlations

TRAIT	LFWT	HFWT	CFWT	YIELD	STLEN	BULK	MFD	COLOUR
WWT	-0.60	-0.18	-0.14	0.18	0.15	0.17	-0.88	-0.29
JWT	-0.36	-0.16	-0.13	0.15	-0.06	0.35	-0.57	-0.24
FWT	-0.23	0.05	0.11	0.41	-0.02	0.26	-0.42	-0.31
AWT	-0.48	0.04	0.09	0.40	0.33	-0.62	-0.34	-0.32
UFD	0.49	0.58	0.56	0.18	0.47	0.12	0.47	0.31
AUFD	1.00	0.84	0.77	-0.02	0.58	0.42	0.78	0.61

ii)Phenotypic correlations

TRAIT	LFWT	HFWT	CFWT	YIELD	STLEN	BULK	MFD	COLOUR
WWT	0.35	0.09	0.07	-0.03	0.05	-0.11	-0.05	-0.04
JWT	0.45	0.14	0.14	0.02	0.01	-0.07	-0.01	-0.07
FWT	0.40	0.19	0.17	0.02	0.07	0.08	0.03	0.01
AWT	0.35	0.37	0.35	0.03	0.15	0.02	0.13	-0.03
UFD	0.13	0.13	0.13	0.02	0.14	-0.01	0.12	-0.05
AUFD	-0.01	-0.03	-0.02	0.003	0.09	0.01	0.06	-0.04

Table 4.11: The Genetic Correlations Between
the Wool and Carcass Traits.

TRAIT	LFWT	HFWT	CFWT	YIELD	STLEN	BULK	MFD	COLOUR
MWWT	0.74	-0.16	-0.22	-0.63	0.19	1.51	-0.07	0.44
PLWT	-0.05	-0.47	-0.48	-0.55	-0.34	0.69	-0.38	-0.14
PUFD	0.74	-0.41	-0.37	-0.14	-0.39	0.76	-0.18	-0.04
PAUFD	1.73	0.16	0.26	0.81	-0.19	0.90	0.10	0.32
HCWT	0.13	-0.45	-0.48	-0.59	-0.25	0.75	-0.27	-0.05
CLEN	-1.48	-0.16	-0.10	0.27	-0.62	-0.89	-0.73	-0.41
GR	1.00	0.64	0.60	0.40	0.13	0.21	0.50	0.47
C	0.91	0.49	0.49	0.49	0.01	0.23	0.12	0.29
TSF	0.55	0.23	0.22	0.19	0.18	-0.23	0.22	0.07
PCSF	0.84	0.41	0.37	0.08	0.03	0.29	0.32	0.46
TIF	0.47	0.12	0.05	-0.33	0.08	0.01	0.22	0.38
PCIF	0.74	0.24	0.16	-0.33	0.14	0.06	0.29	0.44
TLEAN	-0.73	-0.41	-0.35	0.03	-0.16	0.12	-0.20	-0.38
PCLEAN	-0.67	-0.26	-0.23	-0.02	-0.13	0.34	0.01	-0.25
TBONE	-1.05	-0.22	-0.20	-0.07	-0.24	-0.55	-0.60	-0.36
PCBONE	-0.98	-0.10	-0.06	0.17	-0.12	-0.84	-0.64	-0.47

This low to moderate relationship between liveweight and fleeceweight has been observed in the literature eg Baker et al (1979), Tait (1983).

However, low negative estimates between fleeceweight and liveweight have been reported in the literature (eg Baker et al (1979) using regression methodology and also in overseas studies eg Turner and Young (1969), Cunningham and Gjedrem (1970)). But from long term selection experiments, selection for either increased fleeceweight or bodyweight has found to increase the other (eg Blair, 1981; Davis and McGuirk, 1987). In the last 3 years analysed, Blair (1986) reported that liveweight accounted for only 17% of the fleeceweight response in the ewes. Most of the responses could be classified as negligible to low positive. From the Australian Merino lines selected for high and low weaning weight, Pattie and Williams (1967) and Davis (1987) concluded that the main relationship between liveweight and fleeceweight was through the wool growing surface area.

The genetic correlations of YIELD, STLEN and BULK were negligible to moderately positive with liveweight (Table 4.10), with the exception of BULK and AWT which was moderately negative. In contrast, the genetic correlations were moderately negative between MFD and liveweight, and lowly negative between COLOUR and liveweight. For most of the phenotypic correlations between the wool characteristics and liveweight were negligible. This indicated that liveweight generally has little effect on the expression of these traits.

There is little information in the literature on these relationships, but the limited evidence would tend to suggest that in

most cases the correlations are negligible (eg Table 2.4; Davis and McGuirk, 1987). Probably most of these relationships can be attributed to the more general relationship of fleeceweight and liveweight. Davis (1987) considered that the correlated responses in the wool quality traits, after direct selection for weaning weight in Australian Merinos, could be attributed to the correlated response in fleeceweight.

4.4.4 The Correlations Between Fleeceweight and Carcass Traits

There was no clear relationship between liveweight or HCWT and LFWT, however HFWT and CFWT were generally low to moderately negatively correlated with liveweight and HCWT (Table 4.11). In the carcass traits there was little difference between LFWT and HFWT correlations except in the magnitude, which could be attributed to the differences in heritability estimates used. Fleeceweight was low to moderately positively correlated with the various measurements of carcass fatness, and low to moderately negatively associated with lean and bone contents.

The genetic correlations between the wool characteristics and the carcass traits were similar to those between the carcass traits and HFWT and CFWT (Table 4.11). This was except for the low to moderate positive genetic correlation between BULK and lean content. There is no apparent reason for these trends apart from the relationship of these wool characteristics to fleeceweight. There may also be an influence due to the different breeds used, because there were significant breed

mean differences in the wool and carcass traits.

These relationships tended to be very similar to those of Botkin et al (1971), except carcass C. The negative genetic correlation between fleeceweight and carcass C by Botkin et al (1971) appears to be inconsistent with the positive correlation between fleeceweight and total fat weight reported by them and this study. However, it is necessary to keep in mind the differences between the two studies. There were a number of differences involved between the trials of Johnson et al (1968) and Botkin et al (1971) and this study, particularly in the breeds involved (apparel type vs carpet type) and the experimental design. The lambs used in their study were self-fed an pelleted ration before being slaughtered at 50kg liveweight. Overall, the results would tend to support the conclusion of Johnson et al (1968) and Botkin et al (1971) that there is some antagonism in animals fed to a heavy constant weight between the measurements of fleece growth and meatiness at slaughter.

4.4.5 The Correlations Between Ultra-sonic Backfat Depth And The Other Traits

4.4.5.1 Correlations Between Ultra-sonic Backfat Depth, Liveweight and Carcass Traits

Many studies have shown fat to be the most variable tissue, with the greatest influence on the carcass composition (Berg, 1982). In sheep, fatness has become a major concern primarily due to diet concious consumers and many studies have concentrated on the evaluation

of fatness on the live animal, such as the ultra-sonic probe (Thompson, 1985).

The correlations between weight-adjusted UFD and unadjusted UFD were generally highly positive (Tables 4.4, 4.5, 4.8). The UFD's were moderate to highly positive correlated with the measurements of carcass fat, and moderate to highly negative with lean and bone tissue contents (Tables 4.5, 4.6, 4.8). Similar correlations between UFD and C were reported by Bennett et al (1983b) and Parratt et al (1987a) and between UFD and GR by Parratt et al (1987a). In the wool data set, the relationship between the unadjusted UFD and liveweight was low to moderately positive (Table 4.4), with the magnitude increasing to the time when the scan was taken. In contrast, the AWT-adjusted UFD was negligible and suggested the pattern of maturity of the subcutaneous fat depot relative to liveweight. Generally the relationship between UFD and liveweight was low to moderately positive.

The correlations in this study between UFD and liveweight and also hot carcass weight, are moderate to highly positive (Table 4.5). In contrast to this, the genetic correlations between CLEN and UFD were highly negative, and the phenotypic correlations were lowly negative. Purchas et al (1981 and 1982) had noted that in a comparison of Romney and Southdown on the basis of UFDs, the fatter animals were shorter than the leaner animals. Similar results were found later in the Southdown selection lines by Solis (1988) and Kadim (1988). But, Solis (1988) found that selection on weight-adjusted UFD had not affected growth rate or liveweight. In this study, after adjusting for liveweight the UFD the phenotypic correlations between liveweight and

AUFD were small. This would be expected since the variation due to liveweight has been taken into account.

The current lamb export grading system (NZMP, 1987) is based on the measurement of carcass weight and the tissue depth GR. This system has been shown to account for 70 to 80% of the variation in the percentage weight of the fat, lean and bone tissue components (Kirton et al, 1985; Kirton et al, 1986). By using linear measurements for carcass classification, biases due to breed and source of animals (particularly in research) are excepted (Kirton et al, 1986). The immediate aim of any breeding plan would be to exploit this system by the production of large lean animals. While there has been little definition of the required criteria for large lean animals, initially the aim would be to produce animals whose carcass weight is over 17 kg and reduce their tissue depth GR to under 7.5 mm. In the long term, breeding objectives should be for an increase in the total amount of lean tissue and for a reduction in total fat content.

With the high correlations of liveweight with hot carcass weight, selection for increased liveweight at any age would apparently meet the aim to increase carcass weight. Kirton et al (1986) also observed that the combination of the carcass C fat measurement and carcass weight would account for slightly less variation in the percent carcass tissues than using GR and carcass weight. This would tend to suggest that an ultra-sonic backfat assessment of carcass C adjusted for liveweight may be a suitable live-animal measurement of fatness. The high positive correlations of weight-adjusted UFD with GR and C by this and other studies (eg Wolf et al, 1981; Parratt et al, 1987a)

would suggest that this measurement can be used as an live-animal selection criteria to reduce fatness.

Based on these correlations, selection against UFD would be expected to reduce the GR and C measurements in the intermediate period. In the longer term, it would be expected to reduce overall fatness and increase the amount of lean and bone tissues. The results of Fennessey et al (1982) with Coopworths, Bennett et al (1983a) with Southdowns and Suffolks, and Kadim (1988) with Southdowns, have shown that there are have been significant changes possible in carcass C. It is uncertain if there are correlated changes in fat, lean and bone after selection on ultra-sonic backfat depth. Kadim (1988) reported that at a constant carcass side weight that there were significant differences in these tissues, but there was no difference in the actual weight distribution or placement.

However, it would be more realistic to determine whether or not it is necessary to select against fatness. For selection it would result in a further measurement and therefore another trait for selection. There are also problems with the time of measurement of backfat depth, since fat is the most variable carcass tissue. Beatson (1987) reported that weight-corrected backfat depth in Coopworths was more reliable in July (about 10 months of age) than in either April or October. It was thought that the April fat depths may be compromised by low fat depths after unfavourable summers, while accurate October measurements were confounded by fat layers being deposited during rapid spring growth. In the long term, there may be a potential problem of maintaining sheep with adequate fat stores to enable them to survive in

stressful conditions, whilst at the same time producing offspring with lean carcasses at market weights (Butterfield, 1988).

Considering that an important result of the between breed studies was that later maturing breeds were leaner at a constant age or weight (Thompson, 1985), selection against fatness might not be necessary. In the calculation of selection indices has highlighted the importance of carcass weight in the final returns (Simm 1986; Parratt and Simm, 1987; Simm et al, 1987). These various results would appear to relate to the generally positive genetic correlation between the UFD and liveweight. Rae (1984) has provided some estimates of the predicted annual genetic change at a constant age for various selection indices. Selection based solely on liveweight would lead to small increases in the GR measurement and in percent chemical fat. Only selection on weight-adjusted ultra-sonic fat depth and restricting carcass weight would reduce GR and percent chemical fat. Although, selection for liveweight alone at a constant carcass weight would tend to reduce fatness. In the within-flock ranking of rams on their fat-free carcass weight, Nicol and Parratt (1984) reported that the inclusion of fat depth estimation with liveweight would markedly increase the efficiency of ranking of two-tooth rams over liveweight alone.

4.4.5.2 Correlations Between Ultra-sonic Backfat Depth

And The Wool Traits

The positive genetic correlations of both LFWT and BULK with the various UFD measurements is the consistent feature of both data

sets (Tables 4.10, 4.11). For the other wool traits the magnitude of the genetic correlations were smaller in the meat data set than the wool data set. The positive genetic correlation between weight-adjusted UFD is and the other wool traits were also consistent, but the magnitudes are different. The correlations of the unadjusted UFD were of opposite signs.

Botkin et al (1971) had also reported positive, but negligible genetic and phenotypic correlations between greasy fleeceweight and liveweight-adjusted UFD at slaughter. The negative genetic correlations between hogget fleeceweight and UFD reported by McEwan et al (1984) were inconsistent with the positive phenotypic that were also reported. These positive correlations were consistent with Botkin et al (1971) and this study. There may of been an effect due the different times of measurement between the studies, and also McEwan et al (1984) used animals from selection lines. However, the estimated realised genetic correlations, after 9 years of selection, were low positive. Parratt et al (1987b) observed that at a constant age, there was no difference at 8 months of age in ultra-sonic backfat depth between the line selected for hogget fleeceweight and the control line. But at a constant weight the hogget fleeceweight line was significantly fatter than the control line.

CHAPTER FIVE

CONCLUSIONS

An important step in deciding the a breeding objective for the dual-production of meat and wool, is to determine which traits that would meet the current and future market requirements. In the wool industry, clean fleeceweight would appear to remain the major trait in the objective, unless sufficient price premiums appear for certain wool quality traits eg loose wool bulk. However in the long term, the correlations suggest possible problems of increasing MFD, COLOUR, and decreasing BULK. But the presently available information suggests little advantage in the selection of these traits.

While selection for liveweight would apparently reduce fatness at a constant weight, there is likely to be an undesirable correlated increase in the GR grading measurement. The moderately positive correlations of liveweight and fleeceweight with ultra-sonic backfat depth would appear to negate the associated advantages of the reduction in carcass fatness.

The genetic correlations between the wool and meat traits were small to moderate in magnitude. The moderately positive correlations between fleeceweight and the carcass measurements of fatness, particularly GR and C, would cause some long term problems with the current grading system. The low negative correlations between fleeceweight and lean tissue content may reduce selection efficiency for lean meat and wool production. But is unlikely to be a major

concern, similarly with the low negative correlation between fleeceweight and bone content. The correlations between the wool quality traits and the meat traits appeared to follow the same relationship of these traits to fleeceweight.

The estimates of the within-breed heritability indicate that most of the traits would respond to selection. The high estimates of ratio of between-breed genetic variance to the total genetic variance indicate that selection of any of the wool traits and liveweight would be more efficient between the breeds studied, and that selection for the carcass traits should be within a breed. It would be important to initially choose the right breed before any selection for improvement is undertaken.

Overall, there is a rather suprising small quantity of knowledge of the relationship between meat and wool production. A more detailed study of the relationship between liveweight, fleeceweight and carcass characteristics is required, particularly in the growing animal. In addition, the theory of parameters under cross-breeding is inadequate, especially considering that cross-breeding would be the immediate method of obtaining suitable dual-purpose animals for lean growth and wool production.

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