A STUDY OF THE INHERITANCE OF FOLLICLE AND FLEECE CHARACTERISTICS IN MERINOS, NEW ZEALAND ROMNEYS, AND THEIR CROSSBRED PROGENY

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ABSTRACT

A study was carried out to investigate the inheritance of follicle and fleece characteristics in Merinos, New Zealand Romneys and their crossbred progeny under North Island conditions. A total of 637 animals were sampled from the Ministry of Agriculture and Fisherie's flocks at Tokanui. It should be noted that the Romneys studied, were not the parents of the crossbred animals. Six flocks were sampled.

Least squares means of the Romneys, Superfine Merinos, Local Merinos, Superfine Merino x Romneys, Local Merino x Romneys and Backcross (3/4 Superfine Merinos) were respectively as follows: secondary to primary follicle ratio (S/P), 6.68, 18.06, 18.66, 10.92, 10.32 and 15.81; follicle density n(P+S), 35.73, 69.69, 82.07, 49.57, 45.92 and 73.60; primary follicle density (nP), 4.72, 3.70, 4.23, 4.12, 4.23 and 4.40 and mean fibre diameter (MFD) 37.26, 20.71, 22.56, 26.24, 28.23 and 21.21.

Of the fixed effects tested (age, birth/rearing rank and year of sampling) only age exerted a significant effect on most fleece and follicle characteristics. The repeatabilities for all follicle characteristics were greater than 0.4. Most objectively measured fleece characteristics also showed moderate levels of repeatability. Heritability estimates for follicle characteristics, calculated from small numbers of daughter/dam pairs, were moderate to high.

Phenotypic and genetic correlations for 21 fleece and 7 follicle parameters are reported on data corrected and uncorrected for fixed effects. An attempt was made to predict S/P using stepwise multiple regression techniques, but the resultant equations had low accuracy. There was negative heterosis in both crossbred genotypes for most follicle characteristics. LWT showed the highest level of positive heterosis.

Methods of main gene detection were used to investigate the underlying genetic factors controlling follicle inheritance. Although follicle data had skewed distributions there was little evidence for genetic segregation for n(P+S). Multifactorial inheritance of n(P+S) was indicated. Two or more loci are possibly involved in the inheritance of S/P. The S/P genes appeared to behave in a recessive fashion. In contrast, the current results suggest the presence of a main gene for primary follicle density in both types of Merino x Romney flocks.

INTRODUCTION

In animals to be farmed for the production of textile fibres it is necessary to combine maximum rates of fibre formation with the best possible value per kilogram.

Fibre fineness is very important in determining the suitability of fibres for clothing since, with garments of the same weight and shape, those made from finer fibres will have greater warmth, softness and bending flexibility.

With sheep, the combination of high fleeceweight and fine fibre diameter is only attained in sheep of high follicle density. This is best illustrated by comparing the fleece and follicle populations of the Merino and other breeds of sheep. Although the diameter and weight of each fibre produced is very low, Merino sheep rank highly in weight of wool produced because they have far more follicles than other breeds of sheep.

Carter and Clarke (1957a) showed that this high follicle density in the Merino was due to the fact that they develop far more secondary follicles and Carter (1955) developed the technique of using the S/P ratio as the criterion of secondary follicle development.

Traditionally animal breeders have utilized techniques that bring about genetic improvement, even though individual genes are not recognized. More recently, there has been increasing interest in searching for main genes, since this knowledge has potential advantages:

1. It is not too difficult to utilize crossbreeding, followed by backcrossing and selection to transfer a gene from one breed to another. In this way the poll gene from Corriedale and Ryeland sheep was transferred into Dorset Horns to establish a polled strain.

2. With modern techniques of DNA manipulation and injection into the pronucleus of embryos it may soon be possible to take a gene from one individual and transfer it into a newly developing young animal with a very different genotype, at other loci.

The identification of a high follicle density gene may thus allow the gene to be transferred by either of the above means.

The present topic was chosen because of the suspicion that follicle traits, particularly S/P ratio, might be inherited fairly simply. Merinos and Romneys are so different in these traits that it was decided to investigate the inheritance of S/P ratio in Merino x Romneys. A flock, including straightbred Merinos and various classes of crossbreds, was available on the Tokanui research farm. Although these flocks had been established some time earlier and samples had not been taken at the time of establishment of the crossbreds, they provided a reasonable, if not ideal source of data.

ACKNOWLEDGEMENTS

TABLE OF CONTENTS

CHAPTER 1 REVIEW OF LITERATURE   1

CHAPTER 2 MATERIALS AND METHODS

CHAPTER 3 ANALYSIS OF THE EFFECTS AGE, YEAR OF SAMPLING AND BIRTH/REARING RANK ON FOLLICLE AND FLEECE CHARACTERISTICS

CHAPTER 4 GENETIC AND PHENOTYPIC PARAMETERS

CHAPTER 5 METHODS OF GENE DETECTION

CHAPTER 6 GENERAL DISCUSSION AND CONCLUSIONS

LIST OF TABLES

LIST OF FIGURES

CHAPTER 1

REVIEW OF LITERATURE

Definitions of terms used in the review of literature and throughout this dissertation are given in section 2.1 of Chapter 2.

1.1 FLEECE-FOLLICLE RELATIONS

The type of fleece produced is the result of the activity of millions of follicles (Nathusius, 1866, cited by Abouhief, 1980). Both the number of follicles and individual follicle behaviour exert effects on fleece structure.

The arrangement of follicles in follicle groups as well as the size and shape of individual follicles vary markedly between breeds of sheep. Different types of birthcoats and adult fleeces can be attributed to this basic structure. The follicle pattern may be used to demonstrate the evolution of the domestic sheep with a uniform fleece from a wild species of sheep which had a double coat rather than a fleece (Fraser and Hamada, 1952; Fraser, 1953).

Fig 1.1 from Carter (1955), shows the spatial follicle patterns of various breeds of sheep.
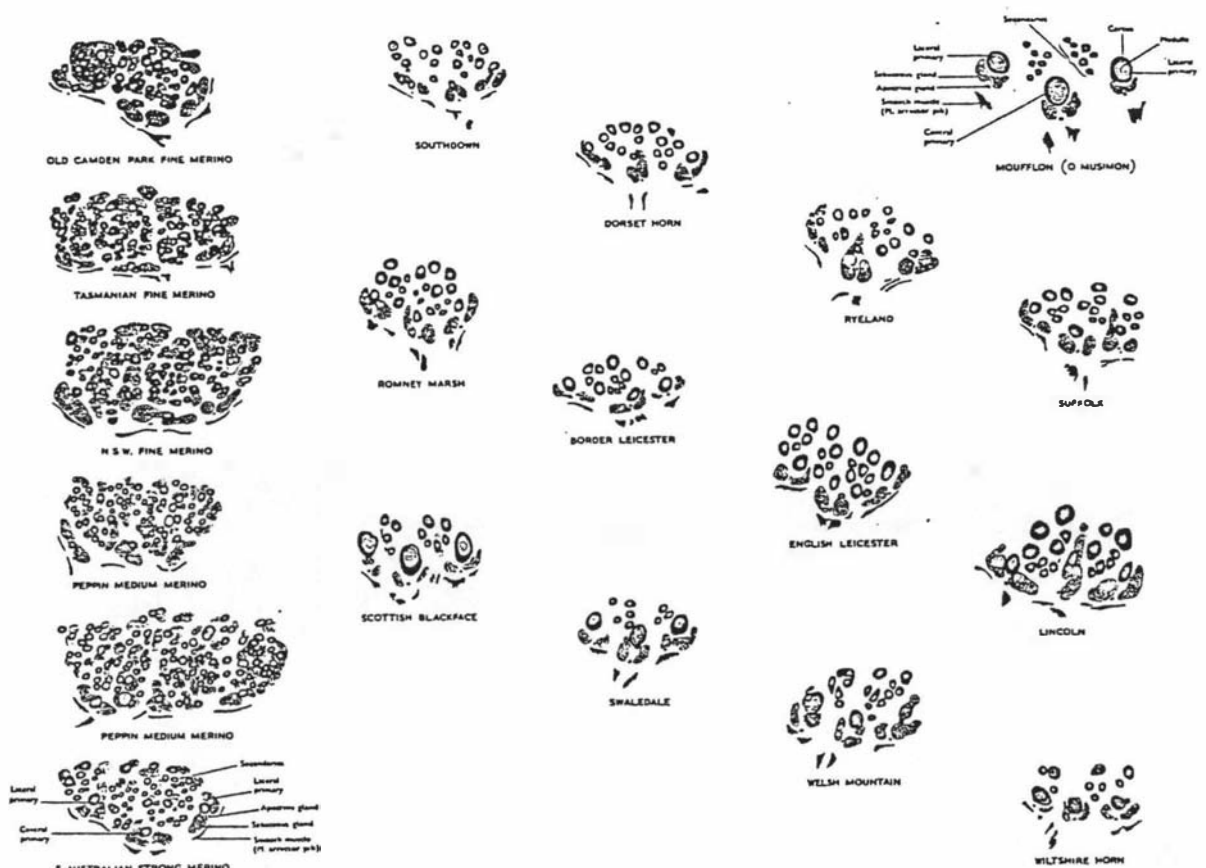
In sheep, wool is produced from two distinct types of follicles. They are classed as secondary and primary follicles due to their developmental sequence (Wildman and Carter, 1939; Carter, 1939a, 1955).

Primaries tend to form in a group of three, the primary trio. This is accompanied by a variable number of secondary follicles. The unit of primaries and secondaries is referred to as the follicle group (Carter, 1939a, 1943, 1955; Hardy and Lyne, 1956b). Figure 1.2 shows a follicle group in transverse section.
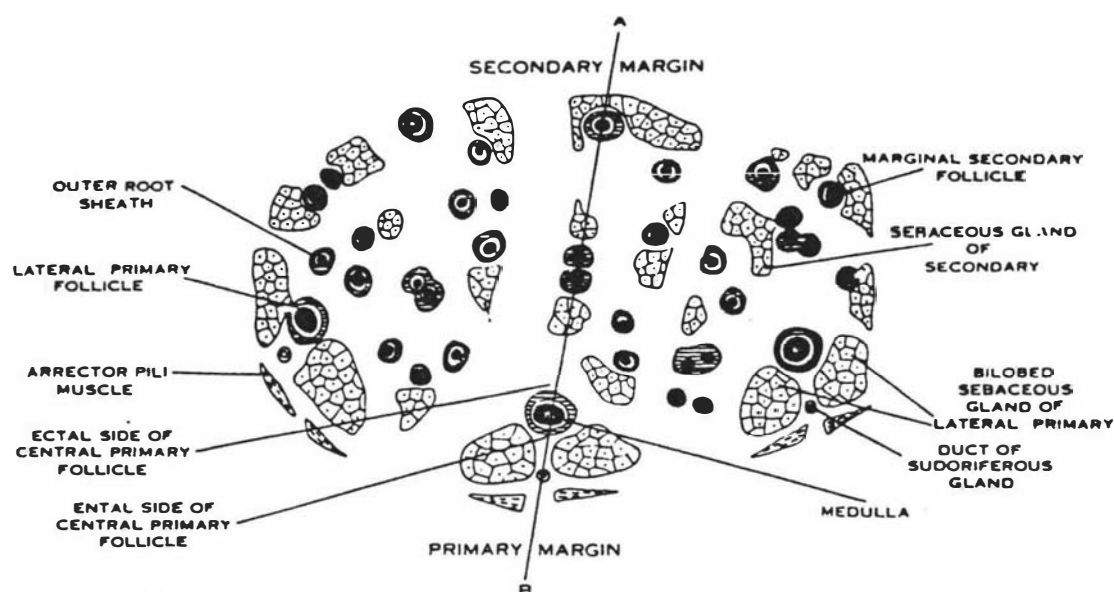
Figure 1.2 A follicle group In transverse section from Hardy and Lyne (1956a).

As well as being more numerous, secondary follicles tend to produce finer fibres. This difference is more noticeable in certain breeds of sheep (Ryder and Stephenson, 1968).

Although both types of follicles can have accessory sebaceous glands, these are small and frequently not present in secondaries. Only primary follicles have a sudoriferous gland and an arrector pili muscle. The sebaceous gland associated with primary follicles is often bi-lobed. In fine woolled sheep, primary and secondary follicles are located at the same level in the skin, the level of the secondaries in coarse woolled sheep (Diomidova, 1961).

The primitive wild sheep such as the Canadian Bighorn (*O. canadensis*) has very large central and lateral primary follicles which produce coarse, heavily, medullated kemps (Ryder and Stephenson, 1968). These fibres form the outer coat and are shed mainly in the spring. The secondaries produce fine non-medullated wool fibres which are shed with the seasonal moult of the whole coat. The outer coat consists of long fibres which cover up the shorter wool fibres and kemps. This wild type fleece and follicle pattern also occurs in the double coated breeds of India, North Africa, and the Middle East. These double coated breeds seem to have evolved in a parallel but separate manner to the British breeds (Ryder and Stephenson, 1968). Indian breeds with a similar fleece structure to British breeds have a consistently lower secondary to primary follicle ratio (S/P). The Herdwick and Scottish Blackface breeds have an S/P ratio of 3:1.

Fraser and Hamada (1952) and Fraser (1953) placed breeds into three categories based on fleece type:

1. The longwool type, e.g., the Lincoln, Romney Marsh and Border Leicester, with a long, fairly even fleece and a birthcoat with few or no halo-hairs. The type has a high fleeceweight, low follicle density and S/P ratio ranging from 5.1 to 7.1.

2. The down or short wool type e.g., the Southdown, Ryeland, and Dorset-Horn breeds. Both fleeceweight and follicle density are low, although the latter is slightly higher than for the longwool types. The short even fleece is finer than that of the longwools and the birthcoat lacks or has very few halo-hairs. This type has an S/P ratio of 6:1 to 9:1.

3. The third fleece type, the Merino with much higher follicle and fibre densities than other breeds. The fleece tends to be very fine, relatively short and fairly heavy (Fraser, 1953). The Merino also has an S/P ratio ranging from 20:1 to 50:1. In comparison with other wool types, the secondaries produce a higher proportion of the fleece fibres (Carter, 1939b). The Merino may have a birthcoat only slightly less coarse than the carpet wool types or fine and woolly like those of the shortwool and longwool breeds, e.g., high halo-hair frequency or low frequency (Schinckel, 1955c, 1958a). Although these differences are seen in the birthcoat, they do not result in an adult carpet or long wool fleece type (Lockhart, 1956). The only carryover effect from a hairy birthcoat is the increased variability of fibre diameter and decreased crimp frequency in the adult fleece. The fleece tends to be short, very fine and fairly heavy (Fraser, 1953).

In coarse woolled sheep such as the N.Z. Romney, the primary follicles tend to be larger than the secondaries, which gives a fleece with wide variation in fibre length and diameter. In contrast, the Merino with its high follicle numbers and low follicle size variation has a dense, even, square-tipped fleece.

The greatly increased follicle population and high number of secondary follicles in the Merino, is caused by budding of the original secondaries to give many derived secondaries (Hardy and Lyne, 1956a, Rougeot et al, 1984). These differences in fleece appearance and follicle population have been used to postulate a different evolutionary pathway for the Merino from the British breeds (Ryder and Stephenson, 1968).

The amount of raw material and energy reaching the follicle will also influence follicle development and fibre output per follicle (Cockrem and Rae, 1961). According to Fraser (1953) the genetic types of fleece structure in different sheep breeds were caused by: 1. the quantity of fibre substrate available, 2. individual follicle differences in competitive efficiency for fibre substrate, the competitive efficiency being related to its time of initiation, i.e., primaries being more efficient than secondaries (Fraser, 1951), 3. between-breed differences in follicle efficiency and 4. between - breed differences in fibre density e.g., inter-follicular competition.

Fraser and Short (1952) measured the spatial patterns of follicle populations in several breeds of sheep. They determined the average relationship of fibre diameter to the diameter and distance of adjacent fibres. They observed a negative relationship between the size of a fibre and the number and size of adjacent fibres e.g., denser fleece types are finer and shorter. According to this concept, the quantity of fibre produced by an individual follicle is affected by the number of follicles close to it (Fraser and Short, 1952, 1960; Fraser 1953).

There has been much research in this area but little real evidence for or against localized competition has been published. Wickham, (personal communication), has suggested that each follicle is part of a generalized pattern of competition for which neighbouring follicles may be no more significant than follicles on a distant region and in which other tissues are also important.

Vertical skin sections have also been used to study follicle and fibre relationships. Follicles vary from short and shallow to long and deep to straight or very curved (Nay and Johnson, 1967). Follicle curvature may affect crimp formation and set in the fleece (Nay and Johnson, 1967; Nay and Williams, 1969).

In a study of the follicle characteristics in sheep selected for increased or decreased fleeceweight, Nay (1970) noted a correlation between follicle depth and follicle width, deeper follicles producing wider fibres. At a given follicle depth, there was a concomitant increase in fibre number and fibre diameter. Sheep with short shallow follicles produced less wool (Nay, 1970). High fleeceweight animals had straight, closely packed deep follicles which produced high yielding fleeces with low crimp frequency. The author suggested the possibility of a genetic correlation between fleeceweight and the percentage of follicle bending.

The differences in the numbers, types, relative sizes and outputs of individual follicles and their relation to the total follicle population determine the ultimate fleece type.

1.2 FOLLICLE INITIATION AND DEVELOPMENT

The sequence and pattern of follicle initiation and development during foetal development has been well studied (Galpin, 1935; Carter, 1942, 1943, 1955; Carter and Hardy, 1947; Schinckel, 1953; Short, 1955a; Hardy & Lyne, 1956a; Lyne, 1957).

Although some between-region variation exists in the time of follicle initiation, on the midside position, follicles tend to begin around 60-70 days for primaries, and from 90-99 days post-conception for secondary follicles.

Follicle initiation occurs in an organized fashion at various times depending on the body region. Waves of follicle development begin on the head and legs and flow caudally and dorsally from the legs to cover the entire foetus (Carter and Hardy, 1947; Ryder, 1956; Stephenson, 1958).

Follicles form in a group around individual follicles laid down during the first two waves of follicle development. At regular intervals new follicles appear around the central follicles.

The three phases of follicle development are: 1. pre-trio, 2. trio and 3. post-trio. The pre-trio phase starts with the first wave of follicle development and by 60-65 days gestation two types of primary central follicles (PCX, PCY), have been formed. During the trio phase, from 75-78 days, follicle plugs appear on either side of the primary central follicles. These are known as primary laterals - PLx and PLy. Not all central primary follicles develop two associated lateral primaries. The number developed ranges from 0-3 (Ryder and Stephenson, 1968).

The post-trio phase involves the initiation of secondary follicles and commences at 90 days post-conception. Secondary waves of secondary follicle initiation produce secondary follicles between the primary trio and the first secondaries. Secondary follicles are initiated until birth. In some breeds, e.g., the Merino, derived secondaries may form by budding off the original secondary follicles (Carter, 1955; Hardy and Lyne, 1956a; Rougeot et al, 1984). As the late maturing follicles are being initiated, those formed earlier are maturing.

The primary central follicles are mature (producing fibres) at 100 days of gestation while the first secondaries reach this stage at 125 days. Secondary follicles continue to mature after birth even until the lamb is 12 months old in Merinos, although the duration of follicle population maturation shows some between-breed variation (Stephenson, 1958). Once fibre production is past the level of the sebaceous gland, the follicle is considered mature (Hardy and Lyne, 1956a).

1.3 ADULT FOLLICLE POPULATIONS

1.3.1 MERINO STRAINS

Carter and Clarke (1957a) studied the follicle populations of 22 Merino studs. A minimum of 20 animals aged 12-18 months were sampled from each stud. As far as possible these sheep had not been selected on any systematic basis except randomisation for sampling.

The traits measured were: mean total follicle density (n(P+S)), secondary to primary follicle ratio (S/P), mean primary fibre diameter (dP), mean secondary fibre diameter (dS), mean fibre diameter of the composite population (d(P+S)) and the ratio of primary to secondary fibre diameter (dP/dS). This is one of the few studies which investigated fibre parameters from skin sections. Table 1.1 summarises the results of Carter and Clarke (1957a).

Table 1.1: The range of individual follicle and fibre parameters observed by Carter and Clarke (1957a).

Sheep Nos.	Fine 295	Medium non-Peppin 69	Peppin 158	S.A. Strong[1] 63
nP	1.5-5.0	1.4-4.2	1.7-4.9	1.9-4.9
n(P+S)	30-118	25-88	32-114	37-82
S/P	11.2-32.8	14.5-34.6	12.5-46.1	10.7-28.3
dP (μm)	12.7-31.2	16.6-35.0	15.2-44.7	22.7-48.8
dS (μm)	12.8-23.2	16.5-27.4	14.1-28.8	19.0-28.4
d(P+S)	12.9-23.6	16.8-27.4	14.5-29.1	19.7-28.7
dP/dS	0.85-1.62	0.80-1.54	0.80-2.15	0.97-2.21

1 South Australian

Between-flock differences for total and primary follicle densities along with follicle group size were noted. The authors concluded that the observed differences were genetic in origin. Camden Park and Fine Merinos had very similar follicle productivity but different group size, while other strains had similar group size but dissimilar follicle productivity. From these results Carter and Clarke (1957a) suggested that one could select for more follicles, e.g. S/P, greater follicle density, or larger area without altering fibre characteristics.

Heydenrych et al, (1977) and Heydenrych et al, (1984) studied South African Merinos and reported S/P follicle ratios ranging from 23.54 to 26.24, in line with the results of Carter and Clarke (1957a).
The results of Steinhagen et al (1984) and Steinhagen et al (1985) are within the range of these studies.

1.3.1.1 ABERRANT FOLLICLE POPULATIONS IN MERINOS

1.3.1.1.1 Low S/P Ratio

The occurrence of some Merinos having a low S/P follicle ratio has been noted by several authors (Carter, 1939b; Carter and Clarke, 1957a; Short, 1958; Fraser and Short, 1960; Jackson, personal communication). Carter and Clarke (1957a) suggested that the occurrence of low S/P ratio sheep in the Peppin medium Merinos is widespread but its incidence is sporadic and rare. A small flock of low ratio (3:1 - 5:1) animals was derived from a mutant ram in a CSIRO Merino flock.

Carter and Clarke (1957a) studied skin samples from a Merino with an S/P ratio of 3.5. Fraser and Short (1960) noted that low ratio animals had no change in primary follicle density or fibre length growth rate. The low ratio animals had a low fibre population, good fibre uniformity and a mid-side $n(P+S)$ of 20/mm^2. Their fleeces were lightweight, yellow and very short with extremely high crimp frequency and a mean fibre diameter of ≤ 28 μm. They resembled those of the Dorset Horn or Ryeland breeds. The yellowness suggested a high suint content (Jackson, personal communication).

Fraser and Short (1960) and Jackson (personal communication), noted that limited evidence from breeding suggested that the low S/P condition might be due to a single gene acting as a simple recessive. Unfortunately, the low S/P flock no longer exists (Jackson, personal communication).

1.3.1.1.2. The Gog

In the Merino, the "Gog" gene very nearly eliminates sweat glands, decreases fibre length growth rate, follicle density and wool production, the latter by 80-90% (Fraser and Short, 1960). At birth the nP of Gogs was similar to that of normal lambs. Fibre diameter was slightly increased.

1.3.1.1.3 Felting Lustre Mutant

Short (1958) studied another unusual fleece mutant which appeared in a flock of Australian Merinos. The adult fleeces were pale yellow and lustrous. Scouring removed the yellow discolouration but, in contrast to normal Merino wools, the fleeces remained lustrous. Crimp frequency resembled that of Romney fleeces of 40-46s. The lustre mutants had finer wool than normal Merinos raised under similar conditions.

Lustre mutant animals had reduced S/P ratios, total fibre and primary densities. These animals had lower than average body weights and were free from skin wrinkles. Wool from lustre mutants felted seven times faster than normal Merino wools of the same fibre diameter, and unprotected fleeces started to cot when only 1/4 inch long. Short (1958) concluded that fleece mutants provided excellent material for genetic, physiological and textile research.

Short (1958) suggested that this condition was controlled by a single dominant autosomal gene. The study by McGuirk and Short (1967) supported Short's earlier (1958) conclusion.

1.3.2 NON-MERINO BREEDS

Carter and Clarke (1957b) studied 484, 8-18 month old animals from Australia and other countries (on average 11-23 sheep per flock). The results are summarized in Table 1.2.

Significant between breed differences in follicle population density were observed. Variation in S/P accounted for the differences. The greatest difference was observed between the British breeds and the Polwarths (3/4 Merino) and Corriedales.

The Corriedales had values for follicle characteristics intermediate to those of the Merinos and British Longwools in line with their crossbred ancestry. Polwarth values were between those of the Corriedale and the Australian Merino.

Table 1.2: Follicle and fibre parameters of several non-Merino breeds
[from Carter and Clarke (1957b)]

Breed n(P+S)	nP	S/P	dP (μm)	dS (μm)	d(P+S) (μm)	dP/dS (μm)
Polwarth						
28.9-85.3	2.6-5.4	8.5-17.4	17.3-35.5	14.3-22.9	14.8-23.5	0.97-1.78
42.6-67.6	3.4-5.2	8.4-16.7	16.0-31.5	17.6-24.6	17.8-24.9	0.82-1.41
37.6-58.5	2.2-3.5	9.5-17.4	22.3-35.3	20.1-27.1	20.4-27.1	0.98-1.34
35.6-57.7	2.8-4.1	10.5-17.0	18.5-25.9	15.7-19.8	15.9-20.3	0.95-1.44
Corriedale						
18.3-30.7	1.6-2.8	7.2-14.8	26.0-44.2	29.3-39.3	29.6-39.3	0.84-1.29
25.8-42.1	2.0-3.7	8.3-14.2	23.4-49.0	28.4-38.0	27.9-38.8	0.81-1.64
25.3-45.5	1.9-3.8	7.9-14.0	22.9-43.4	25.2-34.9	25.1-34.5	0.81-1.44
12.9-35.1	1.4-2.4	5.7-16.4	28.2-47.0	21.9-36.8	22.3-37.0	0.91-1.53
15.0-31.0	1.3-2.9	7.6-16.0	24.8-36.2	28.2-37.6	28.7-37.5	0.79-1.30
Lincoln						
10.9-17.7	1.8-3.3	3.8-7.0	47.1-66.3	35.8-47.9	38.5-51.3	1.20-1.66
English Leicester						
9.8-18.8	1.7-3.1	3.4-5.9	33.7-48.2	29.1-41.0	30.1-42.7	0.98-1.55
Border Leicester						
12.2-20.3	2.4-3.7	3.4-5.5	36.3-55.5	28.2-41.4	30.7-43.9	0.97-1.68
Romney Marsh						
16.0-28.2	2.2-4.7	4.1-8.2	29.5-46.8	28.8-39.2	29.5-39.2	0.90-1.42
Southdown						
20.0-34.5	2.6-4.9	4.1-8.6	20.0-31.9	22.4-30.4	22.0-29.9	0.84-1.33
Dorset Horn						
14.4-23.5	1.8-3.9	3.8-8.5	27.7-38.6	30.4-39.4	30.0-38.5	0.66-1.07
Suffolk						
16.5-29.4	2.7-4.9	3.7-7.5	19.2-32.2	18.2-28.2	18.4-58.9	0.88-1.38
Ryeland						
10.6-20.2	1.9-3.2	3.9-7.7	24.0-40.1	27.2-36.4	27.5-37.1	0.83-1.12
Scottish Blackface						
5.0-9.9	1.4-2.3	1.8-4.7	54.2-121.0	26.2-38.7	34.6-60.4	1.65-3.57
6.0-12.6	1.7-3.1	1.6-3.9	40.6-160.6	17.0-26.9	22.5-46.1	2.10-7.60

Table 1.2:   continued

Breed

n(P+S)	nP	S/P	dP (μm)	dS (μm)	d(P+S) (μm)	dP/dS (μm)
Welsh Mountain						
10.0-19.4	2.0-4.5	2.2-5.8	40.4-106.4	21.5-28.6	27.4-46.7	1.59-3.75
Swaledale						
6.4-11.2	1.6-2.7	2.6-4.3	48.2-92.7	18.8-33.0	26.6-46.0	2.46-2.99
8.2-11.9	2.2-3.0	2.3-3.9	67.1-108.9	26.0-32.8	40.4-50.8	2.19-3.87
Swedish Landrace						
8.3-16.8	1.6-2.7	3.0-7.4	61.0-86.6	29.3-42.4	33.1-47.8	1.64-2.34
Cheviot						
11.6-17.8	2.1-3.5	3.6-5.9	19.3-29.7	14.2-26.3	15.6-26.9	1.04-1.58
Wiltshire						
8.3-14.4	1.8-3.2	2.5-4.8	37.2-67.3	22.7-38.3	28.2-46.6	1.21-2.15

Table 1.3   Follicle and fibre parameters for several breeds.
(from Daly and Carter (1955))

Breed		Lincoln	Corriedale	Polwarth	Fine Merino
Expt 1: Ewe Numbers		4	4	4	4
Character	**Period**				
n(P+S)/mm^2	1	16.1	31.2	51.5	81.8
	10	9.3	19.4	31.8	66.9
nP/mm^2	1	2.5	3.1	4.1	3.5
	10	1.2	2.0	2.3	2.7
S/P	1	5.6	9.0	12.0	21.5
	10	6.8	8.9	13.2	24.0
dP(μm)	1	59.0	34.7	28.7	22.5
	10	58.0	32.2	25.4	19.3
dS(μm)	1	43.6	34.3	29.0	22.0
	10	49.6	34.9	25.6	17.5
dP/dS	1	1.35	1.01	1.00	1.02
	10	1.19	0.92	0.99	1.10

Daly and Carter (1955) studied the fleece growth of young Lincoln, Corriedale, Polwarth and fine Merino maiden ewes under housed conditions. A summary of the follicle and fibre results is given in Table 1.3.

S/P values ranged from 5.6 for the Lincoln, to 21.5 for the fine Merino. There was little between - breed variation for primary follicle density. Total follicle density varied with S/P ratio but was also affected by age and increasing bodyweight. Fibre diameter, dP, dS, d(P+S) and fibre length decreased from the Lincoln to the Merino, the Corriedale and Polwarth animals having intermediate values.

Although only 4 sheep per breed group were used, Daly and Carter (1955) stated that the results for fleece and body characteristics suggested that Lincolns and fine Merinos had multiple genes which acted additively in the two crossbreeds.

Arbiza et al (1966) conducted a study using similar breeds to Daly and Carter (1955) but in a pasture grazing environment in Uruguay. Their results for follicle and fibre parameters are given in Table 1.4. The follicle data showed the expected trends with the Merino having the lowest diameters and the highest S/P and n(P+S).

Table 1.4: Follicle and fibre characteristics for several breeds.
(from Arbiza et al, (1966))

Breed	Romney Marsh	Corriedale	Polwarth	Australian Merino
Number (n)	13	13	13	13
n(P+S)	14.78±1.91	20.14±4.89	34.57±6.88	46.03±6.26
nP	2.21±0.38	1.96±0.26	2.46±0.38	2.18±0.39
S/P	5.88±1.17	9.34±2.09	13.01±1.99	20.64±4.60
dP(μm)	37.31±1.62	29.75±2.88	21.75±3.03	23.30±2.25
dS(μm)	32.25±1.59	26.98±1.71	20.96±2.30	20.95±1.30
d(P+S) (μm)	32.99±1.45	27.30±1.76	20.93±2.19	21.07±1.27
dP/dS (μm)	1.16±0.06	1.10±0.08	1.04±0.04	1.11±0.14
n(P+S):S/P	0.473NS	0.807**	0.702**	0.635*
Between breeds	0.920**			

* $P < 0.05$ ** $P < 0.01$

Burns (1949, 1953, 1954a, b) studied the fleece and follicle characteristics of several British breeds including the Suffolk, Herdwick, and Scottish Blackface. Breed means from these studies are included in Table 1.5. Analysis of repeated samples from lambs showed that follicle density declined rapidly with increasing age, but flattened out when the sheep were one year old.

Ryder (1957) also examined follicle populations of a range of British breeds. The numbers of animals sampled and the results obtained are included in Table 1.5.

1.4 FOLLICLE STUDIES IN MERINO CROSSBREDS
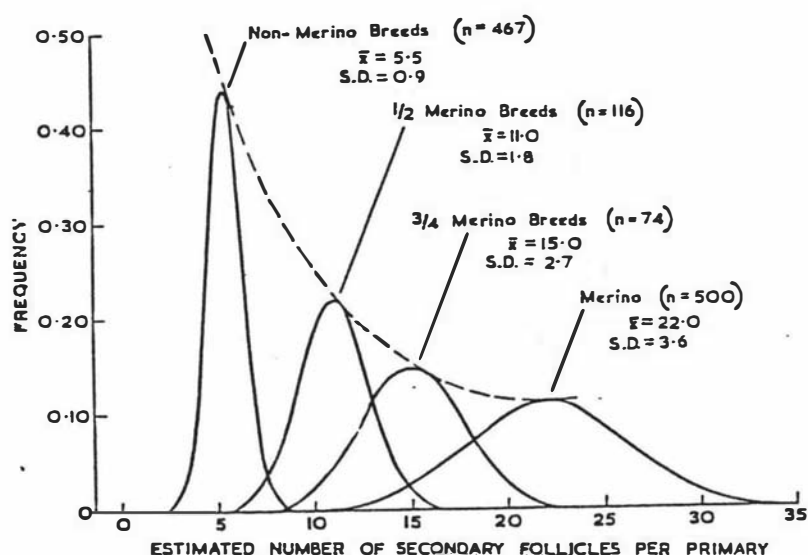
Figure 1.3:   Between Breed Variation in S/P ratio
              (from Carter, 1965)

Figure 1.3 illustrates the change in S/P between non-Merino breeds through to those having some Merino ancestry, to the purebred Merino (Carter, 1965). Carter (1965) and Carter and Clarke (1957a) suggested that the Merino's high S/P shows the clear separation of the Merino from all other breeds. As the proportion of Merino in the breeds' genotype increases so does the secondary to primary follicle ratio. This suggests that the Merino breed has genetic factors which markedly increase the secondary follicle population.

Table 1.5   Summary of follicle population figures in Adult British
             sheep.
                    (from Ryder (1957))

Breed	Number	S/P		n(P+S)	
Source	(n)	Range	Mean	Range	Mean
Mountain Breeds:					
Herdwick (Burns, 1954b)	4	3.3-4.0	3.4	800-1100	1000
Scottish Blackface (Burns, 1953)	3	3.5-4.2	3.7	800-1400	1050
Scottish Blackface (Peart & Ryder, 1954)	24	2.4-5.2	3.7	800-1400	1050
Cheviot (Ryder, 1957)	20	3.9-6.0	4.5	800-2100	1400
Long woolled breeds:					
Devon (Ryder, 1957)	6	3.5-5.0	4.4		
Leicester (Burns, 1949)	1		5.0		3000
Romney (Oliver, unpublished)	25	3.9-7.6	5.6	1450-2550	1975
Romney (Wildman, 1965)	27	3.75-7.45	5.4		
Short woolled breeds:					
Wiltshire (Ryder, 1957)	6	3.1-4.9	4.4		
Ryeland (Ryder, 1957)	6	4.3-4.8	4.4		
Suffolk (Burns, 1954a)	4	4.7-5.6	5.1	1150-1750	1500
Hampshire (Ryder 1957)	6	4.3-6.7	5.4		
Shropshire (Ryder 1957)	6	4.7-7.6	5.9		

Many of the crossbreeding studies between Merinos and longwoolled breeds have been inspired by the contrast between the fleece types of the Merino and other breeds. In many countries crossbreeding or grading up with Merinos will improve the performance of the native stock (Rae, 1952).

Most of the observations on follicle parameters and fleece structure in crossbreeding experiments between low S/P sheep and Merinos have been carried out in Russia. Table 1.6 contains a summary of the results from several trials, some of which will be discussed further.

Builov (1977) crossed meat type rams, e.g. Romney Marsh, Oxford Down, Suffolk and Kalinin to fine-woolled ewes. The results are given in Table 1.6. Daughters of fine-woolled ewes and long woolled rams had values for follicle density and S/P intermediate to their parents. The average values of S/P ranged from 5.4 for the rams to 12.9 for the ewes, and the progeny at 9.2.

In Russia, certain subjective techniques have been used to select sheep on the basis of fleece density. The breeder evaluates the fleece on the following scale: 1. MM+ - very thick, 2. MM - thick, 3. M - normal, 4. M - thin and 5. Mp - very thin. Glembotskii et al (1976) reported a long term selection experiment in fine fleeced sheep that showed: 1. wool uniformity increased so that large primary follicles produced more fine wool and down type fibres and 2. led to the consolidation of mutations which increased the formation of secondary follicles.

In this study, (Glembotskii et al, 1976) skin samples taken from a variety of breeds were used to determine the within-animal repeatabilities (correlations between 1 and 2 years of age), for S/P. The repeatabilites of S/P for the different breeds were: Viatna (0.80), Askranan (0.78), Altai (0.85), German Blackhead (0.74). The high repeatabilities validated the early evaluation and selection of fine-woolled sheep on the basis of S/P ratio.

After comparing the observed results with those expected, the authors concluded that there was an intermediate mode of inheritance, i.e., S/P was polygenically inherited. Glembotskii et al (1976) concluded that the wide within-breed range for S/P suggested additive gene action.

Kroiter and Kroiter (1977) examined the inheritance of individual skin layers in Tien Shan, Altai (fine-woolled), F_1 - Lincoln x Altai, F_2 (LA x LA), Romney Marsh x Altai (RM x Al) and three breed mixtures - RM x L x Al (RM x LAl) Lincoln x Romney Marsh x Altai (L x RM x Al) and Tien Shan x Lincoln x Altai (T x LAl). They found that F_1 Lincoln crosses had 13.7% thicker skin than fine

Table 1.6:   Fleece and Follicle Characteristics of Merino Crossbreds

(a) (from Builov, 1977)

Parents: n = 28	Romney	Kalinin	Suffolk	Oxford Down	Merino	Merino
n(S+P)	21	20	22	18	51	
S/P	5.5	5.5	5.0	5.5	12.9	
Daughters	R x M	K x M	S x M	OD x M		
n(S+P) at birth	76	66	66	71		
at 2.5 yrs	29	32	29	33		
S/P at 2.5 yrs	8.7	9.6	9.0	9.6		

(b) (from Dokov & Samov, 1969)

	Breed Group						
	GMM1	PB2	T3	LP4	XBdFW5	LPxT	LPxGMMxT
n (ewes)	5-10	5-10	5-10	5-10	5-10	5-10	5-10
dP (μm)	26.6	38.3	33.3	43.7	29.9	39.04	21.4
dS (μm)	23.0	30.0	25.0	27.1	25.0	25.2	21.6
S/P	13.89	4.57	6.35	4.40	12.74	4.77	7.05

1   German Mutton Merino   4   Local Planina
2   Pleven Blackhead   5   Crossbred Fine-woolled
3   Tsigai

(c) (Karpova, 1970)

Kazakh finewool (KF), Romney Marsh (RM x KF), Lincoln x KF,
Lincoln x (RM x KF) and RMX (Lincoln XKF) were examined for skin
traits. Proportion of variation in wool density attributable to
sires varied among the different types of sheep: 28-68% S/P,
49-81% wool fibre density.

At weaning, the highest wool fibre density was 80.66/mm^2 in the
KF'S, the lowest at 50.62 for the Lincoln KF. The same pattern
was observed for S/P of 13.5 and 8.4-8.8.

Table 1.6:   continued

(d) (Kroiter and Kroiter, 1970)

	Genotype						
	A1		RM2		RM x A	L x A	L3
n	15	5	5	7	10	7	5
nP (mm^{-2})	5.4	3.5	5.6	3.7	5.8	5.6	3.1
nS (mm^{-2})	72.1	46.7	35.0	17.4	39.2	42.8	20.0
S/P		*		45%	58%	58%	48%

1 Altai   2   Romney Marsh   3   Lincoln
* S/P for Altai equals 100%
   L+A = midparent mean = 74%
   RM+A = midparent mean = 72%

(e) (Pop et al, 1979)

	Breed			
	Romney Marsh			Tsigai
Sex				
n	6		8	8
Age (yrs)	3-4			3-5
dP (μm)	93.93		83.91	71.9
dS (μm)	122.51		104.28	81.26
FD (μm)	37.41		40.03	30.97
n(P+S) (mm^{-2})	39.00		53.87	54.65
S/P	5.93		5.82	2.64
Yield (%)	9.65		5.71	3.31

(f) (Sannikov and Polumiskova, 1974)

Breed	Parameter			
	S/P	n(P+S) (mm^{-2})	dP(μm)	dS(μm)
Askanian	12.2	56.75	26.4	22.4
Caucasian	15.5	62.6	25.6	22.3
Stavropol	12.5	59.48	24.0	21.0
Soviet Merino	11.9	59.74	24.6	21.7
Grozny	12.3	61.18	24.5	21.0

woolled sheep of the same age. F_2 sheep and the three breed crossbreds (RM x LAl and T x LAl) all showed skin thickening compared with the Lincoln F_1 which was used as a dam line.

The shape and depth of follicle characteristics and accessory structures were considered. When Lincoln and Romney rams were crossed with fine-woolled ewes, skin thickness, especially the pilar layer, was under the dominant influence of the sire's breed.

Schinckel and Hayman (1960) examined the inheritance of follicle number per unit area and average fibre weight in Border Leicester-Merino first cross and interbred sheep. To allow for comparison of the two generations at similar ages, the F_2 sheep were not the progeny of the F_1 animals. The results of this trial are shown in Table 1.7.

The output/follicle in the Border Leicester was 6 times greater than that of the Merino but the Merino had 6 times the number of follicles. There was 14-17% within-breed variation for these parameters. The F_1 and F_2 crossbreds had values for follicle density and follicle output intermediate to the parental groups. Variation increased substantially between the F_1 and F_2 groups from 14%-22%. The researchers suggested that: 1. there was evidence for genetic segregation in the F_2 generation for density and fibre weight and 2. that follicle density and the capacity to produce wool/unit area were independently inherited.

Pattie and Smith (1964) set up a trial to investigate breed establishment using the BL x Merino-halfbred. Their wool and skin results are presented in Table 1.8. In this study, 600 Merino ewes and 20 Border Leicester rams were mated to produce 255 F_1 females. The parental Merinos were 75% fine wools (70/74s) and 25% medium Peppin Merinos (60/64s). The 208 F_2 ewes were the progeny of 657 F_1 ewes and 20 F_1 rams. Only 35% of the F_2 ewes were influenced by the fine wool ewes.

There was no significant increase in variation for the characters studied in the F_2 from the F_1, with the exception of horn growth. The authors noted that an increase in variation between the F_1 and F_2 generations was expected when a trait was controlled by a few genes and little influenced by the environment. This is the case for horn growth inheritance as opposed to the polygenic nature of many production traits. Pattie and Smith (1964) concluded that objections to interbreeding first cross animals, (increased variation in the F_2), had little basis for wool production characteristics.

Table 1.7: Total follicle density and fibre weight for F_1 and
F_2 - Border Leicester-Merino sheep.
(from Schinckel and Hayman, 1960)

Generation	Nos.	Sire	Dam	n(P+S)	SD	Fibre Weight (g)	SD
F_1b	27	BL1	M2	31.0	4.5	104	13.8
F_2a	58	F_1(MxBL)	F_1(MxBL)	33.3	7.9**	103.8	21.3*
F_2b	29	F_1(BLxM)	F_1(BLxM)	32.2	9.9**	107.9	26.5**
F_2a	40	F_1(MxBL)	F_1(MxBL)	45.1	10.4**	90.3	19.6*
F_2b	47	F_1(BLxM)	F_1(BLxM)	34.7	7.5**	98.6	19.9*

*, ** all F_2 variances differed significantly from F_1 variances at
either 5% (*) or 1% (**) levels of probability.

Table 1.8   Means and variances of wool characteristics
of F_1 and F_2 ewes
(from Pattie and Smith, 1964)

	F1		F2	
	Mean	Variance	Mean	Variance
Trait				
n (ewes)	255		288	
GFW (lb)	8.0**	1.0	7.7	1.2
Yield (%)	69.2	32.4	8.8	37.1
CFW (lb)	5.5**	0.6	5.3	0.7
SL (cm)	11.4	1.1	1.4	0.8
Crimps (inch-1)	8.9	4.7	8.5	4.6
Colour score	3.7	0.5	3.8	0.5
Character score	3.3	1.3**	3.5	0.9

** F_1 F_2 $P < 0.01$

Table 1.8 contd.   Means and variances of skin section material
of 30 sample ewes from each group

	F1		F2	
	Mean	Variance	Mean	Variance
n (ewes)	30		30	
n(P+S)/mm^2	28.8	40.8	27.4	34.9
S/P	11.3	2.6	11.2	3.5
MFD (μm)	25.6	8.0	25.8	10.4

Henderson, (1968) set out to question whether crossbreeding and interbreeding, as is often claimed, increase the variability of fleece characteristics. This trial evaluated the fleece characteristics and follicle populations of Romneys, Border Leicesters and their F_1 and F_2 crossbred progeny.

With the exception of follicle density, all characteristics had values intermediate to those of the Romney and Border Leicester animals. Although the values for follicle density found in the crossbreds exceeded the purebreds, this was not considered unrealistic because the purebreds were not the parents of the F_1 nor were the F1 animals the parents of the F2. Henderson (1968) cited body area differences as a possible reason for density differences. There were significant between-mean group differences for the characters studied. With the exception of dP, the tests for homogeneity of variance between the F_1 and F_2 groups were not significant. The increased variability of primary fibre diameter was not reflected in the variability of mean fibre diameter in F_1 and F_2. This was attributed to a concurrent high variability of secondary fibre diameter. In contrast to popular belief, no significant increase in variability of fleece or follicle characteristics occurred with interbreeding.

McGuirk et al (1978) examined the effects of forming a interbred halfbred to see if performance in the F_2 declined as reported by other workers (Pattie and Smith; 1964). McGuirk et al (1978), over a five year period, studied four groups of progeny produced from mating Border Leicester and Merino rams to ewes of the same breeds. The progeny groups were: (BB) Border Leicester, (MM) Merino, and reciprocal crosses - Border Leicester x Merino (BM) and Merino x Border Leicester (MB). Follicle and fleece characteristics from this study are given in Table 1.9.

Crossbred ewes produced 8% more greasy and 12% more clean wool than the average of the parent groups. No evidence of hybrid vigour for the components of wool production per unit area was noted, although this was found for total clean wool production. The crossbred means were close to the parental mean for fibre length and diameter, but lower for fibre density (19%) and S/P ratio (16%). Since these differences disappeared when log-transformed data were analysed, McGuirk et al (1978) suggested that the observed differences between the purebreds and crossbreds were due to scale effects and not to non-additive gene action.

For those parameters obtained from skin sections, the crossbreds were more variable than the purebreds and for these traits there was little hybrid vigour. For fleece weight there was considerable hybrid vigour, and the crossbreds were less variable than the purebreds.

Table 1.9:   Breed class means for hogget fleece records and skin
             characteristics
             (from McGuirk et al, 1978)

Mating Group	MxM[1]	MxBL[2]	BLxM	BLxBL	MM-BB[3]	Hybrid Vigour(%)[3]
Ewe numbers	127	48	102	77		
GFW (kg)	4.57	4.59	4.48	3.84	0.73[4]	7.8*
Yield (%)	67.7	73.9	75.4	77.3	-9.6	3.0*
CFW (kg)	3.09	3.39	3.39	2.96	0.13[4]	12.1*
CPC	4.0	2.7	2.4	1.1	2.9	0.8
SL (cm)	9.4	11.9	12.1	17.1	-7.7[4]	-0.4
FL (cm)	11.8	15.4	16.5	19.3	-7.5*	2.6
n(P+S)(mm^{-2})	48.8	25.4	23.0	11.2	37.6*	-19.3
S/P	19.3	10.7	10.4	5.2	14.6*	-15.7
dP (μm)	29.4	36.4	36.9	44.6	-15.2	-0.9
dS (μm)	20.9	26.4	26.8	33.9	-13.0*	-2.9
MFD (μm)	21.3	27.2	27.7	35.9	-14.6*	-0.4
dP/dS	1.41	1.30	2.38	1.31	-0.10*	1.5

[1] = Merino
[2] = Border Leicester
[3] = Breed Effect = MM-BB
    Hybrid Vigour = 1/2 (MB + BM - MM - BB) and given as a % of
      1/2 (BM + MB)
[4] = Breed effect x year interaction significant P < 0.05
  * P < 0.05

Table 1.10:   Least squares means classified by breed type
               for 3 years 1971-1973
               (Woolaston and Roberts, 1976)

	Breed Type				
	PMO1	SAMo2	DR x Mo3	DH x Mo4	BL x Mo5
No.	218	216	179	209	226
GFW (kg)	5.46a	5.46a	4.92c	4.46b	5.41a
Yield (%)	58.2b	59.6b	62.3c	59.7b	68.5a
CFW (kg)	3.23cd	3.29d	3.08c	2.68b	3.72a
FD (μm)	21.9e	23.5d	25.5c	27.7b	30.5a
SL (cm)	8.3b	8.9e	8.7c	8.1b	11.0a
Crimp frequency					
(inch-1)	11.6c	10.3d	10.9bd	11.3bc	5.4a
Fleece value ($)	7.30a	7.26a	6.42c	5.12b	7.12a
Off shears LWT (kg)	39.3e	43.1d	50.5c	54.7b	58.1a

Means within a row with different superscripts differ significantly
(P < 0.05)

1 - Peppin Merino, 2 - South Australian Merino, 3 - Dormer-Merino
4 - Dorset Horn-Merino and 5 - Border Leicester-Merino

Significance of fixed effects for fleece traits and body weight

	GFW	Yield	CFW	FD	SL	CF	FV	OSL
Breed	**	**	**	**	**	**	**	**
Year	**	**	*	**	*	NS	**	**
Pregnancy Status	**	NS	**	*	NS	NS	**	NS
Lactation Status	NS	NS	NS	*	NS	**	NS	**
Breed x Year	**	**	*	*	**	NS	**	**

* P < 0.05   ** P < 0.01   NS - not significant

In another Australian trial, fleece characteristics of five different genotypes were studied; South Australian Merino (SAM), Peppin Merino (PM), F_1 Border Leicester x Merino (BL x M), Dorset Horn x Merino (DH x M), and Dormer x Merino (DR x M) (Woolaston and Roberts, 1976).

When the results were averaged over three years (Table 1.10), the BL x M ewes produced the highest clean fleeceweights with the largest fibre diameter. The finest fleeces were produced by the BL x M ewes while DH x M ewes produced the least amount of clean wool. Fixed effects were also analysed for various fleece characteristics.

Ryder and Wilson (1972) studied the fleece development and adult fleece measurements of Merino, Finnish Landrace and their reciprocal crosses. The results are summarised in Table 1.11.

The fleeces of the crossbred animals were shorter and finer but heavier than the Finnish Landrace. The authors suggested that the heavier fleeceweight was due to greater follicle density and slightly increased grease production. Both crossbreds had similar S/P ratios of 10, well below the parental mean. The fibre diameter of the crossbreds was closer to the Merino, but not significantly. Crimp number showed heterosis because it was higher than the mid-parent average in the crossbreds. The crossbreds's fleece characteristics resembled those of the Merino making their wool commercially valuable (Ryder and Wilson, 1972).

Gjedrem et al (1966) studied Merinos, Columbias and their crossbred progeny as well as the Dala, Cheviot, Rygja and Steigar breeds. The aims were to examine the possibility of producing fine wool in Norway and to determine which breed type had the best production characteristics. Results are shown in Table 1.12.

From wool fibre measurement, fibre finess was mainly additively inherited while non-additive inheritance played some part in the inheritance of medullation. Both Merinos and Columbias had higher wool yields than the Norwegian breeds. For wool production suitable for fine worsted yarn production, the 3/4 Merino was found to be most suited to Norwegian conditions.

There is wide between-breed variation in fleece type, the largest contrast between the Merino and other sheep breeds (Carter and Clarke, 1957a, b; Ryder and Stephenson, 1968). Within-fleece variation may also be large. Woolliams and Wiener (1980) studied the components of fleece and skin traits using 5 British breeds and the Tasmanian Merino. The aim of this project was to measure performance characteristics of the purebreds and their reciprocal crossbred progeny.

Table 1.11: Fleece and follicle characteristics of Finnish
             Landrace, Merino and F x M sheep
             (Ryder and Wilson, 1972)

	Breed Groups							
	FL[1]		FL x M[2]		M x FL		M	
Numbers								
	5	5	2	3	5	4	3	4
CPC	2.0	2.0	5.2	4.6	4.1	5.4	6.6	7.1
GFW (kg)	2.27	2.04	3.92	2.99	4.11	3.01	4.65	4.34
SL (cm)	14.8	17.0	14.2	13.2	13.2	11.0	10.00	10.8
dP (μm)	40.0	38.0	33.4	25.4	31.1	28.2	24.9	25.3
dS (μm)	36.1	28.6	30.4	23.9	27.6	25.6	22.9	22.5
S/P	2.32	2.29	3.33	2.98	3.22	3.10	4.53	4.39

	Breed Difference	Heterosis	Maternal Breed Difference
CPC	-5.6	0.5	0.6
GFW (kg)	-2.35	-0.18	0.04
SL (cm)	79.6	-12.3	-19.7
dP (μm)	14.9	-2.0	-0.5
dS (μm)	10.2	-1.9	0.4
S/P	-2.14	-0.20	-0.03

1 Finnish Landrace; 2 Merino

Table 1.12: Wool fibre measurement of ewes and hoggets
             (from Gjedrem et al, 1966)

Breed Group	Number (ewes and hoggets)	Fibre diameter (μm)	Staple length (cm)
Dala	101	39.2	11.1
Cheviot	62	38.5	9.5
Steigar	150	38.0	9.8
Rygja	68	40.8	9.8
1/2 Merino	293	30.9	6.6
3/4 Merino	295	25.4	5.7
7/8 Merino	11	22.9	5.2
Merino	84	23.7	4.6
1/2 Columbia	41	36.3	10.6
3/4 Columbia	19	32.9	8.6
Columbia	39	29.4	7.1

Scottish Blackface, South Country Cheviot, Welsh Mountain, Lincoln, Southdown and Merino rams were mated to ewes of the same breeds, except that no Merino ewes were used, and Southdown rams were mated to Southdown ewes only. Since this study was not a complete 6 breed diallel cross, the authors used the average effect of breed of sire as a standard for the various fleece and follicle traits. A summary of the results from this trial is shown in Table 1.13.

The Merino crosses were distinguished by high follicle density and fibre fineness when compared to other genotypes with the same maternal breed. The results supported the between-breed relationship of fibre diameter decreasing with increasing fibre density (Ryder and Stephenson, 1968).

Both the Blackface and Lincoln breeds showed a maternal effect. Lambs reared by Blackface ewes had greater fleece weight, mean fibre length, S/P, dP and dP/dS but lower nP and nS. The strong maternal influence on the factors dP and dP/dS was in agreement with their earlier study (Wiener and Slee, 1965) comparing Lincoln and Welsh Mountain ewes.

The only useful heterosis was from Lincoln crosses. S/P was unaffected by birth type or rearing; twin reared animals had denser coats than singles. nS and nP were only affected by rearing rank.

Ragab and Marai (1969) studied wool follicle characteristics of progeny from crossing and grading up of Egyptian coarse wool sheep with fine and long wool sheep. Purebred Texel, Ossimi, Merino and Barki sheep as well as halfbred Texel x Ossimi, and Merino x Barki animals were used. Primary follicle density at birth was intermediate to the parental groups, but by 12 months there was little between breed difference.

Guirgis (1980) evaluated the wool production in coarse wool Barki, Merino and their crossbred progeny - the proportion of Merino in the 5 genotypes ranged from 1/4 to 3/4 in 1/8 increments. Increasing proportion of Merino in the animals' genotype lead to increased wool production and greater fleece uniformity.

In an Indian trial, native Deccani sheep were crossed with 3 Merino strains; Australian Merino, Rambouillet and Stavaropolskya, to give 6 genotypes - pure Deccani, 50% Merino, 50% Merino, 50% Rambouillet, 75% Rambouillet and 50% Stavropolyska (Ghanekar and Soman, 1971). The results are given in Table 1.14.

Table 1.13:   Follicle parameters in some British breeds
              (from Woolliams and Wiener, 1980)

Traits

	nP (mm^{-2})	nS (mm^{-2})	S/P	dP (μm)	dS (μm)	d(P+S) (μm)	dP/dS
Mean	3.83	19.89	5.12	49.17	30.09	33.85	1.371
Southdown							
(purebred)	4.66	27.09	5.95	26.31	26.96	27.02	0.980

Average effect of breed of sire

Blackface	-0.35	-6.64	-1.28	14.01	1.18	4.45	0.38
Cheviot	-0.22	-4.81	0.84	-0.01	2.30	1.97	-0.14
Welsh	-0.11	-4.43	-0.91	9.51	-0.02	1.98	0.26
Lincoln	-0.16	-4.59	-0.88	2.38	2.62	2.66	-0.30
Merino	0.67	20.80	4.08	-17.05	-5.55	-8.69	-0.26
Southdown	0.17	-0.33	-0.17	-8.85	-0.52	-2.38	0.07

Table 1.14:   Fleece and follicle characteristics for Merinos,
              Rambouillets, and their crossbred progeny
              (from Ghanekar and Soman, 1971)

			Breed Groups			
	D1	50%M[2]	50%M	50%R[3]	75%R	50%S
n (ewes)	169	105	16	157	62	40
n(P+S)/(mm^2)	9.8	14.6	19.3	15.0	19.9	12.3
nP/(mm^2)	3.0	2.8	2.7	2.7	2.8	3.0
S/P	2.3	4.2	5.6	4.8	6.0	3.0
Fibre density/mm2	8.8	14.0	18.3	14.3	9.9	11.0
MFD (μm)	34.7	28.1	26.3	15.9	21.1	29.6

1 Deccani   2 Merino   3 Rambouillet   4 Stavropol

Between-genotype values for primary density were not significantly different, but the differences for all other parameters including fibre fineness were significant. Total follicle and fibre densities, as well as S/P, all increased with increasing proportion of Merino or Rambouillet in the crossbreds. The authors concluded that wool quality as determined by follicle structure can be improved from that of the local breed, Deccani, by crossbreeding.

Burns (1967a, b), in the Katsina wool project upgraded Uda and Yankasa Nigerian hair sheep with Merinos. The results of these two studies are shown in Table 1.15. The author found that in the two stages of crossing the mean S/P slowly increased from 4 in the hair sheep to 8 in the F_1 cross and 9.17 in the 3/4 Merinos. This pattern was not characteristic of that expected with polygenic inheritance.

The author suggested that a small number of genes had a decisive effect on S/P. The attainment of upper Merino S/P needs at least 2 of these genes plus a favourable environment and a favourable assembly of polygenes.

In New Zealand, several coastal islands and inland regions contain flocks of feral sheep. Although originally domesticated, these animals have been unselected for many generations and their fleeces now resemble a more primitive sheep. Limited work has been done on the follicle population of feral and domestic crosses.

From Table 1.16 it is interesting to note the low S/P of the feral Merinos, even though the fleece is quite fine. The Merino-Longwool crosses have a low S/P but a relatively fine fleece.

Table 1.15:   A summary of skin data on Merino-Nigerian
              hair sheep crossbreds
              (from Burns, 1967a)

Breed			F$_1$	
	Uda	Yankasa	M x U	M x Y
n	10	8	8	7
S/P	3.4	3.6	7.01	8.04
n			4	5
n(P+S) (mm^{-2})	10.0	10.0	17.1	17.2

Follicle population data, 3/4 Merino
(from Burns, 1967b)

Fleece Type	Sex[1]	n	n(P+S) mm^{-2}	n	S/P
Kempy, white	F	15	17.2	17	8.39
Kempy, black	M			7	8.44
No kemp, white	F	16	20.7	17	11.32
No kemp, white	M			2	11.00
Overall Mean		34	19.3	42	9.17

[1] F = Female;   M = Male

Table 1.16:   New Zealand feral sheep studies
              (from Bigham, M., personal communication)

	Romney	Feral Merino x Longwool	(Merino) Feral
S/P	4.5	4.8	6.0
n(P+S)mm^{-2}	10.4	13.8	17.2
MFD (μm)	30.3	22.1	20.5
dP (μm)	26.9	18.0	20.8

1.5 ENVIRONMENTAL EFFECTS ON FOLLICLE POPULATIONS

1.5.1 NUTRITIONAL EFFECTS

The effects of nutrition on wool follicle populations and consequent effects on wool growth have been reviewed by Schinckel (1963), Sumner (1969), Allden (1970), Butler (1978) and Williams (1987). Since this area is not of major concern to this thesis, only selected studies will be reviewed.

1.5.1.1 Merino Studies

Schinckel (1955a) investigated the post-natal pattern of skin follicle development in Merinos. The total number of mature primary follicles was found to be complete at birth and remained constant until at least 16 months of age. Secondary follicles showed a small lag in post-natal maturation, with a large burst of activity during the second week. The rate of follicle maturation then decreased. Fibres were produced by 70-80% of the secondary follicles at one month of age.

Short (1955a), using Merinos and a few Merino crossbreds, found that all secondary follicles were initiated at birth, although many were still immature. The greatest period of secondary follicle maturation was from 7-21 days after birth, with 65% of all secondaries containing fibres by 28 days. When relating changes in the S/P fibre ratio with age, Short (1955a) noted that secondary follicle maturation followed a sigmoid curve. These results agreed with those of Carter (1943) and Carter and Hardy (1947), and justify the use of the Sf/Pf follicle ratio. Changes in follicle density occurred due to skin expansion.

Differences in secondary follicle maturation between twins and singles apparently arise due to maternal nutritional restrictions. After one month of age, twins which initially showed slower follicle maturation achieved a higher rate of secondary follicle maturation than singles. The twin/single differences were greatly reduced by 15 months (Schinckel, 1955b).

Schinckel (1955b) skin sampled and weighed animals at: a. birth, b. 1 - 4 weeks, c. 4 months and 4. 15 months of age. He observed that the potential follicle ratio at birth set a ceiling for the development of the follicle group size. Pre-natal conditions influenced secondary follicle initiation. The author deduced that factors other than those determining birth weight controlled the number of follicles initiated.

The correlation between log Sf/Pf at 15 months and birth weight indicated that factors which affected pre-natal growth also influenced secondary follicle maturation independently of Si + Sf/Pi + Sf.

In another study (Short, 1955b), birth weight was not closely correlated with the degree of secondary follicle initiation. It should be noted that only 26 animals were used. The author suggested that the level of nutrition during the early post-natal period when secondary follicle maturation peaks, could severely influence the final fibre producing population. The study suggested that the number of secondary follicles initiated was set before birth, and that this placed an upper limit on the adult S/P fibre ratio. Post-natal nutrition would not influence secondary follicle initiation.

Schinckel (1955a, b) concluded that all follicles were initiated prior to birth, although the final number of mature follicles was significantly affected by birth weight and growth from birth to one month. At later stages growth was not significant. Larger animals at birth had a greater total number of primary follicles. This was probably due to greater foetal size and skin area at 90 days of gestation rather than higher follicle density.

Short (1955b) examined the modification of fleece structure resulting from adverse maternal nutrition. During pregnancy two groups of Merino ewes were fed: 1. intermediate (690 g) and 2. low (340 g) levels of an 18% protein ration. Lambs had free access to the ewes' ration. At birth, liveweight and secondary to primary fibre ratio were significantly reduced in the low group but S/P follicle ratio showed little effect. There was a significant correlation between birth weight and S/P fibre ratio. At 168 days, the age when primary and secondary follicles may be considered mature (Schinckel, 1953), S/P fibre ratio and density were higher in the intermediate group. Sex differences were not evident.

Pre-natal nutrition of the dam affected post-natal lamb growth rate probably through effects on milk production. However, by 200 days of age, both groups had the same average liveweight and produced the same amount of clean wool per unit area of skin. In lambs whose dams had been undernourished, S/P follicle ratio and total number of follicles were permanently reduced. In their fleeces, fibres were longer and coarser than those with higher fibre densities. From this study Short (1955b) concluded that wool production/unit area was independent of fibre density.

Hugo (1958) examined the effect of level of feed intake on wool production and follicle development of South African Merinos. Lambs were well fed (H) or restricted (L) over two periods: (a) conception to weaning and (b) weaning to 16 months of age. There were four combinations: H/H, H/L, L/H, L/L. Primary follicles appeared to have completed their development at birth while secondary follicles increased in number until the animals were four months old. Past this age there was no further maturation of secondary follicles. A low level of nutrition did not have a negative effect on the wool follicle population. The decreased wool production noted with animals on low level diets resulted from the production of shorter, finer fibres.

Schinckel and Short (1961) conducted an experiment with a similar design to Hugo (1958). Using Medium Peppin Merinos, they studied the effects of pre-natal and early post-natal (birth to four months) nutrition on adult fleece and body characteristics. The ewes were subjected to high and low planes of nutrition during gestation, and the lambs to high and low nutritional levels from birth to four months. The lambs thus fell into four groups: H/H, H/L, L/H, L/L.

There was a 15% difference between the H/- and L/- groups in nP and nS at birth due to: 1. a greater number of follicle groups and 2. more follicles per group (Si + Sf/Pf). The increased number of follicle groups was attributed to a greater surface area as indicated by the 34% higher average birth weight of H/- lambs compared with L/- animals.

Schinckel and Short (1961) found that secondary follicle maturation was restricted in both the H/L and L/L groups for up to 16 weeks post treatment. Past 4 months of age, the -/L groups showed a marked recovery up to 48 weeks of age but after this all groups remained constant.

Mature follicle density increased from 2-4 weeks of age in the H/H, H/L, and L/H groups and then gradually decreased. In the L/L group density declined from birth.

Low levels of feed intake from birth to four months delayed follicle population maturation but follicle numbers were not permanently reduced. The low level post-natal intake group produced 12% less wool as adults due to a lighter fibre weight.

Those animals on the pre-natal low nutritional level produced fewer but larger fibres. Schinckel and Short (1961) concluded that feed restrictions in the pre-natal period cause a reduced adult follicle population. Early post-natal nutritional deprivation appeared to have little effect on follicle numbers but impaired individual follicle fibre forming capacity.

In order to maximize adult wool production, levels of nutrition which do not restrict birth weight and early post-natal lamb growth should allow maximum follicle initiation and maturation (Schinckel and Short, 1961).

The 2 x 2 nutritional level design (H/H, H/L, L/H and L/L), was also used by Everitt (1967) to study the effects of level of nutrition on the subsequent lamb follicle population. The treatments were applied to Merino ewes in early (0-90 days), and late (90-150 days) pregnancy.

Mature primary follicle density was greater in lambs born to ewes undernourished in early and late pregnancy than to well fed ewes due to reduced lamb size. Mature secondary follicle density (Sf) was reduced by nutritional stress in late rather than early pregnancy. There was a decrease in Sf/Pf in lambs from undernourished ewes.

This study assessed the residual effects of the nutritional treatments on growth, wool follicle development, and clean wool production for three years. Severe undernutrition in late pregnancy led to decreased wool follicle development and clean wool production. The effects of the two periods of low nutrition were cumulative.

Allden (1968) placed Merino lambs on three nutritional regimes for 400 days. Animals were then restored to a normal diet and during the following 27 months the residual effects of the nutritional treatments in terms of wool growth, fleece development, and feed usage for wool production were measured. The sequel to the lowest nutritional treatment (L/L), where wool growth stopped for 400 days at 15 kg weight, was a less dense follicle population, (corrected for bodyweight) and a reduced wool growth rate during the recovery period. Slight reductions in total fibre numbers and wool growth per unit area occurred. Fibre diameter, fibre weight and S/P were not affected. The less severe treatments had only transient effects. Allden (1968) concluded that only extreme undernutrition from the early post-natal stage impaired the animals' wool producing potential.

Turner (1961) noted an average reduction in clean wool weight between unhandicapped animals (singles, progeny of adults) and handicapped animals, (twins, progeny of young ewes) of 0.34 lb. 87% of the difference between the two groups was attributed to a reduced number of secondary follicles. Dun and Grewal (1963) found that Merino twins were handicapped and produced fewer total fibres per sheep.

Gallagher and Hill (1970) reared singles and twins on a high plane of nutrition from birth to eleven months in an attempt to minimize the adverse effects of twin birth and rearing on liveweight, growth and wool fibre uniformity. Twin birth did not have a negative effect on liveweight gain or wool growth rate. S/P ratio for twins and singles was similar at birth and this relativity did not change over the experimental period.

1.5.1.2 Non-Merino Breeds

Henderson (1953) examined the effects of early environment on wool production in Romney sheep. Skin growth, fibre numbers and dimensions were measured on lambs reared for one year on different planes of nutrition. An initial low plane of nutrition retarded fleece development and fibre growth but it was not possible to decide if fibre numbers were permanently affected. The author suggested that this was not of practical importance as a low plane of nutrition during follicle development did not impair production/unit area if subsequent nutrition was adequate.

Ryder (1955) studied the effects of the level of maternal nutrition during pregnancy and lactation on wool follicle development in a small number of Cheviot lambs. There was not a large difference between diet levels, the low level being "normal" so as not to affect lambing.

There was a correlation between the S/P follicle ratio and birth weight of lambs. Ryder suggested that this supported the findings of Schinckel (1953) that the amount of feed available to the foetus influenced secondary follicle initiation and hence S/P ratio. Well fed ewes should produce lambs with greater numbers of secondary follicles. S/P ratio at weaning was correlated with birth weight. Secondary follicle development pre-natally was more sensitive to nutritional level than was post-natal follicle development.

Wildman (1958, 1965) investigated the effects of level of ewe's food intake on their progeny's follicle development using Romney sheep. Wildman (1958) found that variation in the S/P ratio, at birth was partly associated with birth weight. He also suggested that variation in foetal and early post-natal environment affected the rate of secondary follicle population development up to a genetic maximum.

In an extensive study on the post-natal development of the follicle population in Romney Marsh sheep, Wildman (1965) observed the changes in lamb's follicle populations from one week to 12 months of age. For some lambs, and in some years, there was a pause in follicle development

during the first week after birth. In some cases, during the early post-natal period, follicles regressed. Some follicles were initiated post-natally. The author concluded that the S/P follicle ratio, was not completely determined by pre-natal follicle initiation.

Wildman (1965) found that low follicle and fibre ratios restricted due to environmental factors, could increase greatly post-natally. Conversely, high birth S/P ratios could remain constant. In this study, follicle and fibre ratios increased up until the animals were 12 months old.

Some groups showed a high correlation between birth weight and S/P ratio while for others there was no association. This experiment contrasts with previous work (Schinckel and Short, 1961). Twin pregnancy acts as a nutritional limitation on secondary follicle development, which can be overcome by adequate post-natal feeding levels.

Pre-natal and post-natal conditions were found to affect the ratio of mature secondary to primary follicles. Wildman (1965) suggested that a possible coat developing factor, under genetic control might act independently of body growth mechanisms to restrict the levels of mature follicle and fibre ratios.

Doney and Smith (1964) studied the modification of fleece development in Scottish Blackface sheep due to variation in pre- and post-natal nutrition. The pre-natal nutritional limitation was twin pregnancy.

Post-natally there were several groups: 1. born and reared as singles, 2. born as twins, reared as singles after one day, 3. born as twins, reared as singles after 8 days, 4. born as twins, artificially reared after one day and 5. born as twins, artificially reared after 8 days. Samples were taken at 6, 12, 28 and 48 weeks of age.

Pre-natal nutrition limited the number of secondary fibres present at birth but this effect was only temporary, e.g. 6 weeks, when post-natal nutrition was adequate. The authors noted that this result does not support the conclusions of work by Ryder (1955) who found the level of nutrition during pregnancy to be more important, or Schinckel and Short (1961) who found more permanent consequences of impaired pre-natal nutrition.

In the Scottish Blackface breed, there were no permanent effects on fibre number, wool production or fleece structure from moderate nutritional restriction in the late pre-natal stage. Severe early post-natal nutritional restriction markedly affected secondary follicle population maturation. The effects lasted after the nutritional limitation but were not recognizable by 12 months of age. The difference in results for studies with Merinos and the Blackface may be due to the difference in S/P ratios and wool production (Doney and Smith, 1964).

Sumner and Wickham (1970) studied the follicle populations of the progeny of two groups of Romney ewes grazed at two different stocking rates. Primary and secondary follicle density showed birth rank effects related to skin expansion. Twins had a transient delay in secondary follicle maturation, with neither the stocking level nor birth rank permanently affecting the follicle population. The authors suggested that it would be extremely rare for a situation to occur under New Zealand grazing conditions which could permanently alter the follicle population. Dam age had no significant effect on the follicle population at birth or weaning.

Butler (1981) examined the effects of sex and birth status on wool follicle development in Corriedales. S/P ratio of twins and female 10 month old animals were lower than male and single born sheep. Twin born sheep had an 8.6% lower S/P ratio than singles. The follicle population had not recovered by 20 weeks of age. Ewes had an 11.4% lower S/P than rams. Primary follicle density was 20% greater in ewes due to the reduced wool bearing area.

More recently, Hutchinson and Mellor (1983) studied the effects of Scottish Blackface ewe nutrition on foetal secondary follicle initiation. The authors concluded that maternal undernutrition had the greatest effect on follicle initiation form around 115 to 135 days of gestation.

1.5.1.3 Summary

There are conflicting results on the effect of birth status and sex on follicle populations. As previously discussed, some researchers have used twin pregnancy as a restricted nutritional treatment (Doney and Smith, 1964). Schinckel (1955b) noted that single Merino lambs had a higher average S/P than twins although their potential S/P ratios were similar. The limitation to secondary follicle maturation was not overcrowding. Ferguson et al, (1956) found that secondary follicle maturation was slower in twins than singles and that singles had higher S/P ratios than twins.

There is a discrepancy between the findings of Schinckel and Short (1961) and other workers (Ryder, 1955; Wildman, 1965; Sumner and Wickham, 1970). This may reflect a breed difference in type and size of follicle population with the Merino with its larger secondary follicle numbers being more sensitive than the British breeds to nutritional variation. There may have been insufficient difference in nutritional levels between treatments (Schinckel and Short, 1961).

All primary follicles are initiated by 90 days of gestation and although secondary follicles are all initiated pre-natally at least in Merinos, they may not be fully fibre forming until 168 days post-natally. Nutritional limitations in the ewe may affect the follicle population of her progeny depending on: breed, birth status, rearing rank, post-natal nutritional level and severity of the restriction.

Most of the studies using British breeds have involved very limited numbers of animals which limit the accuracy of the conclusions. Birth status and maternal restrictions appear to delay, but not permanently impair, the maturation of secondary follicles in these breeds (Wildman, 1965; Sumner and Wickham, 1970). In contrast, in Merinos adverse maternal nutrition in later pregnancy permanently reduced the lambs' follicle population. When post-natal nutrition was adequate, initiated follicles compensated by producing coarser, longer than normal fibres. In the Merino twin birth, was a handicap to the development of the follicle population. The observed differences between Merinos and other breeds may be due to the larger follicle population of the Merinos which make them more sensitive to nutritional restriction.

1.5.2 AGE EFFECTS

Follicle populations vary with age but are considered mature at 10 to 12 months of age (Carter and Clarke, 1957a). However, as nP and n(P+S) are affected by changing body weight and skin area follicle densities in 1-year-old animals will be higher than in older animals who have reached their mature liveweight. Using skin samples from younger animals may not provide accurate estimates of their adult follicle population parameters. With increasing age, some follicles cease production (Brown et al, 1966; Jackson et al, 1975). The active follicles increase their output as shown by increases with age in both MFD and SL (Brown et al, 1966).

1.5.3 MATERNAL EFFECTS

One experiment involved the transfer of fertilized embryos from Lincoln to Welsh Mountain ewes and *vice versa* (Wiener and Slee, 1965). Lincoln sheep normally weigh twice as much as Welsh Mountains.

At birth, Lincoln lambs born to Welsh Mountain ewes had reduced S/P ratios and follicle densities even though they were smaller than typical Lincoln lambs. Secondary follicle development in transferred Lincoln lambs was depressed by the maternal environment of the Welsh Mountain ewe.

The only effect the Lincoln ewe had on Welsh transferred ewes, was decreased follicle density due to increased body size. The authors suggested that the effects shown in Lincoln lambs merited consideration in crossbreeding schemes.

1.5.4 OTHER FACTORS INFLUENCING FOLLICLE DEVELOPMENT

These factors include: ambient temperature, disease, and hormones. As these factors are not relevant to this thesis only brief mention will be made of a few key papers.

Ambient temperature has been shown so be important (Bowstead and Larose, 1938). Cartwright (1972) and Cartwright and Thwaites (1976) have demonstrated that ewes subjected to high ambient temperatures produce lambs with limited follicle development. There has been little work on disease effects but one form of viral infection has been shown to affect follicle development (Carter et al, 1972; Orr, 1977). There has been considerable work on endocrine effects on follicle development and the area has been reviewed by Wallace, (1979).

1.6 GENETIC EFFECTS ON FOLLICLE POPULATIONS

Relatively few genetic parameters for follicle characterisitics have been published, possibly due to the lengthy process involved in collecting sufficient follicle data.

Using Merinos, Jackson et al (1975) reported h^2 estimates for S/P and n(P+S) of 0.40 ± 0.05 and 0.45 ± 0.06 respectively. These were higher than those of Gregory (1982a) whose estimates for S/P ranged from 0.24 - 0.32 and for n(P+S) from 0.27 - 0.33 and nP from 0.11 - 0.25. Their h^2 estimates using dam-offspring regressions were consistently higher than the paternal-halfsib correlation estimates. Abouhief (1980) studied crossbreds in the U.S.A. and obtained h^2 estimates of: S/P (0.69-0.81), n(P+S) (0.36-0.51) and nP (0.36 -0.39). Jackson et al (1975) calculated repeatability estimates for n(P+S) of 0.52[**] and 0.58[**] and for S/P of 0.70[**] and 0.54[**].

Gregory (1982b) obtained significant positve genetic correlations between n(P+S) x nP and n(P+S) x S/P while the S/P x nP correlations were negative. The n(P+S) x S/P correlation estimates were similar to that of Jackson et al (1975). In the latter study the genetic correlation of n(P+S) x GFW was negative while that of S/P x GFW was 0.46[**]. Both n(P+S) and S/P were negatively correlated with MFD -0.66[**] and -0.45[**] respectively. SL was also negatively correlated with these traits. In these flocks, one genetic route controlling fleeceweight may be through genetic increases in secondary follicle numbers.

These results in conjunction with those of Heydenrych et al, (1977), Rendel and Nay, (1978) and Steinhagen et al (1986), suggest that follicle characteristics are moderately heritable and should respond to selection.

1.6 MAJOR GENE DETECTION

1.6.1 Introduction

Many traits of economic importance to animal production, such as clean fleece weight, show continuous variation; observations are difficult to place in separate classes. Characters showing this pattern of variation are referred to as quantitative or metric characters (Falconer, 1960).

The simultaneous segregation of many genes affecting the trait, together with continuous variation from non-genetic sources, transform underlying discontinuous genetic variation into apparent continuous variation (Falconer, 1981).

For differences arising from the segregation of many genes, Mather (1943), proposed the term polygenic variation, with the genes referred to as polygenes. These have little individual power but an important cumulative effect on a trait. The earlier term, multifactorial inheritance, proposed by Yule (1906; cited by Strickberger, 1968), is equally valid. Today, the terminology is more complex, with references made to main genes, major genes, minor genes, super genes, polygenes, neutral genes and Mendelian genes (Hancock, 1977). These categories represent the level of gene expression but are not distinct i.e., genes may act in a Mendelian manner for one trait and a polygenic manner for another trait or for the same trait in another population.

Major genes tend to be found by accident or as the result of screening large numbers of identified loci (Smith and Webb, 1981). Discrimination between Mendelian genes and those with metric effects depends on their magnitude relative to other sources of variation. A gene having a large enough effect on a trait to be recognized, even in the presence of genes segregating at other loci and under the influence of non-genetic factors, is referred to as a major or main gene and can be studied by Mendelian methods (Falconer, 1981). As noted by Famula (1986), the level of observation is also important, fewer genes being observed at phenotypic than cellular levels.

A major gene has been defined as one having an effect of at least one standard deviation of the metric trait as measured by differences between two homozygotes (Roberts and Smith, 1982). If the gene has a very large effect, causing a difference of at least two standard deviations in a performance trait, (a major gene as defined by Morton and MacLean, 1974; Smith and Webb, 1981), then segregation and kurtosis may be apparent.

1.6.2 METHODS USED IN MAJOR GENE IDENTIFICATION

Techniques from population and biometrical genetics are useful traditional tools for studying the genetic mechanisms controlling productive characters. However, this methodology provides little information about the real nature of genetic segregations underlying observed variability (Robertson, 1967).

Some techniques which have been developed are shown in Table 1.17.

Reviews of this area have been given by Wright (1952), Piper (1971), Hancock (1977), Hanset (1982), Roberts and Smith (1982), Nicholas (1984), Namboodiri and Kaplan (1985) and Hill and Knott (1987).

Many of the methods of major gene identification aim to reduce or eliminate non-genetic sources of variation, or noise, so that genetic factors controlling a trait become apparent.

The power of each of these techniques depends on the magnitude of the effect of the gene and the gene frequency. The power of the technique decreases as.the magnitude of the gene effect falls (Smith and Webb, 1981).

1.6.2.1 Chromosomal and Intra-chromosomal Analysis

To maximize the use of identified major genes in livestock through genetic engineering techniques, chromosomal maps will be needed. Most of the work in this area has been done using *Drosophila melanogaster* or *Triticum aestivum L.* rather than domestic animals. Reduced generation interval, high costs, and limited resources have been important reasons limiting the search for main genes in domestic animals.

Thoday (1961) attempted to bridge the gap between Mendelian and quantitative genetics. Using *Drosophila melanogaster* he showed that both continuous and discontinuous heritable variation have similar properties of segregation, dominance, linkage and interaction.

Thoday's work initially involved the identification of the effects of individual chromosomes using marker chromosomes and cross-over suppressor techniques. He compared a chromosome which

Table 1.17: Methods used in major gene identification

Technique	Researchers
Effective number of genes	Castle (1921); Wright (1952); Lande, (1981); Comstock and Enfield (1981)
(a) Chromosomal and intra-chromosomal analysis	Thoday, (1961); Wehrhahn and Allard (1965); McMillan and Robertson (1974)
Methods using Population Differences	
(a) Segregation in crosses and backcrosses	Wright (1952); Stewart (1969); Lande (1981)
(b) Repeated backcrossing and selection	Wright (1952)
(c) Use of linked markers	Geldermann (1975)
Within Population Analysis	
(a) Departures from normality	
(i) Heterogeneity of variance	Fain (1978); Merat (1968); Penrose (1969)
(ii) Skewness and Kurtosis	O'Donald (1971); Hammond and James (1970)
(b) Maximum Likelihood Methods	Ott (1979)
(i) Complex segregation analysis	Morton and MacLean, (1974); Elston (1981)
(ii) Extended pedigree analysis	Elston and Stewart, (1971); Lange and Elston, (1975); Lange et al, (1976); Go et al (1978)
(iii) Path analysis and linear model techniques	Rao et al., (1974);
(c) Structured Exploratory Data Analysis (SEDA)	Karlin et al (1979); Famula (1986)

resulted in a higher value of a metric character with a homologous chromosome marked with recessive genes. A number of marker stocks were tested in the determination of suitable markers. The active areas of the chromosome were further analyzed to locate and measure the effects of individual loci within these regions. When adequate numbers of recombinants had been obtained, these were classified by progeny testing. The number of quantitatively different subgroups was used to determine the number of loci controlling the trait; a single locus assuming 2 alleles/locus, would show two subgroups, whereas two loci would result in three subgroups.

This technique and its modifications have limited present application in large animals due to the shortage of suitable marker stocks and time. Genes of small effect are hard to isolate as differences are so small that it is difficult to satisfactorily differentiate their effects from other sources of variation. This may lead to non-random samples of polygenes of greater than average effect. Estimates may thus give the minimum number of loci and not reveal the full complexity of each locus (Thoday, 1961).

Other workers, (Wehrhahn and Allard, 1965), used Thoday's method to study heading dates of two different strains of wheat. Their model assumed that parents were chosen at random and all had equal viability. The parental lines were crossed, then the F_1 was crossed back to one parental line. Backcrossing to one parental line over several generations resulted in seeds very similar in genetic makeup to the parental line. The parental, F_2, and inbred backcross lines were analyzed using histograms of the frequency distribution of heading date and probability elipses, to clarify the results. They detected four genes with large effects.

McMillan and Robertson (1974) used a modification of Thoday's technique to study bristle number in *Drosophila melanogaster*. They contended that if a number of small loci were close together giving little chance of crossing over in that chromosomal region, then the combined action of many small loci could be interpreted as a major gene effect. With current gene theory this may now be acceptable since there is mounting evidence that many major genes consist of repeated sequences of a section of DNA in a region of a chromosome (Gillings and Frankham, 1982). With the current work on gene mapping, Thoday's technique (1961) may soon be applicable to livestock.

1.6.2.2 Departures from Normality

Early studies in this area involved chromosome analysis and the use of marker stocks. Recently, workers have used statistical techniques to estimate the number of genes of large effect. Models have been developed (Merat, 1968; Hammond and James, 1970; O'Donald, 1970) based on the shape of curves of frequency distribution of a quantitative character and the use of skewness and kurtosis coefficients. When a major gene is present the distribution of a character will show a departure from normality.

Skewness and bi- and tri-modality are expected depending on the nature of the major genes, gene frequency, the average gene effect, and the number of loci. For example, bimodality would be expected for one pair of additive genes if one allele was at a low frequency or dominant.

According to Hanset (1982), statistics which can be used include:

1. test of skewness ($g1$)
2. test of kurtosis ($g2$)
3. probit analysis, e.g. plotting of cumulative distribution on
   a probability scale
4. the Kolmogoroff-Smirnov test

O'Donald (1970) demonstrated that the 2nd, 3rd, and 4th cumulants of the genotypic distribution of a quantitative character could be used to estimate the number of loci which control variation in the character. Hammond and James (1970) failed to achieve the same success. They noted that non-additive variation, linkage and natural selection also affected skewness and kurtosis statistics.

Hammond and James (1970) studied the inheritance of abdominal chaetae number and number of progeny in a randomly mating group of *Drosophila*. They looked at chaetae number data pooled over families for the shape of individual scores. The variances of family means were calculated in two ways: 1. unpartitioned family means analysis which used the variance of family means, and 2. partitioned family means which used the between-family variance obtained by partitioning the variance due to time, vial and family components. They also carried out a pooled analysis and compared the results gained using these three techniques with that of Merat (1968).

Merat (1968) used skewness and kurtosis coefficients in testing for homogeneity of family variances. Deviations from the family mean for those families with extremely high or low variances were first pooled to form high and low variance groups, then normality statistics were compared. The skewness coefficient is dependent on the relative frequency of high and low alleles. The kurtosis coefficient is negative for intermediate and positive for extreme gene frequencies.

Hammond and James (1970) showed that the frequency distribution of a character would be non-normal if genes of large effect contributed to the genetic variation of that character. With the earlier model (Merat, 1968), groups showing high variance are expected to depart from normality showing assymetry and platykurtosis if genes of large effect are segregating in the population.

Hammond and James (1970) questioned the use of higher-degree statistics for the detection of segregating genes of large effects in traits of low heritability and they suggested that these methods should be reserved for traits demonstrating a greater proportion of genetic variation.

Fain (1978) devised a procedure based upon simple principles which can be applied to relatively small samples of sibships as a preliminary step to more complicated and definitive analyses. Prediction of phenotypic variation amongst members of a sibship from parental phenotype is possible when one or a few loci contribute to variation in a quantitative trait (Penrose, 1969; Fain, 1978).

If a single major locus is responsible for genetic variation and both parents are at extremes of the phenotypic range then it is likely that the parents are homozygous and only environmental variation is expected among members of a sibship. Parents with intermediate phenotypes are likely to be heterozygotes and variation due to segregation at the locus is present among sibs. A similar relationship holds for the phenotypic mean of a sibship and within sibship variance. When a major locus is present, segregating sibships are characterized by intermediate means and higher variance.

Fain (1978) used a regression model, to explain this relationship:

$$Y = A + B_1 X + B_2 X^2 + B_3 X^3$$

Where: Y = log of the within sibship variance
          X = within sibship mean

In the above equation, the regression coefficients do not differ significantly from zero under polygenic inheritance. A single major gene may increase one or more terms due to dominance, gene frequency and/or sex linkage. Fain (1978), compared the effectiveness of regression analysis with Bartlett's test of homogeneity of variance for detection of a variety of major locus models. Both real and computer simulated data were used to examine the power and robustness of test statistics. For each simulated condition a sample of 50 sibships each of size 4 was replicated 100 times.

Bartlett's test of homogeneity of variance was also applied to the within-sibship variances for each sample. The F criterion was used as the test statistic. Fain (1978) found that with random sampling of polymorphic traits, regression analysis of the relationship between within-sibship variance and within-sibship mean was useful for detecting a variety of major locus models, especially with complete dominance or unequal gene frequencies. It was observed that if a main gene affected the distributional properties, significant results remained after transformation. In general, the variance amongst sibships segregating for a major gene was expected to increase.

Bartlett's test of homogeneity of variance was found to be powerful in detecting a major locus, especially with the presence of a background sib correlation which may result from the addition of polygenic or environmental factors affecting the trait. The appropriate statistical method for detection of segregation would vary under different sampling schemes and for different phenotypes. It was observed that the power of the analyses depended on the specific major locus model, but was satisfactory for small samples (Fain, 1978).

1.6.2.3 Maximum Likelihood Methods

The development of more sophisticated computers has enabled large sets of data, both real and simulated, to be manipulated in mathematically complicated ways. Simulation models have provided estimates of expected results from proposed experiments.

As the variation due to single locus segregation decreases relative to other environmental and genetic variation, there is a point where the classes overlap and absolute classification is not possible. Genetic variation then appears continuous. The possibility that a single locus might be responsible for the control of a trait is often not examined, even when the picture is consistent with single locus models with heritability of up to 0.5, as the distributions do not depart significantly from normality (Stewart, 1969).

Stewart (1969) devised a technique to test whether segregation at one or two loci was enough to account for variation in a metric character. If large numbers of loci were involved, then a more biometrical approach could be used. This method involved the comparison of the frequency distribution of the backcross generation with those of corresponding parental and F_1 groups.

The minimum data requirements for this model included: 1. two inbred strains, 2. that the character should have a continuous distribution with a minimum heritability of 0.3 and 3. at least 100 individuals from three successive generations from one backcross population must be measured. If the difference between the parents (P), and the progeny (F_1), was due to a single locus then there should be no significant difference from a composite distribution of 50% parental and 50% of the F_1 distribution. If the backcross differed significantly from this then the form of the backcross could suggest an alternative genetic model to fit to the data.

Much of the recent interest and use of these techniques to identify major genes has occurred in the field of human genetics. Many of the methods of segregation analysis are quite complex and require large data sets with accurate pedigrees. These are frequently unavailable (Elston and Stewart, 1971; Lange et al, 1979; Elston, 1981).

Analysis of the genetic component of disease in the human population is an important research area. The genes may not determine completely the presence or absence of a disease but do influence the probability that the individual will have the disease. Other types of environmental noise and non-heritable incidence of disease may act to obscure the genetic picture (Curnow and Smith, 1975).

Work in this area has concentrated on the single locus two allele model and the multifactorial model since it is difficult to discriminate between these two classifications without trying to decipher more complex models. Associated variables closely correlated with liability of a condition may make discrimination between models easier. Curnow and Smith (1975) fitted a simple Mendelian model using a maximum likelihood method to data on the familial frequency of Schizophrenia. A multifactorial model with two parameters gave a reasonable fit to the data but implied a higher risk within sibships.

Hill and Knott (1987) suggested that maximum likelihood methods and segregation analysis held the most promise for detecting major genes in livestock. Further, they suggested that the size and design of experiments should be considered to provide data for these types of analyses.

1.6.2.4 Estimating the Effective Number of Genetic Factors

In the investigation of genetic mechanisms the choice of scale is important. According to Wright (1952), the best choice of scale for data analysis is one on which both genetic and environmental effects are as nearly additive as possible.

Falconer (1981) noted that the use of a scale was a useful statistical device to simplify data analysis and to make it possible to draw valid conclusions from analyses, and furthermore may help in the interpretation of results. He noted that the justification for the scale transformation must be based on some criterion other than the property about which the conclusions are to be drawn. Falconer (1981) suggested that the basic problem was that a scale which might be appropriate for one population might not be acceptable for another and that the scale best suited for genetic components of variation might not be suited to the environmental components of variation.

Lande (1981) extended a technique first outlined by Student (1934) to estimate NE, the minimum number of freely segregating genetic factors influencing a metric trait in two divergent populations. This method follows from earlier work by Castle (1921) and Wright (1952, 1968), based on the assumption that one line is fixed, with alleles increasing a given character, while the other line is also fixed but in the opposite direction with alleles decreasing the trait (Wright, 1952). This is most likely to occur when the populations have diverged due to sustained artificial or natural selection for a trait (Lande, 1981).

The criteria which must be satisfied before application of this model include:

1. The mean phenotypes in F_1, F_2 and backcross populations must be additive.

2. When the P_1, F_1 and F_2 variances are plotted against their means, there must be constancy or linearity. Also, the extra variance segregating in the backcross populations must be half that in the F_2.

3. Standard errors are based on normal phenotypic distributions in all populations.

If these criteria are satisfied, on an appropriate scale of measurement, then the minimum number of significant factors, NE, can be estimated from a comparison of the phenotypic means and variances of the trait in the parental, F_1, F_2 and backcross populations. This is illustrated in Table 1.18.

At least 20-30 individuals are needed in each of the parental and F_1 groups and at least 100 in F_2 and backcross groups of at least 100 individuals. Lande (1981) estimated the minimum number of genes involved in producing a large difference between populations in a quantitative trait at 5 or 10 with occasional values up to 20.

Angus (1983) wrote a computer programme based on Lande's (1981) model. The findings of Mayo and Hopkins (1985) in testing Lande's (1981) technique are discussed in relation to the present study in Chapter 4.

1.7 APPLICATIONS OF MAIN GENES TO LIVESTOCK BREEDING

Current animal breeding theory is based on multifactorial inheritance i.e., many genes with small effects. Genes with large effects are sometimes important in livestock as evidenced by the Booroola Merino and the N-type Romney or Drysdale (Roberts and Smith, 1982). Ricordeau (1982) reviewed major genes in sheep and goats.

Traditionally, major genes have been studied in relation to: colour and horns as markers and identifiers of breeds; congenital abnormalities such as snorter dwarfism and photosensitivity in the South Down breed (Roberts and Smith, 1982).

Table 1.18:   Phenotypic means and variances of a quantitative
character in parental and hybrid populations
(from Lande, 1981)

Population	Mean	Variance
P_1	μ_1	$\sigma_{g1} + \sigma_e$
$B_1 = F_1 \times P_1$	$3/4\mu_1 + 1/4\mu_2$	$3/4\sigma^2_{g1} + 1/4\sigma^2_{g2} + 1/2\sigma^2_s + \sigma^2_e$
$F_1 = P_1 \times P_2$	$1/2\mu_1 + 1/2\mu_2$	$1/2\sigma^2_{g1} + 1/2\sigma^2_{g2} + \sigma^2_e$
$F_2 = F_1 \times F_1$	$1/2\mu_1 + 1/2\mu_2$	$1/2\sigma^2_{g1} + 1/2\sigma^2_{g2} + \sigma^2_s + \sigma^2_e$
$B_2 = F_1 \times P_2$	$1/4\mu_1 + 3/4\mu_2$	$1/4\sigma^2_{g1} + 3/4\sigma^2_{g2} + 1/2\sigma^2_s + \sigma^2_e$
P_2	μ_2	$\sigma^2_g + \sigma^2_e$

Table 1.19:   Responses expected to different methods of selection
(from Smith, 1967)

Method of selection	Expected genetic response (h^2 units per period)
1. On individual performance	$i_1 c_1$ [1]
2. On known genetic loci	$i_2 c_2 \sqrt{R/h^2}$ [*]
3. On a selection index of (2) and (1)	$i_1 c_1 (1 + \frac{1}{2}R/h^2)$ [**]
4. By two-stage selection first on (2) then on (1)	$i_1 c_1 (1 + i_4/i_1)\sqrt{r/h^2}$
5. By indirect selection on relatives	$i_5 c_5 r/w$
6. On a selection index of (2) and (5)	$(i_5 c_5 r/w)(1 + \frac{1}{2}(R/h^2)(w^2/r^2))$

[1] i -   selection differential   c - reciprocal of the generation
interval

[*] R - proportion of the additive genetic variance controlled by
known loci

[**]   approximately

An example of detection of a main gene in sheep is the F gene for ovulation rate in the Booroola Merino. This strain of Merino, noted for its high fecundity, was developed by the Seears brothers of, "Booroola", Cooma, Australia who continued selection for increased fecundity in the ewes. Turner (1983) examined the genetic background and selection that led to the high fecundity of the Booroola. Piper et al (1985) have recently reviewed the Booroola studies.

Piper and Bindon (1982) studied the records of the original ewes and their daughters. They suggested that the high lambing percentage in the Booroola (170-180% compared with non-Booroola Merinos of 80-110%), could not have been achieved by the accumulation of genes of small effect: the long term increase would have been about 10% for litter size with a heritability of 0.2. They suggested that the increase was due to the presence of individuals carrying a gene or closely linked group of genes of large effect on litter size.

The segregation criterion chosen by Piper and Bindon (1982), was one or more sets of triplets or higher order litter sizes in a ewe's lifetime. Those ewes which were presumed to carry the gene, showed an average difference of one lamb per lambing compared with non-carriers. This corresponds to 2 standard deviations of litter size in the Merino and hence is a main gene according to Morton and Maclean, (1974).

An example of the importance of choosing selection criteria and scale effects was observed in studies on fleece characteristics in the Drysdale. When adult fleece medullation was studied, the results suggested multifactorial inheritance, but when birthcoat hairiness grade on the midback was examined Mendelian inheritance was evident. Studies have shown that the difference in fleece type between the New Zealand Romney and the Drysdale breeds is due to a major gene. In this case, the use of adult fleece medullation gives a more accurate picture of the underlying genetic mechanisms (Stephenson, 1956).

Since the discovery of the F gene in the Booroola, other genes for increased sheep fertility have been found (Hanrahan and Owen, 1985; Jonmundsson and Adalsteinsson, 1985; Bradford et al, 1986). Part of the increased interest in major genes in livestock is due to these discoveries but if the developed transgenic techniques are to achieve their potential, useful genes to transfer need to be identified.

1.8 SELECTION FOR MAJOR GENES

It has been argued that if genes of large effect are present, these will be selected and moved to the desired frequency under current selection strategies. However, quantitative methods are inefficient when gene identification is possible. Gene identification often allows the use of breeding strategies to maximize benefits and minimize drawbacks from a gene of major importance (Smith, 1967; Roberts and Smith, 1982; Hill and Knott, 1987).

Smith (1967), suggested that selection through 'known loci' may prove an efficient means of genetic improvement. Use of these depends on the information they provide about an animal's breeding value for the metric trait (see Table 1.19).

The value of known genetic loci depends on the proportion of the total additive genetic variation due to the known loci relative to the heritability of the trait concerned and on the form of selection practised. Smith (1967) suggested that when normal selection is effective, further information on known loci will add little to the rate of improvement. However, if normal selection is not effective, (for example for a character with a low heritability), or if indirect selection on relatives must be used as in the case with sex-limited traits or carcass traits, or if selection is based on pleiotropic effects or linked effects, then the use of known loci greatly increase the rate of improvement.

1.9 CONCLUSION

Smith and Webb (1981) in their review of the effects of major genes on animal breeding found that genetic parameters were affected by the presence of a main gene and by its current gene frequency in the population. Selection responses were increased due to increased heritability when selection was based on a major gene.

Figure 1.3, from Smith and Webb (1981), after Falconer (1960), shows the effects on the heritability and genetic correlation caused by the presence of a major gene. The researchers noted that the knowledge that a main gene was involved in the genetic control of a productive trait, was of little value unless the phenotypes could be readily identified. They expressed concern about the duration of the period of increased selection response, which could be limited if selection on a major gene led to fixation. They suggested that if normal selection procedures were effective, selection on the basis of a main gene might lead to a small increase in genetic gain and there would be a greater response when the favourable gene is at a low to intermediate frequency.
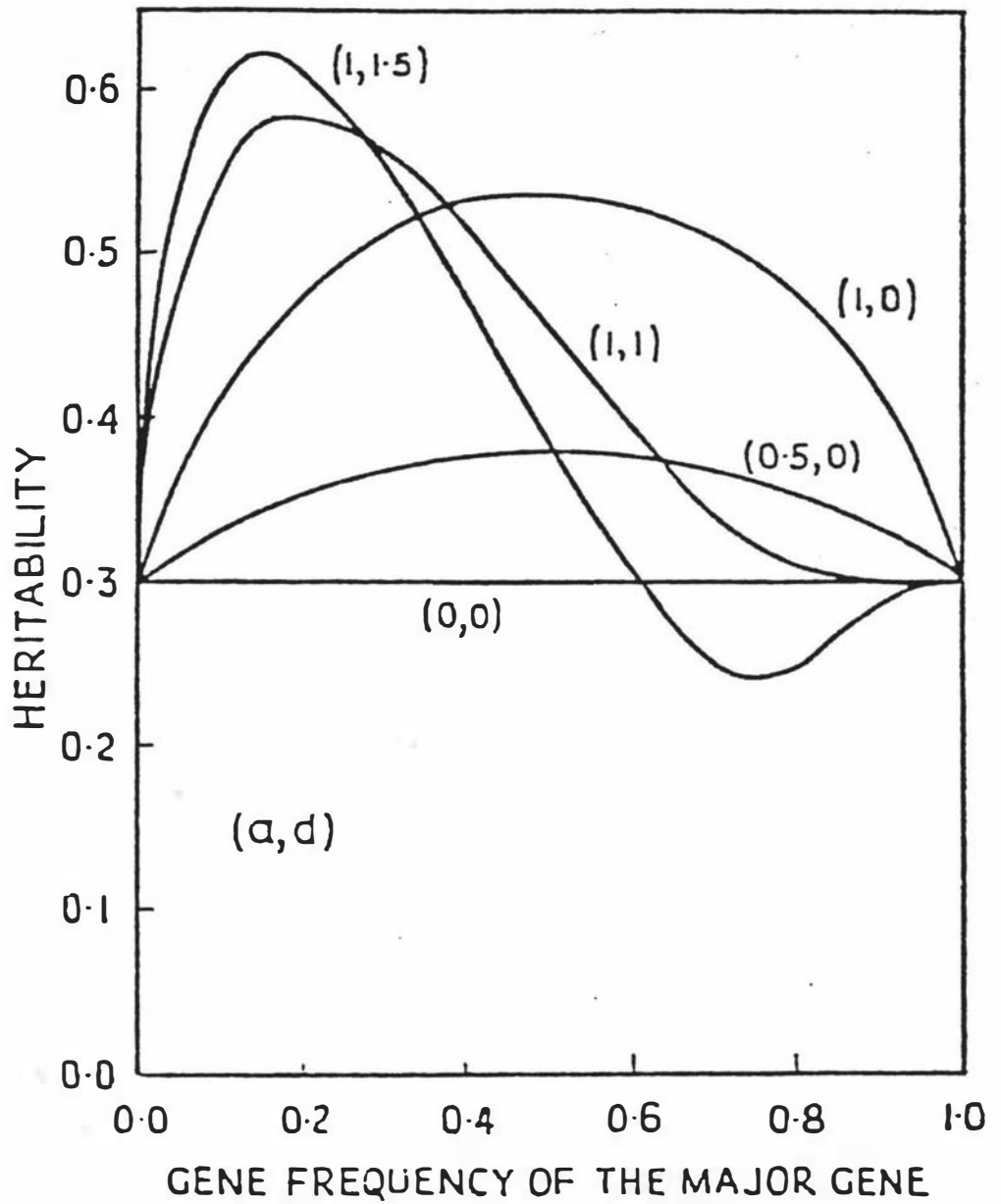
Figure 1.4: Shows the effects of a major gene
on heritability estimates
(from Smith and Webb, 1981)

Roberts and Smith (1982) noted that the presence of a main gene would lead to increased heritability for the trait under control, except if there was overdominance. The authors suggested that one could fix different alleles in different lines and use crossbreeding to produce commercial animals. Their paper outlined some of the genetic theory involved.

Smith and Webb (1981) along with others (Smith, 1967; Hanset, 1982; Roberts and Smith, 1982), pointed out the need for a cost/benefit analysis to estimate the economic value of a major gene in a breeding programme. They noted the need for relevant information on the economic merit of all phenotypes, as well as pleiotropic effects of the main gene and any undesirable genotypic and phenotypic correlations. To maximize the use of a main gene they suggested that it might be desirable to fix the gene or eliminate it. They thought that transferring a major gene from one line to another lacking it, by backcrossing, and then genotyping backcrosses, was possibly beneficial as there would have been no selection for modifying genes which could modify the deleterious effects of a harmful gene.

The ultimate maximization of major gene usage is genetic engineering. In theory, it will permit the transfer of the desired gene without other genetic material, thus leaving the genome relatively intact, apart from the introduction of foreign DNA (Roberts and Smith, 1982; Hill and Knott, 1987).

For sheep the work on the wool keratin gene complex undertaken by Ward et al (1982), was one of the first attempts at using this technology. Robertson (1982) suggested that the initial work in this area could concentrate on the regulating hormones, such as the growth hormone. Currently, there is considerable research aimed at introducing additional growth hormone producing genes.

Recently, Smith (1985) and Hill and Knott (1987) have considered the implications and use of major genes in livestock. The latter authors noted that even after identification of a breed/strain, e.g., the Booroola, with a major gene it may be a lengthy process before the mode of inheritance is illucidated.

Although, gene transfer technology and genetic engineering are still at the pioneer stage, these tools offer scope for livestock improvement not possible with conventional animal breeding techniques. For genetic engineering to become a practical reality in livestock species, the identification of main genes controlling productive characteristics is essential. In large animals this is still in the future.

CHAPTER 2

MATERIALS AND METHODS

2.1 TERMS

Several fleece and follicle traits will be discussed in this dissertation. Their meanings in brief, and the abbreviations that have been used in this thesis, are explained in the following section.

2.1.1 Follicle Parameters

1. Secondary to Primary follicle ratio (S/P), is the ratio of mature secondary to mature primary follicles. The S/P ratio indicates the number of follicles in a follicle group. The secondary to primary follicle ratio is of paramount importance, since it is related to the density of the fibres and to the variability of fibre size in the adult fleece (Daly and Carter, 1955).

2   In S/P is the natural logarithim of S/P.

3   Total Density (n(P+S)), equals the total follicle density or total number of primary and secondary follicles per unit area. Total follicle density is expressed as the number of mature follicles per square mm.

4. Total Density(corr) (n(P+S)corr), is the total follicle density (as given above), corrected for skin shrinkage or n(P+S)/CF.

5. Primary Density (nP), equals the mature primary follicle density or number of primary follicles per square mm. The higher the primary follicle density the smaller the area occupied by the follicle group.

6. Primary Density(corr) (nP(corr)), is the primary follicle density (as given above), corrected for skin shrinkage or nP/CF.

7. Shrinkage Correction Factor (CF), represents the amount of skin shrinkage which occurred from sampling through processing to slide manufacture.

2.1.2 Liveweight and Fleece Characteristics

1. LWT - animal liveweight, in kilograms, taken after shearing in October of the year in which the sheep was skin sampled.

2. GFW - greasy fleece weight in kilograms.

3. CFW - clean fleece weight in kilograms, obtained by multiplying GFW by yield/100.

4. YLD - clean scoured yield obtained from scouring a mid-side sample and expressed as a percentage (%).

5. MFD - fibre diameter in microns (μm), determined by the airflow method.

6. QN_r - quality number, a traditional classfication on fineness, assessed on the fleece by Ruakura staff at Tokanui at the time of shearing.

7. QN_m - quality number as assessed at Massey University using 2 staples from a midside sample. These results were averaged to give one value for data analysis.

8. SL_r - staple length, measured in centimeters by Ruakura staff at the time of shearing.

9. SL_m - staple length, measured in centimeters at Massey University.

10. TCN - total crimp number

11. CPC - crimps per centimeter

12. CHR_r - character grade assessed at shearing at Tokanui, ranging from 1 to 7, with 7 being the optimum.

13. CHR_m - character grade assessed at Massey University, the scale ranges from 1 to 9, the extreme grades 1 and 9 seldom being used.

14. LUS - lustre grade assessed at Massey University, ranging from 1 to 9.

15. TIP - tippiness grade assessed at Massey University, ranging from 1 to 9.

16. COT - degree of cotting as assessed at Massey University. This represents the level of fibre entanglement in the mid-side sample, ranging from 1 (very cotted) to 9 (free of entanglement).

17. SOU - hand breaking grade used to obtain an estimation of staple strength and measured on a scale of 1 - very tender to 9 - very sound.

18. HND - handle grade was assessed with a scale of 1 - very harsh to 9 - very soft.

19. GC_r - greasy colour grade as assessed by Ruakura staff, ranges from 1 to 9. Using this grade, the assessor attempts to estimate scoured colour.

20. GC_m - greasy colour grade as assessed at Massey University, ranging from 1 to 9. With this grade, the assessor does not attempt to estimate scoured colour.

21. SC_m - scoured colour grade as assessed at Massey University, ranging from 1 to 9.

2.2 DATA SOURCES AND COLLECTION

2.2.1 The Sheep Flocks

Sheep at the Ministry of Agriculture and Fisheries Research Station at Tokanui in the Waikato provided the material for these observations.

The flocks used in this study were:

>   Superfine Merino (SFM)
>   Local Merino (LM)
>   Romney (R)
>   Superfine Merino x Romney (SFMxR)
>   Local Merino x Romney (LMxR)
>   Backcross (BX : 3/4 SFM)

These flocks were set up to: 1. assess the potential of Merinos and their Romney crossbreds in high rainfall areas of the North Island and 2. evaluate the performance of the Tasmanian Superfine Merino strains with that of Merinos already present in New Zealand.

The Merino flocks were initiated in 1969. The Superfine group was based on imports of 44 ewes and 6 rams from 9 leading studs in the Australian states of Tasmania and Victoria. These animals had fine wool (>70s quality), of excellent character, soft handle, high yield and good colour.

The two New Zealand Merino flocks were established with 49 medium-woolled and 47 strong-woolled ewes each. In 1971 and 1973 respectively, an additional 54 and 21 ewes were bought from New Zealand Merino flocks. During 1972, the initial separation of the two local strains was abandoned and the flock was subsequently known as the Local Merinos.

Merino and Romney ewes were mated to Romney or Merino rams to produce F_1 crossbred progeny. In total, 424 ewes were involved in these additional matings along with further Romneys to generate Romney controls. Some of the Romneys used in flock establishment came from the Ruakura Fertility Selection flock.

In 1973/74, a Superfine, "Backcross" (BX), (i.e., 3/4 Superfine Merino) flock was created by mating Superfine rams to Superfine x Romney ewes. Since 1974, there has been progressive interbreeding of the backcross progeny, i.e., BX_1 rams x BX_1 ewes.

In 1973, F_1 crossbred rams generated in 1970 and 1971 were mated to F_1 crossbred ewes of the same genotype to produce either F_2 Superfine or New Zealand Merino crossbreds. Interbreeding within the crossbred flocks has continued. Those animals sampled in this study were chosen to give a good coverage of the F_1, F_2 and F_3 generations.

Each flock, with the exception of the Romneys, consisted of 125 ewes and all received similar grazing management. Although 8-10 ram hoggets were selected each year, only 5 two-tooth rams were used. Most of the emphasis in ram and ewe hogget selection was on fleece weight and fibre diameter with some attention to liveweight.

No flock of Romneys of similar ancestry to those used in generating the crossbreds was available. Instead, the Romneys came from the control flock of another genetic study. Figure 2.1 shows Merino x Romneys at Tokanui.

Figure 2.1 Merino x Romney sheep at the Tokanui Research Station

2.2.2 Sampling Procedures

In November 1978 and December 1979, skin samples were collected from the above flocks. Midside wool samples were taken at shearing in October in both 1978 and 1979.

Preliminary analysis of the 1978 data indicated the need for increased animal numbers. For this reason hoggets were included in the 1979 sampling. 143 sheep skin-sampled in 1978 were sampled again in 1979 to provide information on the repeatability of follicle characteristics. For those animals sampled in both years only their 1979 fleece and follicle parameters were used in the general analyses. A total of 637 animals were sampled over the two years. Although age at shearing was closer to 1 year and 3 months to 6 years and 3 months, age has been shortened to 1 to 6 years to simplify the text.

Table 2.1 contains a breakdown of the number of animals sampled and their distribution by age, year born, year sampled and birth/rearing rank.

2.2.3 Follicle Population Determinations

Duplicate skin samples were taken from the right midside of recently shorn ewes using a method derived from that of Carter and Clarke (1957a) (see figures 2.2 - 2.3). After histological processing and wax embedding; 10 μm thick cross sections were taken from the sebaceous gland level. These sections were stained with Haematoxylin, Eosin and Picric acid.

For each sheep, counts were made of the follicles in ten 1-mm^2 areas, the genotype of the sheep being unknown by the observer. From these counts the following parameters were calculated:

   Primary follicle density (nP)
   Secondary follicle density (nS)
   Total follicle density (n(P+S))
   Secondary to primary follicle ratio (S/P)

Figures 2.4 - 2.6 illustrate the follicle groups of Merinos, Romneys and Merino x Romney crossbreds.

Individual skin shrinkage after removal (CF), was also determined (Wickham, 1958) and corrections applied to individual primary and total density data.

TABLE 2.1: Number of sheep in each main group of the fixed effects study

		R		SFM		LM		SFM+LM		SFMxR		LMxR		SFMR+LMR		BX	
Year Born	**Age[1]**																
78	1	18	18	15	15	20	20	35	35	58	58	53	53	111	111	35	35
77	2	2	2	2	3	3	3	5	6	34	43	31	36	65	79	40	40
76	3	9	14	4	7	3	5	7	12	38	35	33	31	71	66	26	30
75	4	13	12	6	6	6	8	10	14	23	20	23	26	46	46	22	25
74	5	5	5	6	5	8	6	14	11	21	27	21	16	42	43	14	7
73	6	5	1	6	3	5	3	11	6	20	11	9	8	29	19	--	
B/Rearing Rank																	
	1/1	38		29		34		63		122		93		215		79	
	2/1	1		5		3		9		7		9		16		5	
	2/2	13		5		8		13		65		68		123		53	
Yr Sampled																	
	1978	13		12		8		20		27		15		42		11	
	1979	39		27		37		65		167		155		322		126	

[1] Under each genotype the first column is the number in the year born class; the second column - the age class

Figure 2.2   The midside skin sampling position

Figure 2.3   Skin sample collection
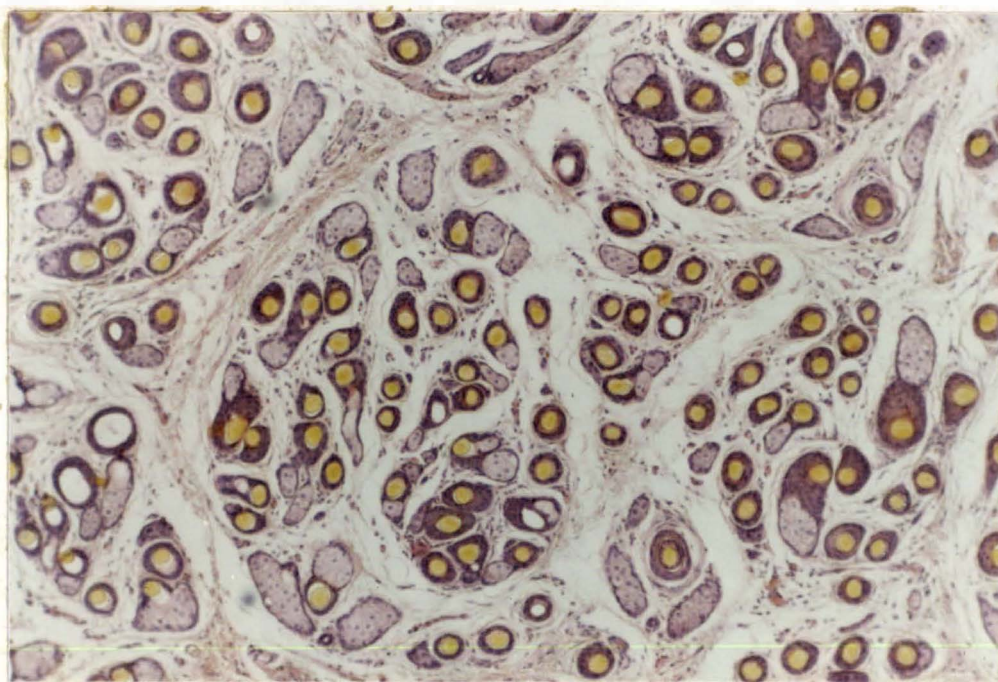
Figure 2.4   A Merino follicle group
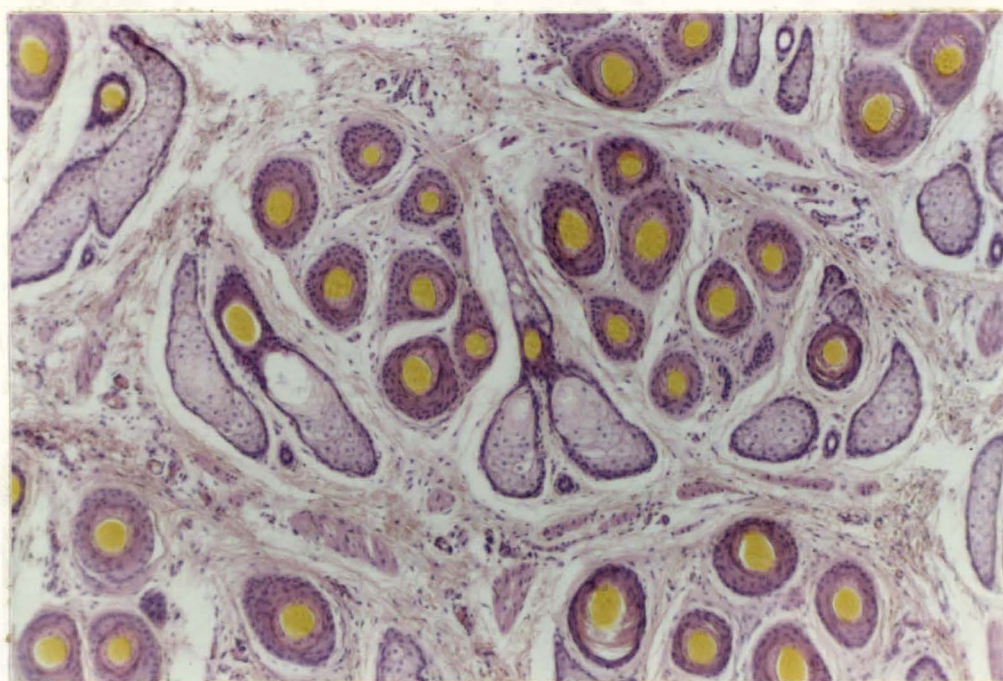
Figure 2.5   A Romney follicle group
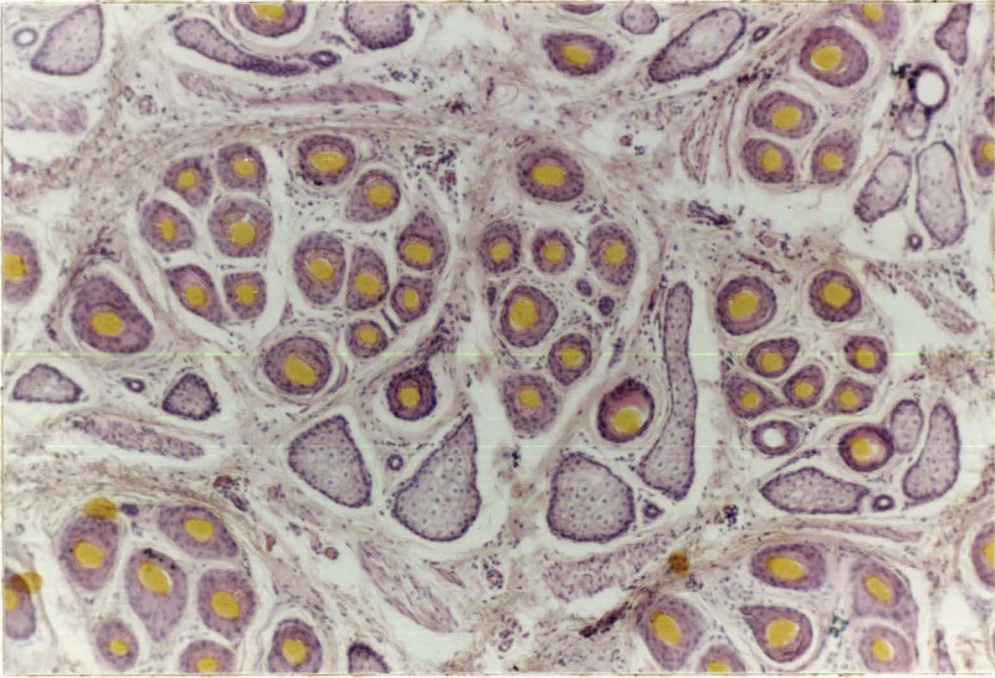
Figure 2.6   A Merino x Romney follicle group

2.2.4 Assessments on Wool Samples

Midside fleece samples were collected at shearing in 1978 and 1979. These were stored in plastic bags until needed. Subjective assessments and measurements were carried out, then the samples were scoured and mean fibre diameter was measured on the scoured sample.

At shearing, assessments of staple length (SL_r), quality number (QN_r) and character grade (CHR_r) were carried out by technical staff from Ruakura Animal Research Station. Later, samples were sent to Massey University where they were appraised using a system that has been described by Sumner (1969), Chopra (1978) and Horton (1978).

Under this system, traits for which standard assessment methods are not available are assessed on a 1 to 9 scale, the higher values being used for the levels most commonly desired. However, since an attempt was made initially to develop a scale on which the observations would tend to follow a distribution approaching the normal curve, 1 and 9 are rare values. Thus 9 represents for:

Lustre (LUS) - very high sheen,
Tip grade (TIP) - a completely blocky (square) tip,
Cotting grade (COT) - no entanglement,
Soundness grade (SOU) - high staple strength,
Handle (HND) - very soft.
Greasy colour (GC_m) - perfectly white,
Scoured colour (SC_m) - perfectly white,

At Massey, a 1 to 9 scale is also used for character (CHR). This is a slight expansion of the 1 to 7 scale commonly used throughout New Zealand and at Tokanui where 7 indicates wool with clear and even staple crimp and a blunt (blocky) staple tip.

Quality number (QN_m, QN_r), is an international system of visually assessing spinnability and fineness on the basis of staple crimp frequency and lustre (Henderson, 1965; Wickham, 1971). At Massey, reference samples of Merino and Halfbred wool were established after consultation with members of the staff of the Wool Department. Two observers then each placed two estimates on the sample. These were averaged to give one value (QN_m).

Staple length (SL_m) was measured to the nearest 5 mm on an unstretched greasy staple taken randomly from the sample. Care was taken not to stretch the wool. The tippy nature of Romney wool, was taken into account in measuring staple length. Tippiness was not a constraint with the Merino and half-bred type samples.

Total crimp number (TCN) was counted on the same staple using a magnifying device.

Crimps per centimetre (CPC) was calculated from TCN and SLm.

Yield (YLD) was measured by first conditioning the sample in a humidity-controlled room at 20°C and 65% RH (48 hrs). The sample was then scoured in a 4 bowl mini scour, dried and conditioned before weighing and calculating the clean weight/greasy weight percentage.

Clean fleece weight (CFW) was derived from the greasy fleece weight (GFW) and YLD.

Mean fibre diameter (MFD) was determined by the Airflow method (Anderson, 1954; Ross, 1958).

2.3 DATA ANALYSIS

Although some of the sheep contributing data were sampled in 1978, most were sampled in 1979. For those animals sampled in both years, fleece and follicle parameters for 1979 only were used in the general analyses. Results from this group were used to obtain repeatability estimates for fleece and follicle characteristics. The collection of data in both 1978 and 1979 enabled the study of the effect of year of sampling on fleece and follicle traits.

The various models used in the analyses are specified in each section.

CHAPTER 3

ANALYSIS OF THE EFFECTS OF AGE, YEAR OF SAMPLING AND BIRTH/REARING
RANK ON FOLLICLE AND FLEECE CHARACTERISTICS.

3.1 Method of Analysis

Much of the statistical analysis for this project was done using REG - a multiple regression
analysis package developed and modified by the Biometrics Section of the New South Wales
Department of Agriculture (Gilmour, 1983).

The effects of age, birth/rearing rank, and year of sampling on follicle and fleece characteristics
were estimated as factors in a linear model. This will be referred to as "age" since it contains an
element of the effect of birth year.

3.2 Results

Tables 3.1 - 3.28 contain the least square estimates of the means for follicle and fleece data
together with the fixed effects within genotype. Age and year born were confounded (see Table
2.1). No interactions were included in the models, as preliminary analysis had shown them to be
non significant. The "age" effect may be due in part to effects of the year in which the sheep was
being reared. In the Merinos and Merino-crosses, year born may have acted through year to year
variation in nutrition affecting pre-natal follicle initiation, post-natal follicle maturation and ultimate
fleeceweight.

The genotypes contained in Tables 3.1 - 3.28 represent 6 actual genotypes and 2 combined
genotypes. The latter were created by combining data from individual groups but without
correcting for genotype.

3.2.1 S/P

BRR was significant (p<0.05) only in the combined Superfine + Local Merino (SFM+LM) data.
This factor was also significant (p<0.05) with ln S/P in the (SFMR+LMR) data.

TABLE 3.1: Least squares estimates of the effects of age, birth/rearing rank and year sampled on S/P[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		6.68±0.55	18.06±1.21	18.66±1.21	18.36±0.83	10.92±0.36	10.32±0.46	10.68±0.28	15.81±0.75
Age	1	0.73±0.42	-1.79±1.50	-0.39±1.05	-0.78±0.89	1.77±0.33	1.40±0.40	1.59±0.25	1.02±0.56
	2	-0.46±1.08	-1.73±2.30	4.69±1.97	-3.22±1.52	0.24±0.35	-0.15±0.45	0.05±0.28	1.06±0.52
	3	-0.22±0.44	3.33±1.71	1.68±1.66	2.59±1.18	-0.72±0.38	-0.01±0.47	-0.43±0.29	-0.44±0.59
	4	0.00±0.44	0.88±1.85	-1.36±1.49	-0.54±1.16	-0.96±0.47	-0.79±0.50	-0.91±0.34	-0.74±0.64
	5	0.21±0.62	4.53±1.91	0.03±1.49	1.86±1.20	-0.15±0.43	-0.43±0.62	-0.21±0.35	-0.89±1.01
	6	-0.26±1.08	-5.03±2.42	4.72±2.00	0.09±1.58	0.19±0.62	-0.01±0.78	-0.08±0.49	-
						**	*	**	
B/Rearing Rank	1/1	-0.66±0.60	1.75±1.14	1.86±1.03	1.79±0.75	0.06±0.35	0.48±0.38	0.27±0.25	0.14±0.57
	2/1	1.14±1.18	0.07±1.64	-0.08±1.66	-0.12±1.13	0.20±0.62	0.05±0.62	0.12±0.43	0.43±1.01
	2/2	-0.48±0.65	-1.82±1.68	-1.11±1.27	1.67±0.99	-0.26±0.36	-0.53±0.38	-0.39±0.26	-0.57±0.60
					*				
Yr Sampled	1978	0.76±0.25	-3.05±1.03	-1.48±0.92	-2.04±0.69	-0.11±0.26	-0.25±0.38	-0.12±0.21	0.21±0.56
	1979	-0.76±0.25	3.05±1.03	1.48±0.92	2.04±0.69	0.11±0.26	0.25±0.38	0.12±0.21	0.21±0.56
		**	**		**				

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

TABLE 3.2: Least squares estimates of the effects of age, birth/rearing rank and year sampled on ln S/P[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		1.89±0.09	2.88±0.07	2.90±0.06	2.89±0.04	2.36±0.03	2.29±0.04	2.33±0.02	2.73±0.05
Age	1	0.12±0.07	-0.08±0.08	-0.01±0.05	-0.03±0.04	0.15±0.03	0.13±0.04	0.14±0.02	0.06±0.04
	2	-0.07±0.19	-0.06±0.12	-0.24±0.09	-0.15±0.08	0.03±0.03	-0.00±0.04	0.02±0.02	0.07±0.03
	3	-0.05±0.08	0.16±0.09	0.10±0.08	0.14±0.06	-0.07±0.03	0.00±0.04	-0.04±0.03	-0.02±0.04
	4	0.01±0.88	-0.00±0.10	-0.06±0.07	-0.04±0.06	-0.08±0.04	-0.08±0.05	-0.09±0.03	-0.05±0.04
	5	0.02±0.11	0.23±0.10	0.02±0.07	0.11±0.06	-0.02±0.04	-0.03±0.05	-0.02±0.03	-0.06±0.07
	6	-0.03±0.19	-0.24±0.13	0.18±0.09	-0.02±0.08	-0.01±0.05	-0.02±0.07	-0.01±0.04	-
						**	*	**	
B/Rearing Rank	1/1	-0.12±0.10	0.08±0.06	0.09±0.05	0.08±0.04	0.01±0.03	0.05±0.03	0.03±0.02	0.01±0.04
	2/1	0.20±0.20	0.02±0.09	-0.04±0.08	0.00±0.06	0.01±0.05	0.01±0.06	0.01±0.04	0.04±0.07
	2/2	-0.08±0.11	-0.09±0.09	0.05±0.06	-0.08±0.05	-0.02±0.03	-0.06±0.03	-0.04±0.02	-0.05±0.04
							*	*	
Yr Sampled	1978	0.13±0.04	-0.15±0.06	-0.08±0.04	-0.10±0.03	-0.02±0.02	-0.03±0.03	-0.02±0.02	-0.01±0.04
	1979	-0.13±0.04	0.15±0.06	0.08±0.04	0.10±0.03	0.02±0.02	0.03±0.03	0.02±0.02	0.01±0.04
		**	*		**				

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

TABLE 3.3:   Least squares estimates of the effects of age, birth/rearing rank and year sampled on Total Follicle Density [n(P+S)][1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		35.73±3.21	69.69±4.56	82.07±5.78	74.61±3.69	49.57±1.74	45.92±1.86	47.50±1.26	73.60±3.70
Age	1	7.34±2.47	5.58±5.64	20.35±5.02	14.82±3.94	19.11±1.57	13.13±1.58	16.31±1.14	13.08±2.78
	2	-3.70±6.29	-4.84±8.66	-6.89±9.39	-6.98±6.77	4.23±1.71	2.58±1.79	3.58±1.26	2.34±2.61
	3	-2.85±2.55	0.70±6.42	5.45±7.91	2.11±5.27	-4.47±1.82	-1.10±1.90	-3.02±1.33	-4.08±2.93
	4	-0.08±2.56	-0.12±6.97	-13.65±7.11	-6.55±5.16	-5.38±2.27	-6.14±2.02	-5.92±1.53	-6.95±3.17
	5	-5.09±3.61	12.16±7.18	-9.08±7.11	1.05±5.34	-4.83±2.08	-4.87±2.42	-4.83±1.59	-4.38±5.02
	6	5.11±6.29	-13.48±9.10	3.82±9.56	-4.45±7.03	-8.66±2.98	-3.60±3.30	-6.13±2.25	-
		*		**	*	**	**	**	**
B/Rearing Rank	1/1	-3.66±3.53	2.88±4.30	4.70±4.93	4.37±3.34	-2.50±1.70	0.94±1.52	-0.39±1.15	-6.52±2.84
	2/1	5.74±6.91	0.95±6.18	-2.31±7.91	-2.09±0.01	5.38±2.98	1.10±2.47	2.70±1.95	13.04±5.00
	2/2	-2.07±3.81	-3.82±6.32	-2.39±6.08	-2.28±4.42	-2.88±7.76	-2.05±1.53	-2.31±1.18	-6.51±2.99
Yr Sampled	1978	5.27±1.43	-7.61±3.89	1.52±4.41	-3.36±3.05	-0.74±1.27	0.61±1.51	0.02±0.97	-0.69±2.78
	1979	-5.27±1.43	7.61±3.89	-1.52±4.41	3.36±3.05	0.74±1.27	-0.61±1.51	-0.02±0.97	0.69±2.78
		**							

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

TABLE 3.4: Least squares estimates of the effects of age, birth/rearing rank and year samples on corrected total follicle density [n(P+S)]corr[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		14.28±1.84	40.67±3.46	51.30±5.03	47.58±2.86	26.69±1.02	24.39±1.30	25.40±0.79	41.88±2.70
Age	1	2.82±1.42	11.63±4.29	3.35±4.37	6.74±3.06	5.74±0.93	4.02±1.12	4.93±0.72	2.07±2.02
	2	-3.57±3.60	-5.12±6.58	5.43±8.18	0.21±5.25	3.58±1.00	3.41±1.26	3.53±0.79	4.78±1.90
	3	-2.14±1.46	-2.84±4.87	9.21±6.88	4.17±4.09	-2.36±1.07	-3.02±1.34	-2.81±0.84	-2.55±2.13
	4	-0.26±1.47	-3.21±5.29	-12.08±6.19	-8.50±4.00	-3.38±1.34	-2.36±1.42	-2.92±0.97	-3.95±2.31
	5	-1.31±2.07	4.47±5.46	-4.81±6.19	0.13±4.14	-1.33±1.23	-2.10±1.76	-1.74±1.02	-0.35±3.66
	6	4.46±3.60	-4.93±6.91	-1.12±8.32	-2.76±5.45	2.25±1.76	0.06±2.22	-1.00±1.39	-
						**	**	**	*
B/Rearing Rank	1/1	-0.42±2.02	2.38±3.26	1.79±4.29	0.11±2.59	-1.50±1.00	0.92±1.08	0.05±0.73	-2.14±2.07
	2/1	0.61±3.96	5.37±4.70	-1.76±6.88	1.81±3.89	2.69±1.75	-1.25±1.76	0.24±1.23	4.74±3.64
	2/2	-0.18±2.18	-7.75±4.80	-0.41±5.29	-1.92±3.43	-1.19±1.04	0.32±1.09	-0.29±0.75	-2.60±2.18
Yr Sampled	1978	1.43±0.82	-1.07±2.95	0.63±3.84	-0.34±2.37	-0.10±0.75	1.01±1.07	0.56±0.61	0.32±2.03
	1979	-1.43±0.82	1.07±2.95	-0.63±3.84	0.34±2.37	0.10±0.75	-1.01±1.07	-0.56±0.61	-0.32±2.03

[1] Effects are not significant unless * indicates level

* $P < 0.05$
** $P < 0.01$

TABLE 3.5: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Primary Follicle Density (nP)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		4.72±0.42	3.70±0.20	4.23±0.18	3.90±0.14	4.12±0.11	4.23±0.12	4.11±0.08	4.40±0.16
Age	1	0.64±0.38	0.60±0.25	0.98±0.16	0.82±0.15	0.87±0.10	0.61±0.10	0.76±0.07	0.53±0.12
	2	-0.32±0.83	0.01±0.38	0.54±0.30	0.22±0.25	0.31±0.11	0.21±0.12	0.28±0.08	-0.12±0.11
	3	-0.30±0.34	-0.44±0.28	-0.14±0.25	-0.34±0.20	-0.06±0.11	0.00±0.12	-0.03±0.08	-0.12±0.13
	4	-0.15±0.34	-0.17±0.31	-0.44±0.23	-0.23±0.19	-0.13±0.14	-0.34±0.13	0.22±0.10	-0.26±0.14
	5	-0.85±0.48	-0.17±0.32	-0.41±0.23	-0.26±0.20	-0.37±0.13	-0.25±0.16	-0.35±0.10	-0.03±0.22
	6	0.98±0.83	0.17±0.40	-0.53±0.30	-0.20±0.26	-0.62±0.19	-0.24±0.22	-0.44±0.14	-
				**	**	**	**	**	**
B/Rearing Rank	1/1	-0.15±0.47	-0.16±0.19	-0.15±0.16	-0.12±0.12	-0.17±0.11	-0.06±0.10	-0.09±0.07	-0.39±0.12
	2/1	0.15±0.91	-0.09±0.27	0.02±0.25	-0.13±0.19	0.25±0.19	0.03±0.16	0.11±0.12	0.59±0.22
	2/2	0.01±0.50	0.24±0.28	0.13±0.19	0.25±0.16	-0.08±0.11	0.03±0.10	-0.02±0.07	-0.20±0.13
									**
Yr Sampled	1978	0.26±0.19	0.15±0.17	0.34±0.14	0.19±0.11	-0.02±0.08	0.28±0.10	0.10±0.06	-0.03±0.12
	1979	-0.26±0.19	-0.15±0.17	-0.34±0.14	-0.19±0.11	0.02±0.08	-0.28±0.10	-0.10±0.06	0.03±0.12
				*			**		

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

TABLE 3.6: Least squares estimates of the effects of age, birth/rearing rank and year sampled on primary follicle density nP(corr)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		1.93±0.26	2.14±0.118	2.70±0.17	2.49±0.10	2.26±0.08	2.22±0.10	2.21±0.06	2.51±0.13
Age	1	0.22±0.20	0.70±0.15	0.14±0.15	0.35±0.11	0.15±0.07	0.11±0.08	0.13±0.05	0.02±0.10
	2	-0.45±0.51	-0.10±0.22	0.89±0.27	0.40±0.19	0.25±0.08	0.31±0.09	0.28±0.06	0.13±0.09
	3	-0.29±0.21	-0.40±0.17	0.13±0.23	-0.08±0.15	-0.06±0.08	-0.19±0.10	-0.13±0.06	-0.08±0.10
	4	-0.08±0.21	-0.23±0.18	-0.50±0.21	-0.37±0.15	-0.14±0.10	-0.12±0.11	-0.12±0.07	-0.17±0.11
	5	-0.22±0.29	-0.21±0.19	-0.22±0.21	-0.18±0.15	0.08±0.10	-0.05±0.13	-0.10±0.08	0.09±0.18
	6	0.82±0.51	0.24±0.23	-0.45±0.28	-0.12±0.20	-0.13±0.14	-0.05±0.17	-0.08±0.11	-
		**	**	*	**	**	**	**	
B/Rearing Rank	1/1	0.06±0.29	-0.06±0.11	-0.18±0.14	-0.21±0.09	-0.13±0.08	0.04±0.08	-0.02±0.06	-0.14±0.10
	2/1	-0.16±0.56	0.21±0.16	0.02±0.23	0.10±0.14	0.17±0.14	-0.18±0.13	-0.04±0.09	0.19±0.18
	2/2	0.10±0.31	-0.15±0.16	0.16±0.18	0.12±0.13	-0.04±0.08	0.13±0.08	0.06±0.06	-0.04±0.11
Yr Sampled	1978	0.004±0.12	0.23±0.10	0.22±0.13	0.19±0.09	0.02±0.06	0.21±0.08	0.10±0.05	0.03±0.10
	1979	-0.004±0.12	-0.23±0.10	-0.22±0.13	-0.19±0.09	-0.02±0.06	-0.21±0.08	-0.10±0.05	-0.03±0.10
			**		*		**	*	

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

TABLE 3.7: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Skin Shrinkage Correction Factor (CF)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		0.41±0.05	0.59±0.03	0.64±0.01	0.55±0.22	0.53±0.02	0.53±0.02	0.54±0.01	0.58±0.03
Age	1	-0.02±0.04	0.11±0.03	-0.10±0.04	-0.07±0.01	-0.05±0.02	-0.05±0.02	-0.06±0.01	-0.06±0.02
	2	-0.08±0.10	-0.04±0.05	0.13±0.07	0.02±0.01	0.04±0.02	0.04±0.02	0.03±0.01	0.05±0.02
	3	-0.03±0.04	-0.05±0.04	0.07±0.06	-0.01±0.02	-0.05±0.02	-0.05±0.02	-0.03±0.01	-0.01±0.02
	4	0.00±0.04	-0.04±0.04	-0.06±0.05	-0.02±0.02	0.01±0.02	0.01±0.02	-0.00±0.01	-0.00±0.02
	5	0.06±0.06	-0.03±0.04	0.01±0.05	0.03±0.02	0.01±0.03	0.01±0.03	0.02±0.01	0.02±0.04
	6	0.07±0.10	0.05±0.05	-0.05±0.07	0.04±0.03	0.04±0.03	0.04±0.03	0.04±0.02	-
				*	**	**	**	**	**
B/Rearing Rank	1/1	0.02±0.05	0.01±0.03	-0.01±0.04	-0.01±0.01	0.01±0.02	0.01±0.02	0.00±0.01	0.01±0.02
	2/1	-0.06±0.11	0.06±0.04	0.01±0.06	0.01±0.03	-0.03±0.03	-0.04±0.03	-0.02±0.02	-0.03±0.04
	2/2	0.03±0.06	-0.07±0.04	0.00±0.04	-0.00±0.02	0.02±0.02	0.02±0.02	0.01±0.01	0.02±0.02
Yr Sampled	1978	-0.03±0.02	0.05±0.02	0.00±0.03	0.01±0.01	0.01±0.02	0.01±0.02	0.01±0.01	0.01±0.02
	1979	0.03±0.02	-0.05±0.02	0.00±0.03	-0.01±0.01	-0.01±0.02	-0.01±0.02	-0.01±0.01	-0.01±0.02
			*						

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

TABLE 3.8:   Least squares estimates of the effects of age, birth/rearing rank and year sampled on Liveweight (LWT) (kg)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		54.72±2.89	44.50±2.36	47.73±1.70	45.93±1.55	48.42±0.97	61.15±1.74	50.38±0.82	44.64±1.27
Age	1	-15.81±3.57	-13.70±2.80	-12.68±1.67	-13.54±1.68	-11.37±0.86	-17.91±1.69	-10.57±0.77	-11.43±0.96
	2	-0.04±6.61	-0.13±3.50	0.06±2.86	-1.04±2.53	1.40±0.94	-7.76±1.79	0.96±0.83	-0.32±1.03
	3	6.33±3.30	0.36±2.72	1.05±2.31	-0.11±1.89	7.29±0.99	-1.56±1.82	7.01±0.86	4.36±1.08
	4	1.71±3.31	0.86±2.64	2.72±1.94	2.28±1.80	8.42±1.15	3.19±1.87	10.53±0.93	4.81±1.15
	5	-	-	-	-	9.12±1.13	-	8.20±1.01	2.58±1.72
	6	7.81±13.41	12.61±9.39	8.30±6.62	12.41±6.23	-14.86±2.57	24.03±6.42	-16.13±2.75	-
		**	**	**	**	**	**	**	**
B/Rearing Rank	1/1	2.35±1.14	-1.26±1.10	0.07±0.92	-0.23±0.79	0.95±0.85	1.25±0.75	0.86±0.60	1.95±0.99
	2/1	-	0.82±1.68	2.68±1.47	1.52±1.21	1.22±1.50	-0.26±1.21	0.74±1.01	-1.00±1.70
	2/2	2.35±1.14	0.45±1.55	-2.75±1.44	-1.30±1.02	-2.17±0.87	-0.99±0.75	-1.60±0.61	-0.96±1.06
						**	*	**	*
Yr Sampled	1978	0.83±1.24	-2.16±1.06	-0.80±0.82	-2.11±0.72	-1.62±0.60	0.29±0.75	-1.03±0.50	-0.96±0.97
	1979	-0.83±1.24	2.16±1.06	0.80±0.82	2.11±0.72	1.62±0.60	-0.29±0.75	1.03±0.50	0.96±0.97
		**	**	**	**	**	**	*	

[1] Effects are not significant unless * indicates level

* P < 0.05

** P < 0.01

TABLE 3.9: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Fleeceweight (GFW) (kg)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		3.60±0.32	3.40±0.29	3.75±0.27	3.58±0.22	3.64±0.08	4.09±0.10	3.85±0.07	3.12±0.12
Age	1	-0.91±0.29	-0.21±0.35	-0.17±0.27	-0.25±0.25	-0.09±0.07	-0.24±0.08	-0.17±0.06	-0.10±0.09
	2	0.44±0.55	-0.43±0.44	-0.08±0.40	-0.41±0.34	-0.44±0.08	-0.64±0.09	-0.54±0.07	-0.25±0.09
	3	0.42±0.27	-0.09±0.35	0.57±0.34	0.07±0.28	0.34±0.08	0.52±0.10	0.42±0.07	0.09±0.10
	4	0.46±0.27	0.21±0.37	0.46±0.31	0.38±0.27	0.17±0.10	0.45±0.11	0.38±0.08	0.30±0.11
	5	-	-	-	-	0.04±0.92	0.09±0.13	0.02±0.08	-0.04±0.16
	6	0.40±1.12	0.52±1.20	-0.79±1.03	0.20±0.91	-0.01±0.15	-0.19±0.19	-0.10±0.13	-
		**				**	**	**	**
B/Rearing Rank	1/1	0.42±0.23	-0.22±0.15	0.09±0.15	-0.03±0.12	-0.03±0.08	0.09±0.08	-0.01±0.06	0.27±0.09
	2/1	-0.48±0.46	0.24±0.22	0.29±0.24	0.18±0.18	0.13±0.14	-0.15±0.13	0.03±0.10	-0.39±0.16
	2/2	0.07±0.25	-0.02±0.22	-0.38±0.18	-0.15±0.16	-0.09±0.08	0.06±0.08	-0.02±0.06	0.12±0.10
									*
Yr Sampled	1978	-0.15±0.10	-0.26±0.14	-0.20±0.13	-0.30±0.11	-0.30±0.06	-0.27±0.08	-0.32±0.05	-0.25±0.09
	1979	0.15±0.10	0.26±0.14	0.20±0.13	0.30±0.11	0.30±0.06	0.27±0.08	0.32±0.05	0.25±0.09
		*				**	**	**	**

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

TABLE 3.10: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Clean Fleeceweight (CFW) (kg)[1]

	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean	2.74±0.63	2.36±0.21	2.84±0.19	2.57±0.16	2.56±0.10	2.88±0.10	2.74±0.07	2.25±0.11
Age 1	-	-0.16±0.25	-0.18±0.19	-0.20±0.18	-0.16±0.07	-0.30±0.08	-0.22±0.06	-0.16±0.08
2	0.66±0.79	-0.19±0.38	-0.06±0.27	-0.19±0.27	-0.26±0.07	-0.50±0.08	-0.38±0.06	-0.13±0.08
3	0.48±0.60	0.02±0.25	0.40±0.24	0.08±0.20	0.26±0.07	0.49±0.09	0.35±0.06	0.07±0.08
4	0.72±0.60	0.30±0.26	0.14±0.24	0.28±0.21	0.18±0.09	0.41±0.09	0.34±0.07	0.27±0.09
5	-	-	-	-	-0.00±0.08	0.01±0.12	-0.02±0.08	-0.04±0.14
6	-1.86±1.80	0.03±0.89	-0.31±0.71	0.03±0.67	-0.02±0.13	-0.11±0.18	-0.08±0.12	-
					**	**	**	*
B/Rearing Rank 1/1	0.26±0.28	-0.15±0.11	-0.02±0.10	-0.04±0.09	0.09±0.09	0.14±0.07	0.05±0.06	0.20±0.09
2/1	-0.34±0.54	0.14±0.16	0.37±0.17	0.14±0.13	-0.16±0.17	-0.19±0.12	-0.09±0.11	-0.27±0.16
2/2	0.09±0.33	0.10±0.17	-0.35±0.13	-0.10±0.12	0.07±0.10	0.05±0.07	0.04±0.06	0.07±0.09
			*					*
Yr 1978		-0.19±0.11	-0.09±0.10	-0.19±0.08	-0.24±0.06	-0.37±0.09	-0.32±0.05	-0.21±0.08
Sampled	a							
1979		0.19±0.11	0.09±0.10	0.19±0.08	0.24±0.06	0.37±0.09	0.32±0.05	0.21±0.08
					**	**	**	

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.11: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Yield (YLD) (%)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		77.56±2.39	70.33±1.58	72.46±1.80	71.00±1.08	71.77±1.01	72.96±1.01	72.30±0.67	72.43±1.29
Age	1	-	-0.71±1.77	-1.82±1.59	-1.29±1.13	-2.20±0.74	-2.80±0.73	-2.42±0.52	-2.59±0.90
	2	3.24±4.29	-1.20±3.35	-0.75±2.91	-1.13±2.10	1.99±0.84	0.69±0.83	1.43±0.59	1.55±0.87
	3	1.97±2.35	1.98±2.08	1.26±2.42	1.25±1.49	0.40±0.81	1.86±0.86	1.13±0.58	0.01±0.94
	4	2.31±2.28	3.60±2.30	2.16±2.69	3.48±1.61	2.05±1.01	1.11±0.92	1.75±0.67	1.40±1.03
	5	-5.26±4.29	-0.48±2.33	0.61±2.17	0.22±1.51	-0.32±0.96	0.08±1.13	-0.12±0.71	-0.38±1.61
	6	-2.26±4.29	-3.18±2.85	-1.46±2.95	-2.52±1.97	-1.93±1.32	-0.93±1.72	-1.77±1.03	-
						**	**	**	*
B/Rearing Rank	1/1	-1.20±2.51	-0.20±1.40	-0.15±1.54	0.16±0.96	0.73±0.93	0.67±0.70	0.47±0.56	-0.04±1.00
	2/1	1.90±4.79	-1.22±1.98	1.76±2.54	-0.15±1.42	-1.73±1.71	-0.83±1.17	-0.96±0.98	0.62±1.81
	2/2	-0.70±2.92	1.41±2.13	-1.60±1.99	-0.02±1.30	1.00±0.98	0.17±0.71	0.49±0.58	-0.57±1.06
Yr Sampled	1978	a	-0.62±1.32	-0.95±1.44	-1.04±0.92	-1.19±0.71	-1.56±0.83	-1.49±0.52	-0.65±0.94
	1979		0.65±1.32	0.95±1.44	1.04±0.92	1.19±0.71	1.56±0.83	1.49±0.52	0.65±0.94
								**	

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.12: Least squares estimates of the effects of age, birth rank/rearing rank and year sampled on fibre diameter (MFD) (μm)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		37.26±0.57	20.71±0.52	22.56±0.45	21.43±0.37	26.24±0.53	28.23±0.57	27.31±0.40	21.21±0.50
Age	1	-	1.03±0.58	-1.00±0.39	-0.96±0.39	-1.85±0.38	-1.40±0.43	-1.62±0.30	-0.31±0.36
	2	1.04±1.87	1.59±1.11	0.48±0.71	0.87±0.73	-0.13±0.43	-0.93±0.48	-0.51±0.34	0.09±0.35
	3	0.92±1.02	-0.55±0.68	-1.11±0.60	-0.98±0.52	0.47±0.53	-0.37±0.50	0.06±0.35	-0.40±0.38
	4	1.17±0.99	-0.27±0.75	-0.33±0.59	-0.04±0.54	-0.25±0.53	1.27±0.52	0.83±0.39	-0.07±0.40
	5	-1.16±1.87	0.04±0.76	0.96±0.54	0.65±0.53	0.29±0.50	0.58±0.64	0.29±0.42	0.67±0.64
	6	-1.97±1.87	0.21±0.93	1.02±0.73	0.46±0.68	1.47±0.69	0.85±1.01	0.95±0.61	-
			*	**		**	*	*	*
B/Rearing Rank	1/1	0.67±1.09	-1.11±0.46	-0.70±0.38	-0.72±0.33	0.41±0.48	0.37±0.41	0.13±0.33	0.92±0.40
	2/1	-0.53±2.09	0.83±0.65	1.27±0.60	0.86±0.49	-1.06±0.89	-0.41±0.68	-0.39±0.58	-1.84±0.71
	2/2	-0.14±1.27	0.27±0.70	-0.57±0.46	-0.13±0.44	0.65±0.51	0.04±0.41	0.26±0.34	0.93±0.42
Yr Sampled	1978	a	-0.25±0.43	0.02±0.35	-0.31±0.32	-0.20±0.37	-0.59±0.46	-0.42±0.31	-0.64±0.35
	1979		0.25±0.43	-0.02±0.35	0.31±0.32	0.20±0.37	0.59±0.46	0.42±0.31	0.64±0.35

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.13: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Quality Number (QN_r)[1]

		R	SFM	LM	SFM+LM	SFM×R	LM×R	SFMR+LMR	BX
Least SQ Mean		46.67±1.07	70.88±1.83	63.27±1.07	68.03±1.50	56.79±0.46	55.76±0.40	56.47±0.31	61.72±1.56
Age	1	-	-	-	-	-	-	-	-
	2	0.66±1.88	0.78±2.13	0.58±1.50	1.88±2.16	0.76±0.36	0.78±0.35	0.72±0.26	0.51±0.70
	3	-0.21±0.93	-0.10±1.77	-0.90±1.27	0.73±1.65	-0.07±0.38	0.19±0.37	0.01±0.28	0.36±0.76
	4	-	-1.00±1.71	0.78±1.39	-1.16±1.72	-0.39±0.46	-0.55±0.38	-0.60±0.31	-0.14±0.81
	5	-0.45±2.31	-	-0.47±1.18	-1.45±1.72	-0.30±0.42	-0.42±0.49	-0.13±0.33	-0.73±1.23
	6	-	-	-	-	-	-	- *	-
B/Rearing Rank	1/1	-0.33±0.87	2.92±1.92	0.29±1.16	1.13±1.62	0.19±0.50	0.29±0.39	0.21±0.32	0.09±1.44
	2/1	-0.33±1.64	1.10±2.30	-1.06±1.83	1.59±2.12	-0.93±0.87	0.99±0.63	0.12±0.54	-1.28±2.76
	2/2	0.66±1.03	-4.03±3.41	0.76±1.68	-2.73±2.46	0.73±0.50	-1.28±0.39 **	-0.32±0.32	1.19±1.45
Yr Sampled	1978	a	2.76±1.04	0.30±0.79	2.35±1.08	0.66±0.28	0.06±0.31	0.51±0.21	0.95±0.72
	1979		-2.76±1.04 **	-0.30±0.79	-2.35±1.08 *	-0.66±0.28 *	-0.06±0.31	-0.51±0.21 *	-0.95±0.72

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.14:   Least squares estimates of the effects of age, birth/rearing rank and year sampled on Quality Number (QN_m)[1]

	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean	47.53±2.28	68.68±0.89	62.23±0.02	65.31±0.87	57.24±0.56	53.73±0.60	55.84±0.43	63.51±0.89
Age 1	–	-1.57±1.03	2.54±0.89	0.92±0.91	0.54±0.45	0.11±0.44	0.34±0.34	-1.79±0.66
2	-1.39±4.10	7.46±1.95	-0.24±1.64	2.76±1.71	0.79±0.51	0.46±0.51	0.66±0.39	0.89±0.62
3	-2.57±2.24	-0.12±1.21	2.77±1.37	1.65±1.22	0.27±0.50	0.98±0.52	0.69±0.39	1.76±0.70
4	0.76±2.18	-3.98±1.33	-0.33±1.36	-2.25±1.26	0.86±0.63	-0.50±0.55	-0.33±0.44	1.29±0.75
5	-1.39±4.09	-1.75±1.35	-3.65±1.23	-3.07±1.24	-0.91±0.59	-0.36±0.70	-0.25±0.48	-2.15±1.19
6	4.69±4.09	-0.04±1.66	-1.08±1.67	-0.00±1.61	-1.54±0.82	-0.69±0.99	-1.12±0.68	–
		**	**	*				**
B/Rearing Rank 1/1	-0.13±2.40	0.50±0.78	0.37±0.88	0.41±0.77	0.68±0.53	-0.03±0.44	0.37±0.36	-0.47±0.67
2/1	-0.13±4.57	-0.81±1.13	-0.23±1.38	0.15±1.14	-0.72±0.90	0.69±0.73	-0.00±0.64	1.03±1.18
2/2	0.27±2.79	0.31±1.15	-0.14±1.05	-0.57±1.01	0.05±0.57	-0.65±0.44	-0.37±0.38	-0.56±0.11
Yr Sampled 1978	a	3.14±0.76	3.86±0.80	3.88±0.74	2.47±0.43	0.00±0.50	1.56±0.34	2.88±0.68
1979		-3.14±0.76	-3.86±0.80	-3.88±0.74	-2.47±0.43	0.00±0.50	-1.56±0.34	-2.88±0.68
		**	**	*	**		**	**

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.15: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Staple Length (SL$_r$)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		15.33±0.94	7.27±0.48	8.96±0.44	8.19±0.30	9.65±0.25	10.98±0.28	10.22±0.19	8.25±0.56
Age	1	-	-	-	-	-	-	-	-
	2	-0.97±1.66	-0.57±0.56	-0.66±0.61	0.61±0.43	-1.00±0.20	-1.88±0.25	-1.39±0.17	-0.81±0.25
	3	-0.14±0.84	0.42±0.42	0.10±0.51	0.22±0.33	0.63±0.21	0.49±0.26	0.59±0.18	0.75±0.27
	4	-	0.13±0.47	0.32±0.57	0.24±0.34	0.81±0.25	0.93±0.24	1.04±0.19	0.48±0.29
	5	-	0.02±0.45	0.24±0.48	0.16±0.34	-0.43±0.25	0.46±0.35	-0.25±0.21	-0.41±0.44
	6	1.10±2.06	-	-	-	-	-	-	-
							**	**	**
B/Rearing Rank	1/1	-0.37±0.77	0.55±0.51	-0.23±0.47	0.09±0.32	-0.41±0.27	-0.49±0.28	-0.54±0.20	0.33±0.51
	2/1	1.63±1.46	0.12±0.61	0.22±0.74	-0.12±0.42	0.61±0.48	0.37±0.44	0.63±0.35	0.37±0.98
	2/2	-1.26±0.94	-0.66±0.90	0.01±0.68	0.03±0.49	-0.19±0.28	0.12±0.28	-0.09±0.21	-0.70±0.52
								*	**
Yr Sampled	1978	a	-0.27±0.28	-0.34±0.32	-0.38±0.22	-0.57±0.16	-0.38±0.22	-0.60±0.14	-0.70±0.26
	1979		0.27±0.28	0.34±0.32	0.38±0.22	0.57±0.16	0.38±0.22	0.60±0.14	0.70±0.26
								**	**

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.16: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Staple Length (SL_m) (cm)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		13.90±0.85	8.12±0.25	9.11±0.32	8.41±0.22	9.99±0.26	11.23±0.31	10.49±0.20	8.68±0.33
Age	1	-	0.42±0.30	0.66±0.28	0.59±0.23	0.49±0.21	0.11±0.23	0.33±0.16	0.60±0.24
	2	0.27±1.51	-1.02±0.54	-0.58±0.51	-0.85±0.43	-1.12±0.23	-1.53±0.26	-1.30±0.18	-1.21±0.23
	3	2.10±0.83	0.50±0.34	0.50±0.43	0.32±0.31	0.34±0.23	0.68±0.27	0.52±0.18	0.66±0.26
	4	1.08±0.81	0.73±0.37	0.13±0.42	0.64±0.32	0.91±0.29	0.95±0.29	1.11±0.21	0.30±0.28
	5	-1.73±1.52	-0.10±0.38	0.61±0.39	0.32±0.31	-0.63±0.27	0.18±0.36	-0.45±0.23	-0.36±0.44
	6	-1.73±1.52	-0.52±0.46	-1.31±0.52	-1.01±0.40	0.02±0.37	-0.38±0.52	-0.20±0.32	-
				*	**	**	**	**	**
B/Rearing Rank	1/1	0.17±0.89	-0.36±0.20	-0.26±0.27	-0.13±0.19	-0.30±0.24	-0.20±0.23	-0.34±0.17	0.31±0.25
	2/1	0.83±1.70	-0.37±0.32	0.71±0.43	-0.05±0.29	0.27±0.44	-0.01±0.38	0.23±0.30	-0.13±0.44
	2/2	-0.66±1.04	0.73±0.32	-0.45±0.33	0.18±0.25	0.04±0.26	0.21±0.23	0.11±0.18	-0.18±0.26
Yr Sampled	1978	a	-0.27±0.21	-0.13±0.25	-0.31±0.19	-0.56±0.20	-0.27±0.26	-0.55±0.16	-0.51±0.24
	1979		0.27±0.21	0.13±0.25	0.31±0.19	0.56±0.20	0.27±0.26	0.55±0.16	0.51±0.24
						**		**	*

[1] Effects are not significant unless * indicates level

$* \ P < 0.05$
$** \ P < 0.01$

a Romneys were only fleece sampled in 1979

TABLE 3.17: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Total Crimp Number (TCN)[1]

	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean	15.46±1.87	49.37±2.24	38.26±2.51	43.86±1.89	32.17±1.53	27.98±1.21	29.89±1.01	41.43±2.33
Age 1	-	-5.39±2.60	-1.53±2.17	-3.20±1.96	6.66±1.23	3.92±0.90	5.37±0.81	2.30±1.77
2	-3.07±3.36	1.70±4.92	-9.23±4.02	-4.91±3.70	-1.69±1.38	-1.79±1.03	-1.62±0.91	-4.53±1.65
3	-1.92±1.84	7.13±3.06	7.04±3.37	8.23±2.65	0.49±1.37	2.34±1.05	1.39±0.91	5.34±1.85
4	-0.09±1.79	-1.10±3.36	4.60±3.34	1.31±2.73	2.12±1.71	-0.88±1.12	0.17±1.04	4.76±1.99
5	-3.07±3.36	-2.05±3.42	-1.14±3.03	-2.21±2.67	-1.89±1.62	-1.52±1.42	-1.41±1.13	-7.87±3.16
6	8.93±3.36	-0.30±4.18	0.28±4.10	0.78±3.48	-5.69±2.23	-2.08±2.01	-3.89±1.59	-
				**	**	**	**	**
B/Rearing Rank 1/1	0.61±1.97	-0.95±1.98	-2.34±2.16	-1.85±1.66	-2.35±1.45	-0.76±0.89	-1.14±0.86	-1.05±1.79
2/1	-1.39±3.76	5.06±2.85	5.14±3.40	6.54±2.48	4.22±2.64	2.36±1.48	2.75±1.50	1.16±3.15
2/2	0.78±2.29	-4.11±2.91	-2.80±2.59	-4.70±2.18	-1.87±1.54	-1.60±0.89	-1.61±0.89	-0.12±1.90
Yr Sampled 1978	a	-2.87±1.93	-2.13±1.96	-1.87±1.61	0.04±1.17	0.31±0.99	0.29±0.81	-0.07±1.75
1979		2.87±1.93	2.13±1.96	1.87±1.61	-0.04±1.17	-0.31±0.99	-0.29±0.81	0.07±1.75

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.18:   Least squares estimates of the effects of age, birth/rearing rank and year sampled on Crimps per Centimetre (CPC)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		1.16±0.15	6.24±0.28	4.25±0.31	5.34±0.27	3.27±0.18	2.54±0.12	2.92±0.12	4.78±0.29
Age	1	-	-1.05±0.33	-0.51±0.27	-0.75±0.28	0.50±0.15	0.29±0.09	0.40±0.10	0.00±0.22
	2	-0.31±0.27	1.06±0.62	-0.90±0.50	-0.08±0.53	0.20±0.16	0.18±0.10	0.20±0.11	0.18±0.20
	3	-0.30±0.15	0.45±0.38	0.47±0.42	0.71±0.38	-0.02±0.16	0.02±0.11	0.00±0.11	0.23±0.23
	4	-0.16±0.14	-0.61±0.42	0.35±0.41	-0.29±0.39	-0.04±0.20	-0.24±0.11	-0.23±0.12	0.37±0.25
	5	-0.11±0.27	-0.20±0.43	-0.24±0.38	-0.31±0.39	-0.06±0.19	-0.21±0.14	-0.05±0.13	-0.79±0.39
	6	0.89±0.27	0.34±0.53	0.83±0.51	0.73±0.50	-0.58±0.27	-0.04±0.20	-0.32±0.19	-
		*	*		*	*	**	**	
B/Rearing Rank	1/1	0.05±0.16	0.06±0.25	-0.12±0.27	-0.13±0.24	-0.10±0.17	-0.03±0.09	-0.01±0.11	-0.22±0.22
	2/1	-0.15±0.30	0.81±0.36	0.25±0.42	0.82±0.36	0.29±0.32	0.21±0.15	0.17±0.18	0.12±0.39
	2/2	0.09±0.18	-0.87±0.37	-0.14±0.32	-0.70±0.32	-0.19±0.18	-0.18±0.09	-0.17±0.11	0.09±0.23
Yr Sampled	1978		-0.19±0.24	-0.20±0.24	-0.06±0.23	0.19±0.14	0.08±0.10	0.19±0.10	0.23±0.22
	1979	a	0.19±0.24	0.20±0.24	0.06±0.23	-0.19±0.14	-0.08±0.10	-0.19±0.10	-0.23±0.22

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.19: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Character Grade (CHR$_r$)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		3.68±0.36	5.66±0.51	5.67±0.27	5.68±0.23	4.18±0.20	4.45±0.22	4.37±0.15	5.06±0.41
Age	1	-	-	-	-	-	-	-	-
	2	0.13±0.66	-0.64±0.59	0.57±0.38	-0.04±0.34	0.01±0.16	-0.40±0.19	-0.19±0.13	-0.45±0.18
	3	-0.28±0.41	0.13±0.43	-0.01±0.32	0.02±0.26	0.02±0.16	0.25±0.20	0.13±0.13	0.14±0.20
	4	0.15±0.42	0.09±0.49	0.07±0.35	0.13±0.27	0.25±0.20	0.24±0.21	0.28±0.15	0.11±0.21
	5	-	0.43±0.47	-0.63±0.30	-0.11±0.27	-0.28±0.18	-0.09±0.26	-0.22±0.18	0.21±0.32
	6	-	-	-	-	-	-	-	-
B/Rearing Rank	1/1	0.19±0.48	-0.07±0.53	0.08±0.29	-0.06±0.25	0.01±0.21	-0.21±0.21	-0.01±0.15	-0.24±0.38
	2/1	-0.81±0.90	-0.04±0.64	0.25±0.46	0.15±0.33	-0.09±0.38	-0.22±0.34	-0.05±0.26	0.55±0.72
	2/2	0.63±0.56	0.10±0.95	-0.33±0.42	-0.10±0.38	0.10±0.22	0.01±0.21	0.06±0.16	-0.31±0.38
Yr Sampled	1978	a	-0.15±0.29	-0.15±0.20	-0.14±0.17	0.30±0.12	-0.21±0.17	0.06±0.10	0.16±0.19
	1979		0.15±0.29	0.15±0.20	0.14±0.17	-0.30±0.12 *	0.21±0.17	-0.06±0.10	-0.16±0.19

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.20: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Character Grade (CHR_m) [1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		3.81±0.33	5.66±0.16	5.67±0.27	5.68±0.15	5.17±0.13	5.28±0.13	5.16±0.09	5.43±0.15
Age	1	-	0.21±0.19	0.45±0.23	0.33±0.15	0.32±0.11	0.27±0.10	0.31±0.07	0.19±0.11
	2	0.65±0.59	-0.69±0.35	0.85±0.43	0.21±0.29	-0.10±0.12	-0.04±0.11	-0.06±0.08	-0.14±0.10
	3	-0.74±0.32	0.23±0.22	-0.10±0.36	0.04±0.21	0.02±0.12	0.04±0.11	0.03±0.08	-0.05±0.12
	4	-0.20±0.31	0.40±0.24	-0.22±0.36	0.05±0.21	0.23±0.15	-0.15±0.12	0.07±0.09	-0.13±0.13
	5	-0.35±0.59	0.20±0.24	0.17±0.32	0.13±0.21	-0.20±0.14	0.02±0.15	-0.14±0.10	0.12±0.20
	6	0.65±0.59	-0.36±0.30	-1.15±0.44	-0.76±0.27	-0.27±0.19	-0.15±0.22	-0.21±0.14	-
				*		*		**	
B/Rearing Rank	1/1	0.54±0.34	-0.08±0.14	-0.16±0.23	-0.11±0.13	-0.21±0.13	0.06±0.10	-0.07±0.08	0.03±0.11
	2/1	-1.46±0.65	0.10±0.20	0.34±0.36	0.19±0.19	0.21±0.23	-0.02±0.16	0.08±0.14	0.09±0.20
	2/2	0.92±0.40	-0.20±0.21	-0.17±0.28	-0.09±0.17	0.00±0.13	-0.05±0.10	-0.01±0.08	-0.12±0.12
Yr Sampled	1978	a	-0.12±0.14	0.03±0.21	-0.02±0.13	-0.26±0.10	-0.14±0.11	-0.24±0.07	-0.16±0.11
	1979		0.12±0.14	-0.03±0.21	0.02±0.13	0.26±0.10	0.14±0.11	0.24±0.07	0.16±0.11
						**		**	

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.21:   Least squares estimates of the effects of age, birth/rearing rank and year sampled on Lustre (LUS)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		6.73±0.30	2.93±0.17	3.83±0.23	3.29±0.16	4.47±0.14	5.00±0.16	4.71±0.10	3.66±0.18
Age	1	-	-1.06±0.20	-0.54±0.20	-0.79±0.17	-0.26±0.11	-0.21±0.12	-0.26±0.08	0.07±0.14
	2	0.16±0.53	0.29±0.37	-0.04±0.36	0.10±0.31	-0.22±0.12	-0.05±0.14	-0.17±0.09	-0.15±0.13
	3	0.41±0.29	-0.22±0.23	-0.05±0.30	-0.18±0.22	-0.08±0.12	0.01±0.14	-0.07±0.09	-0.13±0.14
	4	0.11±0.28	0.14±0.25	-0.05±0.30	0.16±0.23	-0.08±0.15	0.34±0.15	0.20±0.11	-0.10±0.16
	5	0.16±0.53	0.23±0.26	0.57±0.27	0.43±0.23	0.07±0.14	0.04±0.19	-0.01±0.12	0.31±0.25
	6	-0.84±0.53	0.62±0.32	0.11±0.37	0.27±0.29	0.57±0.20	-0.12±0.26	0.29±0.16	-
			**		**	*		*	
B/Rearing Rank	1/1	0.11±0.31	0.02±0.15	-0.30±0.19	-0.06±0.14	-0.09±0.13	0.04±0.12	-0.08±0.09	0.12±0.14
	2/1	0.11±0.59	-0.15±0.22	0.15±0.31	-0.17±0.21	-0.12±0.24	-0.07±0.20	-0.05±0.15	-0.17±0.25
	2/2	-0.21±0.36	0.13±0.22	0.14±0.23	0.22±0.18	0.21±0.14	0.07±0.12	0.13±0.09	0.06±0.15
Yr Sampled	1978	a	-0.76±0.15	-0.69±0.18	-0.81±0.14	-0.48±0.10	-0.12±0.13	-0.35±0.08	-0.48±0.14
	1979		0.76±0.15	0.69±0.18	0.81±0.14	0.48±0.10	0.12±0.13	0.35±0.08	0.48±0.14
			**	**	**	**		**	**

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.22: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Tip Grade (TIP)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		3.80±0.25	5.49±0.16	4.96±0.17	5.32±0.13	5.45±0.11	5.28±0.13	5.35±0.08	5.25±0.14
Age	1	-	-0.01±0.18	0.01±0.15	-0.01±0.13	-0.06±0.09	-0.15±0.10	-0.09±0.07	0.21±0.11
	2	0.72±0.44	0.13±0.34	0.67±0.27	0.49±0.25	-0.12±0.10	0.07±0.11	-0.02±0.07	0.10±0.10
	3	-0.86±0.24	0.27±0.21	-0.26±0.23	-0.09±0.18	0.10±0.10	0.27±0.11	0.19±0.07	0.23±0.11
	4	-0.30±0.23	0.15±0.24	-0.20±0.23	-0.21±0.19	0.18±0.13	-0.27±0.12	-0.08±0.09	-0.02±0.12
	5	-0.28±0.44	-0.18±0.25	0.12±0.21	0.00±0.18	-0.03±0.12	-0.08±0.15	-0.02±0.09	-0.52±0.19
	6	0.72±0.44	-0.36±0.29	-0.33±0.28	-0.32±0.23	-0.08±0.16	0.16±0.22	0.02±0.13	-
		*					*		*
B/Rearing Rank	1/1	0.48±0.26	-0.22±0.14	0.36±0.15	0.01±0.11	-0.08±0.11	-0.04±0.10	-0.05±0.07	0.13±0.11
	2/1	-1.52±0.49	0.43±0.20	-0.72±0.23	-0.01±0.17	0.18±0.20	0.06±0.16	0.10±0.13	-0.24±0.19
	2/2	1.04±0.30	-0.21±0.20	0.36±0.18	0.00±0.15	-0.10±0.11	-0.03±0.10	-0.05±0.07	0.11±0.11
		*		*					
Yr Sampled	1978	a	-0.10±0.14	0.32±0.13	0.18±0.11	-0.15±0.09	-0.26±0.11	-0.20±0.07	0.00±0.11
	1979		0.10±0.14	-0.32±0.13	-0.18±0.11	0.15±0.09	0.26±0.11	0.20±0.07	0.00±0.11
				*			*	**	

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		5.02±0.47	5.72±0.13	5.76±0.13	5.73±0.08	5.49±0.11	5.60±0.13	5.52±0.08	5.62±0.11
Age	1	–	0.19±0.14	0.34±0.11	0.26±0.08	0.16±0.90	0.22±0.10	0.20±0.06	0.28±0.08
	2	-0.34±0.84	0.34±0.27	-0.26±0.21	-0.30±0.16	-0.12±0.10	-0.12±0.11	-0.12±0.07	0.00±0.07
	3	-1.13±0.46	-0.03±0.17	-0.25±0.17	-0.12±0.11	0.10±0.10	0.03±0.11	0.08±0.07	-0.26±0.08
	4	0.15±0.45	0.03±0.19	-0.05±0.17	-0.02±0.12	0.09±0.19	-0.14±0.12	-0.02±0.08	0.11±0.09
	5	0.66±0.84	-0.00±0.20	0.17±0.15	0.08±0.12	-0.02±0.11	0.15±0.15	0.04±0.09	-0.13±0.14
	6	0.66±0.84	0.16±0.23	0.05±0.21	0.10±0.15	-0.21±0.16	-0.13±0.21	-0.18±0.12	–
					*			*	**
B/Rearing Rank	1/1	0.32±0.49	-0.04±0.11	-0.07±0.11	-0.04±0.07	0.02±0.10	-0.01±0.09	0.01±0.07	0.03±0.08
	2/1	-0.68±0.94	0.29±0.16	0.19±0.17	0.24±0.11	-0.06±0.18	0.05±0.16	0.00±0.12	0.08±0.14
	2/2	0.35±0.58	-0.29±0.16	-0.12±0.13	-0.20±0.09	0.04±0.11	-0.05±0.09	-0.01±0.07	-0.11±0.09
Yr Sampled	1978	a	-0.17±0.11	0.08±0.10	-0.05±0.07	-0.07±0.08	-0.03±0.10	-0.07±0.06	-0.07±0.08
	1979		0.17±0.11	-0.08±0.10	0.05±0.07	0.07±0.08	0.03±0.10	0.07±0.06	0.07±0.08

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.24: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Soundness Grade (SOU)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		6.87±0.86	6.37±0.41	7.18±0.40	6.73±0.27	5.31±0.27	5.50±0.28	5.37±0.19	6.09±0.37
Age	1	–	-1.18±0.48	-2.32±0.35	-1.84±0.28	-0.64±0.22	-0.24±0.21	-0.46±0.15	-1.08±0.28
	2	-0.04±1.54	-0.08±0.91	0.97±0.65	0.53±0.53	-0.11±0.24	0.37±0.24	0.09±0.17	0.22±0.26
	3	-0.70±0.85	0.48±0.57	-0.07±0.54	0.15±0.38	0.14±0.24	-0.56±0.24	-0.20±0.17	-0.38±0.29
	4	-0.16±0.82	0.71±0.62	-0.15±0.54	0.35±0.39	0.06±0.30	0.16±0.26	0.13±0.20	0.44±0.31
	5	0.96±1.54	0.16±0.63	1.11±0.49	0.70±0.39	-0.09±0.29	0.50±0.33	0.10±0.21	0.80±0.50
	6	-0.04±1.54	-0.08±0.77	0.46±0.66	0.12±0.50	0.64±0.39	-0.23±0.47	0.33±0.30	–
				**	**			**	**
B/Rearing Rank	1/1	0.17±0.90	-0.42±0.37	-0.53±0.35	-0.42±0.24	0.02±0.26	0.01±0.21	0.03±0.16	0.00±0.28
	2/1	0.17±1.73	0.12±0.53	0.62±0.55	0.22±0.36	-0.54±0.47	-0.04±0.34	-0.30±0.28	-0.03±0.50
	2/2	-0.35±1.05	0.30±0.54	-0.08±0.42	0.20±0.32	0.52±0.27	0.03±0.21	0.27±0.17	0.03±0.30
Yr Sampled	1978		0.88±0.36	0.78±0.31	0.76±0.23	0.78±0.21	1.11±0.23	0.90±0.15	1.04±0.28
		a							
	1979		-0.88±0.36	-0.78±0.31	-0.76±0.23	-0.78±0.21	-1.11±0.23	-0.90±0.15	-1.04±0.28
			*	*	**	**	**		**

[1] Effects are not significant unless * indicates level

* P < 0.05

** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.25: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Handle (HND)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		4.93±0.35	5.81±0.17	5.53±0.23	5.66±0.14	5.26±0.13	5.58±0.14	5.32±0.09	5.87±0.20
Age	1	-	0.65±0.20	1.01±0.20	0.86±0.15	0.75±0.10	0.51±0.10	0.66±0.07	0.60±0.15
	2	0.15±0.62	-1.21±0.38	-0.24±0.37	-0.67±0.27	0.17±0.12	-0.08±0.11	-0.11±0.08	0.24±0.14
	3	-0.29±0.34	0.44±0.24	-0.08±0.31	0.18±0.20	0.02±0.11	-0.03±0.12	0.00±0.08	-0.19±0.16
	4	-0.16±0.33	0.19±0.26	-0.16±0.31	-0.01±0.20	0.18±0.14	-0.37±0.13	-0.06±0.09	0.05±0.17
	5	0.15±0.62	0.14±0.26	-0.18±0.28	0.09±0.20	-0.34±0.13	0.06±0.16	-0.21±0.10	-0.22±0.27
	6	0.15±0.62	-0.21±0.32	-0.71±0.38	-0.45±0.26	-0.40±0.19	-0.09±0.22	-0.28±0.14	-
			**	**	**	**	**	**	**
B/Rearing Rank	1/1	-0.07±0.36	0.15±0.15	0.09±0.20	0.15±0.12	0.02±0.12	0.02±0.10	0.03±0.08	0.02±0.15
	2/1	-0.07±0.69	-0.14±0.22	0.21±0.32	0.07±0.18	0.06±0.22	0.10±0.17	0.06±0.14	0.10±0.26
	2/2	0.15±0.42	-0.02±0.22	-0.30±0.24	-0.22±0.16	-0.08±0.13	-0.11±0.10	-0.09±0.08	-0.12±0.16
Yr Sampled	1978	a	-0.25±0.15	-0.08±0.18	-0.13±0.12	-0.40±0.10	-0.15±0.11	-0.35±0.07	-0.20±0.15
	1979		0.25±0.15	0.08±0.18	0.13±0.12	0.40±0.10	0.15±0.11	0.35±0.07	0.20±0.15
						**		**	

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.26: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Greasy Colour (GC_r)[1]

	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean	3.88±0.39	5.81±0.54	5.03±0.29	5.02±0.43	3.97±0.14	4.32±0.18	4.22±0.11	4.03±0.43
Age 1	-	-	-	-	-	-	-	-
2	0.83±0.92	-0.85±0.63	-0.18±0.41	-0.25±0.58	0.11±0.11	-0.39±0.16	-0.14±0.09	0.03±0.19
3	-0.79±0.46	0.22±0.47	0.20±0.35	0.40±0.48	-0.01±0.11	0.08±0.17	0.05±0.10	-0.01±0.21
4	-0.04±0.46	0.52±0.53	0.44±0.38	0.89±0.49	0.00±0.14	0.12±0.17	0.07±0.11	-0.16±0.22
5	-	0.11±0.51	-0.46±0.32	-1.04±1.23	-0.09±0.13	0.19±0.22	0.02±0.12	0.14±0.34
6	-	-	-	-	-	-	-	-
B/Rearing Rank 1/1	0.29±0.52	-0.31±0.57	-0.33±0.32	-0.18±0.29	0.28±0.15	-0.13±0.18	0.00±0.11	0.77±0.39
2/1	-0.71±0.52	-1.31±0.68	0.03±0.50	-0.56±0.38	-0.64±0.26	0.02±0.28	-0.18±0.19	-1.18±0.75
2/2	0.42±0.62	1.63±1.02	0.29±0.46	0.74±0.44	0.37±0.15	0.10±0.17	0.18±0.12	0.41±0.40
Yr Sampled 1978	a	-0.04±0.31	-0.27±0.21	-0.13±0.19	0.19±0.08	-0.17±0.14	0.01±0.08	-0.11±0.20
1979		0.04±0.31	0.27±0.21	0.13±0.19	-0.19±0.08 *	0.17±0.14	-0.01±0.08	0.11±0.20

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.27:   Least squares estimates of the effects of age, birth/rearing rank and year sampled on Greasy Colour (GC_m)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		3.95±0.27	5.76±0.16	5.36±0.21	5.58±0.14	5.01±0.13	5.18±0.15	5.06±0.10	5.37±0.20
Age	1	-	0.78±0.18	0.31±0.18	0.51±0.14	0.51±0.11	-0.02±0.11	0.28±0.08	0.18±0.15
	2	1.50±0.48	-1.09±0.35	0.10±0.33	-0.42±0.27	0.09±0.12	-0.12±0.13	0.01±0.09	-0.10±0.14
	3	-0.54±0.26	0.34±0.21	0.01±0.28	0.16±0.19	-0.19±0.12	0.04±0.13	-0.05±0.09	-0.20±0.16
	4	0.04±0.25	0.40±0.24	0.53±0.27	0.44±0.20	0.12±0.15	-0.09±0.14	0.04±0.10	0.20±0.17
	5	-0.50±0.48	-0.01±0.24	0.16±0.25	0.05±0.20	-0.15±0.14	0.17±0.18	-0.03±0.11	-0.08±0.28
	6	-0.50±0.48	-0.42±0.29	-1.11±0.34	-0.74±0.26	-0.38±0.19	0.02±0.25	-0.25±0.15	-
		*	**	*	**	**		*	
B/Rearing Rank	1/1	0.55±0.28	0.14±0.14	0.25±0.18	0.18±0.12	0.06±0.12	-0.01±0.11	0.01±0.08	0.07±0.16
	2/1	-1.45±0.53	-0.09±0.20	0.13±0.28	0.08±0.18	-0.04±0.23	0.02±0.19	0.01±0.14	-0.10±0.27
	2/2	0.90±0.32	-0.05±0.20	-0.38±0.21	-0.26±0.16	-0.01±0.13	-0.01±0.11	-0.02±0.09	0.03±0.16
		*							
Yr Sampled	1978	a	-0.19±0.14	-0.16±0.16	-0.15±0.12	-0.05±0.10	-0.15±0.12	-0.12±0.08	-0.21±0.15
	1979		0.19±0.14	0.16±0.16	0.15±0.12	0.05±0.10	0.15±0.12	0.12±0.08	0.21±0.15

[1] Effects are not significant unless * indicates level

* P < 0.05
** P < 0.01

a Romneys were only fleece sampled in 1979

TABLE 3.28: Least squares estimates of the effects of age, birth/rearing rank and year sampled on Scoured Colour (SC$_m$)[1]

		R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
Least SQ Mean		4.88±0.30	6.23±0.16	6.16±0.19	6.12±0.12	5.62±0.15	5.69±0.20	5.66±0.11	6.04±0.17
Age	1	-	-0.28±0.18	-0.30±0.16	-0.31±0.12	-0.08±0.12	-0.46±0.15	-0.26±0.09	-0.18±0.12
	2	0.98±0.54	0.09±0.34	-0.20±0.30	-0.10±0.23	0.23±0.14	0.13±0.17	0.19±0.11	0.25±0.12
	3	-0.39±0.29	0.16±0.21	0.07±0.26	0.14±0.17	-0.23±0.14	0.09±0.17	-0.07±0.11	-0.17±0.12
	4	0.46±0.28	0.00±0.24	-0.12±0.25	-0.03±0.17	0.18±0.17	0.07±0.18	0.13±0.12	0.05±0.13
	5	-0.02±0.54	0.29±0.24	0.62±0.23	0.44±0.17	-0.10±0.16	-0.06±0.23	-0.05±0.13	0.05±0.21
	6	-1.02±0.54	-0.25±0.29	-0.07±0.31	-0.14±0.22	-0.01±0.22	0.22±0.35	0.05±0.19	-
		*				*		*	*
B/Rearing Rank	1/1	0.14±0.31	-0.19±0.14	-0.29±0.16	-0.20±0.11	-0.03±0.14	0.22±0.14	-0.14±0.10	0.05±0.13
	2/1	0.14±0.60	0.09±0.20	0.18±0.26	0.12±0.16	0.07±0.26	0.44±0.24	0.30±0.17	0.05±0.24
	2/2	-0.27±0.37	0.11±0.22	0.11±0.20	0.08±0.14	-0.04±0.15	-0.22±0.14	-0.15±0.10	-0.10±0.14
Yr Sampled	1978	a	-0.88±0.13	-0.54±0.15	-0.72±0.10	-0.41±0.11	-0.51±0.16	-0.47±0.09	-0.59±0.12
	1979		0.88±0.13	0.54±0.15	0.72±0.10	0.41±0.11	0.51±0.16	0.47±0.09	0.59±0.12
			**	**	**	**	**	**	**

[1] Effects are not significant unless * indicates level

* $P < 0.05$
** $P < 0.01$

a Romneys were only fleece sampled in 1979

The effect of year sampled was significant ($p < 0.01$) on S/P for the Romney, Superfine Merino and combined (SFM+LM) Merino data and on ln S/P for the SFM and combined Merino data.

The estimate of the effect of year sampled in these groups may be unreliable due to the low numbers of animals sampled in 1978 compared with 1979 (see Table 2.1). The results of the present study may also have been slightly influenced by improved operator skill in histological techniques and follicle identification between 1978 and 1979.

"Age" was significant for S/P ratio in the Romney and LMxR ($p < 0.05$) and in the SFMxR and combined Halfbred data ($p < 0.01$). Log transformation of the S/P data changed the level of significance in the SFM+LM group ($p < 0.05$), and for the SFMxR, LMxR, and (SFMR+LMR) groups ($p < 0.01$).

3.2.2 Total Follicle Density

n(P+S)corr was significantly affected ($p < 0.01$) by "age" in the Superfine Merino x Romney, Local Merino x Romney and Backcross genotypes. This contrasts with uncorrected total follicle density which was significantly affected by "age": SFM+LM ($p < 0.05$) and LM, SFMxR, LMxR, SFMR+LMR and BX ($p < 0.01$).

Neither BRR nor year sampled were statistically significant for corrected total follicle density for any group. Year sampled significantly ($p < 0.05$) affected uncorrected total density in the Romneys. Birth/rearing rank was significant ($p < 0.05$) for this factor in the BX group.

3.2.3 Primary Follicle Density

With the data corrected for skin shrinkage, "age" exerted a significant influence in the SFM ($p < 0.01$), LM ($p < 0.05$), SFM+LM ($p < 0.01$), SFMxR ($p < 0.01$), LMxR ($p < 0.01$) and SFMR+LMR ($p < 0.01$) groups. The pattern was similar for uncorrected primary follicle density with "age" also being significant in the BX animals ($p < 0.01$) and of increased importance in the Local Merinos ($p < 0.01$).

Birth/rearing rank was not significant for (nP)corr in any data set, and for uncorrected primary follicle density it was significant only in the BX class.

The SFM+LM, SFMxR and LMxR data were affected by year sampled (p<0.01); the SFM and LMxR classes were less affected (p<0.05). Year sampled was important for uncorrected primary follicle density in the LMxR (p<0.01) and LM (p<0.05) genotypes only.

Correction for skin shrinkage tended to lower the significance of the fixed effects.

3.2.4 Skin Shrinkage Correction Factor

"Age" exerted a significant effect on skin shrinkage (p<0.01, p<0.05) in all genotypes except the R and SFM groups. There was a slight variation between ages, with skin shrinkage increasing with "age".

3.2.5 Liveweight

Liveweight was significantly affected (p<0.01) by "age" in all genotypes. BRR was significant in the SFMxR and SFMR+LMR groups (p<0.01) and LMxR and BX groups (p<0.05). With the exception of the BX animals YRSAMP was significant in all groups.

3.2.6 Fleeceweight

For GFW and CFW; "age" was significant in the SFMxR, LMxR, SFMR+LMR (p<0.01) and the BX (p<0.05). "Age" also affected GFW (p<0.01) in the Romneys. In most genotypes both GFW and CFW peaked at "age" 3, the LMxR animals having the heaviest fleeces. YRSAMP also influenced GFW in these groups (p<0.01), BX (p<0.05).

3.2.7 Staple Length

"Age" significantly affected both SL_m and SL_r in the LMxR, SFMR+LMR and BX groups (p<0.01) and SL_m in the LM (p<0.05), SFM+LMLM and SFMxR (p<0.01) data sets. Both SL_r and SL_m peaked in the 4 year olds.

3.2.8 Fibre Diameter

As indicated in Table 3.9, MFD generally increased with "age", the differences being significant in data from LM, (SFM+LM) and BX (p<0.05) and SFMxR and (SFMR+LMR) (p<0.01).

Neither birth/rearing rank nor year sampled exerted a statistically significant effect on fibre diameter.

3.2.8 Total Crimp Number

In the crossbreds, TCN increased from "age" 1 to "age" 2, increased in 3 and 4 year olds, and declined again in the oldest animals. "Age" was significant in the crossbred and BX ($p<0.01$) and SFM+LM ($p<0.05$) groups. With the exception of the LM and BX groups, "age" also had a significant effect on CPC.

3.3 Discussion

Across all genotypes, "age" was the most consistently significant fixed effect for all traits. For traits such as primary and total follicle density this would be expected as both body weight and skin area vary with "age". A number of authors, usually using Merinos, (e.g., Brown et al, 1966; Jackson et al, 1975), observed that some follicles cease production with increasing "age".

A similar trend was noted in the present study in the crossbreds in that S/P increased from "age" 1 to "age" 2 and then steadily declined. Increases in both S/P and n(P+S) of 0.4% and 4.3%, between "age" 1 to "age" 2 were reported by Dun and Grewal (1963).

In one study LWT increased until 3 1/2 years and then declined (Brown et al, 1966). In the current results LWT peaked slightly later at 4 years. "Age" affects fleeceweight. Brown et al (1966) noted that GFW and CFW reached maxima at 3 1/2 years and declined thereafter. Lewer et al (1983) reported an earlier peak at 2 years. The current data due to the range of breeds concur with these studies.

Several authors (Dun and Grewal, 1963; Ross, 1965; Brown et al, 1966; Lewer et al, 1983), using various breeds, found "age" to affect MFD significantly. In the study by Brown et al (1966), MFD reached a maximum at 5 1/2 to 6 1/2 years and then declined. In the present project, in some genotypes e.g., R, SFM and LMxR, MFD was greatest at "age" 2. In the remaining groups MFD peaked at either "age" 5 or 6. The changes in MFD reflect changes in the follicle population, with older animals having less active follicles and these producing coarser fibres per follicle.

Lewer et al (1983) and Brown et al (1966) found that 2-year-olds had the longest staples. In the present project, maximum staple length occurred at 4 years which coincided with maximum fleeceweight but not fibre diameter. This suggests that with "age" although some follicles cease production, others compensate by increasing their output.

Crimp frequency has been shown to be affected by age, peaking at 4 1/2 years (Brown et al, 1966). Although "age" influenced both TCN and CPC no consistent pattern was observed in the present study.

The lack of consistent significance of age across genotypes may reflect: 1. the difference in numbers of animals per age class per genotype and 2. true breed differences - the low S/P Romneys being less affected than the high S/P Merinos.

Birth rank and rearing rank reflect nutritional differences in the pre-natal and post-natal periods. These can be considered as maternal effects. BRR had the largest effect in the combined genotype groups. For several genotypes, the least squares mean of both n(P+S)corr and nP(corr) were greater for the 2/1 animals than for either the 1/1 or 2/2 sheep. Generally the 1/1 animals had greater corrected follicle densities than the 2/2 sheep. These results reflect the unbalanced nature of the data for BRR. The data indicate the influence of post-natal nutrition on follicle population maturation. The present results confirm those of Schinckel (1953; 1955b) who found that twins had lower S/P than singles.

Gregory and Ponzoni (1981) found type of birth to be significant in both flocks studied for S/P ($p < 0.01$; $p < 0.001$). Total follicle number, secondary follicle number and primary follicle number were all significantly affected ($p < 0.001$) by birth type in a flock selected on an index. Only secondary follicle number was significantly affected ($p < 0.001$) in a visual selection flock.

The estimates of the effects of BRR are not particularly accurate because of the unbalanced nature of the data (see Table 2.1).

Year of sampling may affect primary and total follicle density as the sheep's condition at the time of sampling will affect these traits. Jackson et al (1975), found that year of measurement was significant ($p < 0.01$) for total follicle density, secondary follicle density and primary follicle density. Year of sampling may also reflect seasonal differences, hence the differences in levels of significance of this effect on LWT, GFW and CFW.

The between-breed/genotype differences in significance of the fixed effects partly reflect the variation in their follicle populations. Those having Merino backgrounds, with much larger follicle numbers (S/P), were more significantly affected by these fixed effects.

CHAPTER 4

GENETIC AND PHENOTYPIC PARAMETERS

4.1 REPEATABILITIES

4.1.1 Method of Analysis

Repeatabilities were estimated using product-moment correlations (Turner and Young, 1969) with data not corrected for fixed effects and ignoring genotypes. The Minitab computer package was used. The data set included 143 records of sheep measured both in 1978 and 1979.

4.1.2 Results

Repeatabilites are given in Table 4.1. The repeatabilities for follicle characterisitcs were generally high and ranged from 0.439^{**} to 0.775^{**}. The repeatabilities of the follicle densities corrected for skin shrinkage were lower. The repeatability of this correction factor was very low (-0.111).

The high repeatabilities of S/P, ln S/P and n(P+S) were expected due to the high heritability estimates and frequent non-significance of fixed effects on these traits (see Tables 3.1 - 3.4).

Both LWT; GFW and CFW were moderately repeatable (0.659^{**}, 0.586^{**}, 0.804^{**} respectively). The repeatabilities for MFD, QN, SL, and TCN were also high, ranging from 0.506^{**} to 0.890^{**}.

Those traits (TIP, COT, SOU, HND, GC and SC) affected by seasonal factors (e.g., weather and climate), had low repeatabilities. The subjective nature of these assessments may also be important in the low repeatabilities.

4.1.3 Discussion

Young et al (1960) obtained repeatabilities of 0.70 for S/P and 0.52 for n(P+S). Jackson et al (1975) reported repeatability estimates of 0.52^{**} and 0.58^{**} for n(P+S) and 0.70^{**} and 0.54^{**} for S/P. With the exception of that for n(P+S)corr, the estimates in the current study are slightly higher.

TABLE 4.1:   Repeatability estimates for fleece and follicle characteristics

Trait	n=	r
S/P	143	0.759**
ln S/P	143	0.775**
n(P+S)	143	0.745**
n(P+S)corr	143	0.584**
nP	143	0.439**
nP(corr)	143	0.113 NS
CF	143	-0.110 NS
LWT	110	0.659**
GFW	133	0.586**
CFW	105	0.804**
YLD	105	0.354**
MFD	103	0.890**
QN_r	119	0.829**
QN_m	106	0.724**
SL_r	119	0.506**
SL_m	106	0.654**
TCN	106	0.705**
CPC	106	0.760**
CHR_r	118	0.537**
CHR_m	106	0.289**
LUS	100	0.476**
TIP	106	0.169 NS
COT	106	0.207*
SOU	106	0.195*
HND	106	0.285**
GC_r	119	0.384**
GC_m	106	0.276**
SC_m	105	0.308**

* P < 0.05
** P < 0.01
NS not significant

Jackson et al (1975) concluded that n(P+S), was subject to more temporary environmental effects than was S/P. This was only moderately suggested from the present results but this may reflect the uncorrected nature of the data.

Using Merinos and Merino derivatives, Young et al (1960) and Mullaney et al (1970) respectively reported repeatability estimates for the following traits of: GFW (0.637; 0.62 - 0.84), CFW (0.588; 0.60 - 0.86), LWT (0.669), SL (0.578; 0.57 - 0.69), and MFD (0.501; 0.66 - 0.68). Using Perendales, Lewer et al (1983) obtained repeatabilities of: 0.62 (GFW), 0.42 to 0.61 (SL), 0.46 to 0.87 (MFD), 0.31 to 0.63 (QN), and 0.08 to 0.32 (CHR). The current results concur with these estimates. Only CFW, QN_r, QN_m and CHR_r had higher repeatabilities. The higher repeatability of CFW vs GFW and YLD may indicate the randomness of fleece contamination between seasons.

The results indicate that follicle traits, with the exception of CF, are moderately repeatable. Skin sampling of hoggets should give an indication of an animal's lifetime follicle parameters.

As LWT and several important fleece characteristics were also moderately repeatable, an accurate indication of an animal's production merit would be provided by only one measurement. The high levels of repeatability, would allow earlier animal selection for these traits and greater genetic gain in a selection programme.

4.2 PHENOTYPIC CORRELATIONS

4.2.1 Method of Analysis

Phenotypic correlations were calculated both within each genotype and ignoring genotype using data sets with one year's data per sheep (Turner and Young, 1969; Becker, 1984). It should be noted that correlations for Total, SFM+LM and SFMR+LMR data sets correlations were calculated on combined data uncorrected for genotype. As genotype variances were often heterogeneous, pooling sums of products and calculating a single correlation may have introduced some bias (Steel and Torrie, 1981). A specially written programme that checked that both items in each data set were non-zero before accumulating into the cross products and numbers was used. The numbers of sheep per genotype and per correlation are shown in Tables 4.2 and 4.3. The significance of each correlation (Ho: $\rho = 0$) is also indicated.

4.2.2 Results

Correlations calculated within and across genotypes using data uncorrected and corrected for the fixed effects - age, year sampled and birth/rearing rank are given in Tables 4.2 - 4.3. The correlations from the total data set are associated with both between and within "breed" components.

The discussion of results will concentrate on those obtained using data corrected for fixed effects. Variations in the numbers of records explains many of the changes in level of significance between data sets.

4.2.2.1 S/P

The correlation between total density and S/P ranged from 0.63 to 0.85 across genotypes (p<0.01). This indicates the importance of the number of secondaries in determining total density. The correlation between n(P+S)corr and S/P, although positive and significant (p<0.01), was not as high as that for uncorrected total density. The relationship was better within genotype than across genotypes.

TABLE 4.2: PHENOTYPIC CORRELATIONS FOR FLEECE AND FOLLICLE TRAITS USING DATA CORRECTED FOR AGE, YEAR SAMPLED AND BIRTH/REARING RANK

TRAIT   GENOTYPE

S/P	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
ln S/P	0.96^{**}	0.95^{**}	0.97^{**}	0.98^{**}	0.97^{**}	0.98^{**}	0.98^{**}	0.98^{**}	0.98^{**}
n(P+S)	0.85^{**}	0.72^{**}	0.67^{**}	0.69^{**}	0.64^{**}	0.67^{**}	0.63^{**}	0.65^{**}	0.69^{**}
n(P+S)corr	0.29^{**}	0.52^{**}	0.59^{**}	0.57^{**}	0.55^{**}	0.44^{**}	0.49^{**}	0.45^{**}	0.54^{**}
nP	-0.28^{**}	-0.20^{NS}	-0.35^{*}	-0.21^{NS}	-0.26^{*}	-0.27^{**}	-0.35^{**}	-0.30^{**}	-0.16^{NS}
nP(corr)	0.04^{NS}	-0.27^{NS}	-0.17^{NS}	-0.04^{NS}	-0.09^{NS}	-0.32^{**}	-0.23^{**}	-0.26^{**}	-0.11^{NS}
CF	0.25^{**}	-0.10^{NS}	0.16^{NS}	0.10^{NS}	0.12^{NS}	-0.14^{NS}	0.00^{NS}	-0.06^{NS}	-0.02^{NS}
LWT	-0.45^{**}	0.21^{NS}	-0.24^{NS}	-0.10^{NS}	-0.16^{NS}	-0.05^{NS}	-0.07^{NS}	-0.08^{NS}	0.01^{NS}
GFW	-0.20^{**}	0.33^{*}	-0.13^{NS}	0.04^{NS}	-0.08^{NS}	-0.01^{NS}	0.08^{NS}	-0.00^{NS}	0.07^{NS}
CFW	-0.27^{**}	0.00^{NS}	-0.09^{NS}	0.02^{NS}	-0.09^{NS}	0.01^{NS}	0.13^{NS}	0.04^{NS}	0.09^{NS}
YLD	-0.09^{NS}	0.06^{NS}	0.06^{NS}	0.20^{NS}	0.12^{NS}	0.06^{NS}	0.14^{NS}	0.09^{NS}	0.04^{NS}
MFD	-0.69^{**}	-0.31^{NS}	-0.23^{NS}	-0.27^{NS}	-0.22^{*}	-0.43^{**}	-0.33^{**}	-0.36^{**}	-0.35^{**}
QN_r	0.66^{**}	0.50^{*}	-0.48^{*}	-0.28^{NS}	-0.11^{NS}	0.17^{NS}	0.11^{NS}	0.16^{*}	0.16^{NS}
QN_m	0.62^{**}	0.12^{NS}	0.18^{NS}	-0.06^{NS}	0.04^{NS}	0.29^{**}	0.03^{NS}	0.18^{**}	0.23^{*}
SL_r	-0.46^{**}	-0.41^{NS}	0.06^{NS}	-0.13^{NS}	-0.09^{NS}	-0.04^{NS}	-0.14^{NS}	-0.11^{NS}	0.05^{NS}
SL_m	-0.51^{**}	-0.46^{*}	-0.13^{NS}	-0.17^{NS}	-0.13^{NS}	-0.12^{NS}	-0.20^{*}	-0.17^{**}	0.00^{NS}
TCN	0.51^{**}	0.06^{NS}	0.19^{NS}	0.19^{NS}	0.16^{NS}	0.15^{NS}	0.05^{NS}	0.13^{*}	0.15^{NS}
CPC	0.60^{**}	0.25^{NS}	0.23^{NS}	0.29^{NS}	0.19^{NS}	0.16^{NS}	0.14^{NS}	0.16^{**}	0.12^{NS}
CHR_r	0.35^{**}	0.17^{NS}	0.15^{NS}	0.06^{NS}	0.12^{NS}	0.21^{*}	0.15^{NS}	0.16^{*}	0.23^{*}
CHR_m	0.26^{**}	0.12^{NS}	0.14^{NS}	-0.34^{*}	-0.14^{NS}	0.08^{NS}	0.08^{NS}	0.07^{NS}	0.11^{NS}
LUS	-0.50^{**}	-0.26^{NS}	0.05^{NS}	-0.04^{NS}	0.01^{NS}	-0.05^{NS}	0.06^{NS}	-0.01^{NS}	-0.14^{NS}
TIP	0.06^{NS}	0.09^{NS}	0.22^{NS}	-0.28^{NS}	-0.05^{NS}	-0.11^{NS}	0.10^{NS}	0.00^{NS}	-0.05^{NS}
COT	0.19^{**}	0.42^{NS}	0.13^{NS}	-0.14^{NS}	0.00^{NS}	0.11^{NS}	0.10^{NS}	0.11^{NS}	0.10^{NS}
SOU	0.06^{NS}	-0.07^{NS}	-0.03^{NS}	0.02^{NS}	-0.01^{NS}	0.01^{NS}	-0.05^{NS}	-0.01^{NS}	0.07^{NS}
HND	0.29^{**}	0.33^{NS}	0.23^{NS}	-0.16^{NS}	0.02^{NS}	0.14^{NS}	0.16^{NS}	0.14^{**}	0.10^{NS}
GC_r	0.28^{**}	0.14^{NS}	0.25^{NS}	-0.03^{NS}	0.20^{NS}	0.01^{NS}	-0.01^{NS}	-0.01^{NS}	-0.03^{NS}
GC_m	0.37^{**}	0.12^{NS}	0.09^{NS}	0.11^{NS}	0.09^{NS}	0.14^{NS}	0.15^{NS}	0.14^{*}	0.02^{NS}
SC_m	0.35^{**}	-0.06^{NS}	0.32^{NS}	-0.05^{NS}	0.12^{NS}	0.04^{NS}	0.12^{NS}	0.08^{NS}	-0.05^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

$*$ $p<0.05$

$**$ $p<0.01$

NS not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

In S/P	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
n(P+S)	0.83^{**}	0.61^{**}	0.68^{**}	0.67^{**}	0.63^{**}	0.63^{**}	0.63^{**}	0.63^{**}	0.69^{**}
n(P+S)corr	0.22^{**}	0.47^{**}	0.58^{**}	0.56^{**}	0.53^{**}	0.44^{**}	0.48^{**}	0.43^{**}	0.55^{**}
nP	-0.29^{**}	-0.26^{NS}	-0.33^{*}	-0.21^{NS}	-0.24^{*}	-0.31^{**}	-0.36^{**}	-0.32^{**}	-0.12^{NS}
nP(corr)	0.04^{NS}	-0.25^{NS}	-0.16^{NS}	-0.03^{NS}	-0.08^{NS}	-0.31^{**}	-0.24^{**}	-0.27^{**}	-0.07^{NS}
CF	0.27^{**}	-0.04^{NS}	0.13^{NS}	0.12^{NS}	0.12^{NS}	-0.11^{NS}	-0.02^{NS}	-0.06^{NS}	0.00^{NS}
LWT	-0.42^{**}	0.18^{NS}	-0.26^{NS}	-0.19^{NS}	-0.19^{NS}	-0.04^{NS}	-0.09^{NS}	-0.10^{NS}	0.02^{NS}
GFW	-0.17^{**}	0.25^{NS}	0.08^{NS}	0.04^{NS}	-0.04^{NS}	0.00^{NS}	0.09^{NS}	0.00^{NS}	0.08^{NS}
CFW	-0.27^{**}	0.00^{NS}	-0.03^{NS}	0.02^{NS}	-0.05^{NS}	0.03^{NS}	0.16^{NS}	0.05^{NS}	0.10^{NS}
YLD	-0.11^{*}	0.03^{NS}	0.03^{NS}	0.17^{NS}	0.10^{NS}	0.07^{NS}	0.16^{NS}	0.10^{NS}	0.06^{NS}
MFD	-0.75^{**}	-0.39^{NS}	-0.17^{NS}	-0.33^{*}	-0.20^{NS}	-0.42^{**}	-0.33^{**}	-0.37^{**}	-0.34^{**}
QN_r	0.67^{**}	0.52^{*}	-0.48^{*}	-0.27^{NS}	-0.14^{NS}	0.20^{*}	0.16^{NS}	0.19^{**}	0.14^{NS}
QN_m	0.65^{**}	0.09^{NS}	0.24^{NS}	-0.06^{NS}	0.07^{NS}	0.28^{**}	0.07^{NS}	0.20^{**}	0.23^{**}
SL_r	-0.52^{**}	-0.46^{NS}	0.13^{NS}	-0.12^{NS}	-0.02^{NS}	-0.06^{NS}	-0.18^{NS}	-0.14^{*}	0.07^{NS}
SL_m	-0.57^{**}	-0.48^{*}	-0.09^{NS}	-0.15^{NS}	-0.09^{NS}	-0.10^{NS}	-0.23^{**}	-0.19^{**}	0.00^{NS}
TCN	0.55^{**}	0.11^{NS}	0.22^{NS}	0.23^{NS}	0.18^{NS}	0.13^{NS}	0.07^{NS}	0.13^{*}	0.17^{NS}
CPC	0.61^{**}	0.26^{NS}	0.25^{NS}	0.30^{NS}	0.19^{NS}	0.14^{NS}	0.17^{*}	0.17^{**}	0.13^{NS}
CHR_r	0.34^{**}	0.21^{NS}	0.11^{NS}	0.07^{NS}	0.09^{NS}	0.22^{**}	0.17^{NS}	0.16^{*}	0.25^{*}
CHR_m	0.31^{**}	0.09^{NS}	0.13^{NS}	-0.28^{NS}	-0.09^{NS}	0.06^{NS}	0.10^{NS}	0.07^{NS}	0.14^{NS}
LUS	-0.54^{**}	-0.27^{NS}	0.08^{NS}	0.00^{NS}	0.05^{NS}	-0.04^{NS}	0.03^{NS}	-0.02^{NS}	-0.17^{NS}
TIP	0.14^{**}	0.02^{NS}	0.22^{NS}	-0.27^{NS}	-0.03^{NS}	-0.11^{NS}	0.13^{NS}	0.01^{NS}	-0.05^{NS}
COT	0.24^{**}	0.47^{*}	0.16^{NS}	-0.13^{NS}	0.02^{NS}	0.09^{NS}	0.13^{NS}	0.11^{NS}	0.09^{NS}
SOU	0.03^{NS}	-0.02^{NS}	0.02^{NS}	0.05^{NS}	0.04^{NS}	0.04^{NS}	-0.03^{NS}	0.01^{NS}	0.07^{NS}
HND	0.33^{**}	0.44^{*}	0.25^{NS}	-0.13^{NS}	0.05^{NS}	0.12^{NS}	0.17^{NS}	0.14^{*}	0.11^{NS}
GC_r	0.27^{**}	0.15^{NS}	0.18^{NS}	-0.01^{NS}	0.15^{NS}	0.00^{NS}	-0.02^{NS}	-0.02^{NS}	-0.01^{NS}
GC_m	0.38^{**}	0.09^{NS}	0.06^{NS}	0.12^{NS}	0.07^{NS}	0.12^{NS}	0.15^{NS}	0.13^{*}	0.03^{NS}
SC_m	0.38^{**}	0.00^{NS}	0.29^{NS}	0.03^{NS}	0.15^{NS}	0.03^{NS}	0.10^{NS}	0.07^{NS}	-0.03^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

* p<0.05
** p<0.01
NS not significant

TABLE 4.2: (continued)

TRAIT	GENOTYPE

n(P+S)	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
n(P+S)corr	0.41**	0.74**	0.69**	0.63**	0.53**	0.64**	0.72**	0.62**	0.69**
nP	0.22**	0.46**	0.44**	0.52**	0.55**	0.51**	0.43**	0.49**	0.59**
nP(corr)	0.30**	0.14NS	0.31NS	0.24NS	0.33**	0.16NS	0.24**	0.20**	0.32**
CF	0.17**	-0.16NS	-0.03NS	-0.04NS	-0.07NS	-0.21**	-0.01NS	-0.11NS	-0.14NS
LWT	-0.48**	0.15NS	-0.43*	-0.15NS	-0.06NS	-0.22**	-0.17*	-0.25**	-0.13NS
GFW	-0.23**	0.37**	-0.27NS	-0.15NS	0.00NS	-0.11NS	0.00NS	-0.13*	0.00NS
CFW	-0.30**	-0.17NS	-0.21NS	-0.19NS	0.02NS	-0.08NS	0.07NS	-0.09NS	0.02NS
YLD	-0.07NS	-0.06NS	0.14NS	0.13NS	0.18NS	0.09NS	0.16NS	0.09NS	0.03NS
MFD	-0.69**	-0.27NS	-0.42*	-0.42**	-0.17NS	-0.48**	-0.41**	-0.48**	-0.47**
ON_r	0.60**	0.53*	-0.26NS	-0.47*	-0.34*	0.16NS	0.23*	0.21**	0.20*
QN_m	0.57**	0.47*	0.17NS	0.20NS	-0.08NS	0.22*	0.12NS	0.23**	0.11NS
SL_r	-0.41**	-0.40NS	0.15NS	0.22NS	0.24NS	0.00NS	-0.14NS	-0.11NS	0.08NS
SL_m	-0.43**	-0.39NS	-0.03NS	0.10NS	0.20NS	-0.04NS	-0.04NS	-0.10NS	0.07NS
TCN	0.46**	0.33NS	0.02NS	0.08NS	-0.15NS	0.19*	0.18*	0.23**	0.05NS
CPC	0.51**	0.49*	0.06NS	0.03NS	-0.19NS	0.16NS	0.14NS	0.21**	-0.01NS
CHR_r	0.36**	0.48NS	0.22NS	0.23NS	0.22NS	0.26**	0.23*	0.20**	0.27**
CHR_m	0.26**	0.19NS	0.17NS	-0.14NS	-0.07NS	0.20**	0.04NS	0.11*	0.11NS
LUS	-0.44**	-0.19NS	0.01NS	-0.16NS	0.13NS	0.02NS	0.02NS	-0.02NS	-0.10NS
TIP	0.00NS	0.24NS	0.00NS	-0.28NS	-0.26*	-0.17*	-0.01NS	-0.09NS	-0.03NS
COT	0.17**	0.64**	0.06NS	-0.03NS	-0.03NS	0.11NS	0.08NS	0.09NS	0.03NS
SOU	0.04NS	-0.05NS	-0.09NS	-0.18NS	0.11NS	-0.02NS	-0.09NS	-0.04NS	0.06NS
HND	0.30**	0.36NS	0.32NS	0.04NS	0.04NS	0.20*	0.19NS	0.19**	0.12NS
GC_r	0.26**	0.02NS	0.36NS	-0.28NS	0.08NS	0.11NS	0.08NS	0.08NS	-0.03NS
GC_m	0.31**	-0.10NS	0.05NS	0.17NS	-0.04NS	0.13NS	0.11NS	0.11NS	-0.01NS
SC_m	0.32**	-0.04NS	0.07NS	-0.05NS	-0.08NS	0.07NS	0.18*	0.13*	-0.06NS
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

*   p<0.05
** p<0.01
NS not significant

TABLE 4.2: (continued)

| TRAIT | GENOTYPE | | | | | | | | |

n(P+S)corr	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
nP	0.24^{**}	0.37^{*}	0.09^{NS}	0.16^{NS}	0.03^{NS}	0.32^{**}	0.27^{**}	0.27^{**}	0.36^{**}
nP(corr)	0.62^{**}	0.63^{**}	0.68^{**}	0.78^{**}	0.65^{**}	0.69^{**}	0.69^{**}	0.67^{**}	0.76^{**}
CF	0.48^{**}	0.49^{**}	0.67^{**}	0.71^{**}	0.70^{**}	0.56^{**}	0.64^{**}	0.58^{**}	0.57^{**}
LWT	-0.14^{**}	-0.06^{NS}	-0.28^{NS}	-0.02^{NS}	-0.22^{NS}	-0.18^{*}	-0.15^{NS}	-0.09^{NS}	-0.13^{NS}
GFW	-0.01^{NS}	0.11^{NS}	-0.06^{NS}	-0.03^{NS}	-0.15^{NS}	-0.02^{NS}	0.06^{NS}	0.10^{NS}	0.07^{NS}
CFW	0.00^{NS}	-0.21^{NS}	-0.01^{NS}	-0.09^{NS}	-0.16^{NS}	-0.02^{NS}	0.05^{NS}	0.09^{NS}	0.08^{NS}
YLD	0.02^{NS}	-0.19^{NS}	0.07^{NS}	-0.05^{NS}	-0.04^{NS}	0.05^{NS}	0.03^{NS}	0.06^{NS}	0.03^{NS}
MFD	-0.14^{**}	-0.37^{NS}	-0.13^{NS}	-0.21^{NS}	-0.25^{*}	-0.39^{**}	-0.34^{**}	-0.23^{**}	-0.38^{**}
QN_r	0.11^{NS}	0.31^{NS}	-0.18^{NS}	-0.39^{NS}	-0.08^{NS}	0.09^{NS}	0.23^{*}	0.10^{NS}	0.25^{*}
QN_m	0.13^{**}	0.41^{NS}	0.09^{NS}	0.14^{NS}	0.21^{NS}	0.24^{**}	0.09^{NS}	0.10^{NS}	0.19^{*}
SL_r	-0.03^{NS}	-0.48^{NS}	-0.03^{NS}	-0.03^{NS}	-0.06^{NS}	-0.11^{NS}	-0.12^{NS}	-0.02^{NS}	-0.03^{NS}
SL_m	-0.03^{NS}	-0.64^{**}	-0.21^{NS}	0.03^{NS}	-0.14^{NS}	-0.03^{NS}	-0.11^{NS}	-0.01^{NS}	-0.03^{NS}
TCN	0.06^{NS}	0.43^{NS}	-0.23^{NS}	0.15^{NS}	0.09^{NS}	0.14^{NS}	0.16^{NS}	0.07^{NS}	0.06^{NS}
CPC	0.08^{NS}	0.66^{**}	-0.12^{NS}	0.14^{NS}	0.14^{NS}	0.11^{NS}	0.17^{*}	0.05^{NS}	0.06^{NS}
CHR_r	0.19^{**}	0.40^{NS}	-0.02^{NS}	0.40^{NS}	0.14^{NS}	0.13^{NS}	0.14^{NS}	0.19^{**}	0.21^{*}
CHR_m	0.05^{NS}	0.36^{NS}	0.02^{NS}	-0.04^{NS}	0.00^{NS}	0.12^{NS}	0.06^{NS}	0.11^{NS}	0.12^{NS}
LUS	-0.07^{NS}	-0.42^{NS}	-0.37^{*}	-0.13^{NS}	-0.29^{**}	-0.08^{NS}	0.02^{NS}	0.01^{NS}	-0.07^{NS}
TIP	-0.07^{NS}	0.43^{NS}	0.09^{NS}	-0.08^{NS}	0.05^{NS}	-0.04^{NS}	-0.02^{NS}	-0.03^{NS}	-0.05^{NS}
COT	0.02^{NS}	0.61^{*}	0.08^{NS}	-0.23^{NS}	-0.07^{NS}	0.04^{NS}	0.03^{NS}	0.04^{NS}	0.06^{NS}
SOU	0.09^{NS}	0.06^{NS}	-0.08^{NS}	0.07^{NS}	-0.01^{NS}	-0.03^{NS}	0.00^{NS}	-0.03^{NS}	0.17^{NS}
HND	0.08^{NS}	0.37^{NS}	0.27^{NS}	-0.06^{NS}	0.12^{NS}	0.16^{*}	0.20^{*}	0.18^{*}	-0.02^{NS}
GC_r	0.00^{NS}	0.07^{NS}	0.21^{NS}	-0.17^{NS}	0.09^{NS}	0.07^{NS}	-0.04^{NS}	0.04^{NS}	-0.15^{NS}
GC_m	0.06^{NS}	-0.10^{NS}	0.22^{NS}	0.12^{NS}	0.23^{*}	0.13^{NS}	0.09^{NS}	0.12^{*}	-0.11^{NS}
SC_m	0.00^{NS}	-0.29^{NS}	0.05^{NS}	-0.03^{NS}	0.05^{NS}	0.02^{NS}	-0.00^{NS}	0.00^{NS}	-0.03^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

*   p<0.05
** p<0.01
NS not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

nP	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
nP(corr)	0.53^{**}	0.62^{*}	0.51^{**}	0.35^{*}	0.48^{**}	0.59^{**}	0.60^{**}	0.59^{**}	0.59^{**}
CF	-0.14^{**}	-0.03^{NS}	-0.32^{NS}	-0.21^{NS}	-0.27^{*}	-0.11^{NS}	0.00^{NS}	-0.05^{NS}	-0.14^{NS}
LWT	-0.08^{NS}	-0.19^{NS}	-0.24^{NS}	-0.20^{NS}	0.01^{NS}	-0.28^{*}	-0.11^{NS}	-0.22^{**}	-0.18^{NS}
GFW	-0.07^{NS}	-0.15^{NS}	-0.20^{NS}	-0.25^{NS}	0.05^{NS}	-0.12^{NS}	-0.09^{NS}	-0.13^{*}	-0.08^{NS}
CFW	-0.06^{NS}	-0.21^{NS}	-0.17^{NS}	-0.27^{NS}	0.08^{NS}	-0.12^{NS}	-0.08^{NS}	-0.14^{*}	-0.07^{NS}
YLD	0.05^{NS}	-0.08^{NS}	0.09^{NS}	0.03^{NS}	0.12^{NS}	0.05^{NS}	0.02^{NS}	0.02^{NS}	0.00^{NS}
MFD	0.01^{NS}	-0.01^{NS}	-0.27^{NS}	-0.22^{NS}	0.00^{NS}	-0.14^{NS}	-0.14^{NS}	-0.18^{*}	-0.26^{**}
ON_r	-0.14^{*}	0.21^{NS}	0.19^{NS}	-0.38^{NS}	-0.36^{**}	-0.02^{NS}	0.05^{NS}	0.02^{NS}	0.09^{NS}
ON_m	-0.10^{*}	0.42^{NS}	0.00^{NS}	0.18^{NS}	-0.18^{NS}	-0.04^{NS}	0.03^{NS}	0.03^{NS}	-0.08^{NS}
SL_r	0.13^{*}	0.08^{NS}	0.13^{NS}	0.53^{*}	0.43^{**}	0.06^{NS}	0.04^{NS}	0.04^{NS}	0.04^{NS}
SL_m	0.18^{**}	0.03^{NS}	0.14^{NS}	0.31^{NS}	0.36^{**}	0.13^{NS}	0.23^{**}	0.13^{*}	0.07^{NS}
TCN	-0.06^{NS}	0.26^{NS}	-0.16^{NS}	-0.05^{NS}	-0.29^{**}	0.09^{NS}	0.15^{NS}	0.14^{*}	-0.08^{NS}
CPC	-0.14^{**}	0.19^{NS}	-0.17^{NS}	-0.20^{NS}	-0.38^{**}	0.02^{NS}	-0.02^{NS}	0.04^{NS}	-0.13^{NS}
CHR_r	0.02^{NS}	0.47^{NS}	0.15^{NS}	0.25^{NS}	0.17^{NS}	0.05^{NS}	0.06^{NS}	0.05^{NS}	0.11^{NS}
CHR_m	0.00^{NS}	0.06^{NS}	0.05^{NS}	0.15^{NS}	0.04^{NS}	0.19^{*}	-0.05^{NS}	0.08^{NS}	0.04^{NS}
LUS	0.12^{**}	0.03^{NS}	0.03^{NS}	-0.11^{NS}	0.19^{NS}	0.06^{NS}	0.03^{NS}	0.02^{NS}	0.00^{NS}
TIP	-0.11^{*}	0.14^{NS}	-0.25^{NS}	-0.01^{NS}	-0.24^{*}	-0.06^{NS}	-0.20^{*}	-0.12^{*}	-0.01^{NS}
COT	-0.03^{NS}	0.27^{NS}	-0.08^{NS}	0.11^{NS}	-0.03^{NS}	0.01^{NS}	-0.01^{NS}	-0.00^{NS}	-0.08^{NS}
SOU	-0.02^{NS}	0.01^{NS}	-0.06^{NS}	-0.13^{NS}	-0.05^{NS}	-0.05^{NS}	0.00^{NS}	-0.02^{NS}	0.01^{NS}
HND	0.03^{NS}	0.13^{NS}	0.15^{NS}	0.16^{NS}	0.03^{NS}	0.14^{NS}	0.04^{NS}	0.09^{NS}	0.05^{NS}
GC_r	-0.02^{NS}	-0.03^{NS}	0.26^{NS}	-0.47^{*}	-0.12^{NS}	0.12^{NS}	0.09^{NS}	0.10^{NS}	0.00^{NS}
GC_m	-0.10^{*}	-0.17^{NS}	-0.08^{NS}	0.12^{NS}	-0.15^{NS}	0.04^{NS}	-0.05^{NS}	-0.01^{NS}	-0.04^{NS}
SC_m	-0.04^{NS}	0.00^{NS}	-0.27^{NS}	-0.04^{NS}	-0.23^{*}	0.04^{NS}	0.08^{NS}	0.07^{NS}	-0.03^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

*   p<0.05
** p<0.01
NS not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

nP(corr)	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CF	0.71^{**}	0.72^{**}	0.63^{**}	0.81^{**}	0.70^{**}	0.68^{**}	0.74^{**}	0.71^{**}	0.68^{**}
LWT	-0.24^{**}	-0.35^{*}	-0.15^{NS}	0.00^{NS}	0.05^{NS}	-0.16^{*}	-0.12^{NS}	-0.15^{**}	-0.17^{NS}
GFW	-0.09^{*}	-0.33^{*}	0.01^{NS}	-0.06^{NS}	0.12^{NS}	0.00^{NS}	0.03^{NS}	-0.04^{NS}	0.01^{NS}
CFW	-0.12^{**}	-0.27^{NS}	0.04^{NS}	-0.09^{NS}	0.14^{NS}	-0.04^{NS}	-0.08^{NS}	-0.09^{NS}	0.02^{NS}
YLD	-0.08^{NS}	-0.25^{NS}	0.05^{NS}	-0.18^{NS}	-0.04^{NS}	-0.01^{NS}	-0.10^{NS}	-0.06^{NS}	0.01^{NS}
MFD	-0.21^{**}	-0.29^{NS}	0.01^{NS}	-0.03^{NS}	0.11^{NS}	-0.07^{NS}	-0.15^{NS}	-0.13^{*}	-0.19^{*}
QN_r	0.14^{*}	0.03^{NS}	0.15^{NS}	-0.22^{NS}	-0.44^{**}	-0.04^{NS}	0.14^{NS}	0.06^{NS}	0.18^{NS}
QN_m	0.17^{**}	0.47^{*}	-0.05^{NS}	0.18^{NS}	-0.10^{NS}	0.02^{NS}	0.04^{NS}	0.05^{NS}	0.06^{NS}
SL_r	-0.16^{**}	-0.07^{NS}	-0.09^{NS}	0.07^{NS}	0.24^{NS}	-0.07^{NS}	-0.02^{NS}	-0.05^{NS}	-0.10^{NS}
SL_m	-0.11^{*}	-0.43^{NS}	-0.13^{NS}	0.18^{NS}	0.17^{NS}	0.07^{NS}	0.04^{NS}	0.02^{NS}	0.06^{NS}
TCN	0.13^{**}	0.52^{*}	-0.43^{**}	0.05^{NS}	-0.28^{**}	0.05^{NS}	0.16^{NS}	0.11^{NS}	-0.02^{NS}
CPC	0.11^{*}	0.55^{*}	-0.34^{*}	-0.05^{NS}	-0.30^{**}	0.00^{NS}	0.09^{NS}	0.06^{NS}	0.01^{NS}
CHR_r	0.07^{NS}	0.40^{NS}	-0.16^{NS}	0.53^{*}	0.09^{NS}	-0.03^{NS}	0.00^{NS}	-0.02^{NS}	0.10^{NS}
CHR_m	0.10^{*}	0.34^{NS}	-0.11^{NS}	0.20^{NS}	0.06^{NS}	0.08^{NS}	-0.02^{NS}	0.03^{NS}	0.06^{NS}
LUS	-0.14^{**}	-0.33^{NS}	-0.45^{**}	-0.08^{NS}	-0.05^{NS}	-0.06^{NS}	0.01^{NS}	-0.04^{NS}	0.01^{NS}
TIP	0.02^{NS}	0.48^{*}	-0.10^{NS}	0.11^{NS}	-0.06^{NS}	0.05^{NS}	-0.14^{NS}	-0.04^{NS}	0.00^{NS}
COT	0.02^{NS}	0.42^{NS}	-0.03^{NS}	-0.19^{NS}	-0.14^{NS}	-0.04^{NS}	-0.04^{NS}	-0.04^{NS}	-0.03^{NS}
SOU	0.04^{NS}	0.15^{NS}	-0.07^{NS}	0.12^{NS}	0.06^{NS}	-0.06^{NS}	0.06^{NS}	0.00^{NS}	0.12^{NS}
HND	0.09^{*}	0.29^{NS}	0.20^{NS}	0.03^{NS}	0.01^{NS}	0.09^{NS}	0.10^{NS}	0.09^{NS}	-0.09^{NS}
GC_r	0.01^{NS}	0.14^{NS}	0.10^{NS}	-0.15^{NS}	-0.15^{NS}	0.08^{NS}	-0.06^{NS}	0.00^{NS}	-0.11^{NS}
GC_m	0.03^{NS}	-0.13^{NS}	0.18^{NS}	0.07^{NS}	0.00^{NS}	0.04^{NS}	-0.03^{NS}	0.00^{NS}	-0.13^{NS}
SC_m	0.04^{NS}	-0.24^{NS}	-0.21^{NS}	0.01^{NS}	-0.13^{NS}	0.00^{NS}	-0.10^{NS}	-0.05^{NS}	0.01^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

* $p<0.05$
** $p<0.01$
NS   not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

CF	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
LWT	-0.19^{**}	-0.20^{NS}	0.11^{NS}	0.03^{NS}	0.01^{NS}	0.06^{NS}	-0.04^{NS}	0.00^{NS}	-0.08^{NS}
GFW	-0.06^{NS}	-0.24^{NS}	0.21^{NS}	0.06^{NS}	0.06^{NS}	0.10^{NS}	0.03^{NS}	0.04^{NS}	0.07^{NS}
CFW	-0.11^{*}	-0.10^{NS}	0.23^{NS}	0.07^{NS}	0.07^{NS}	0.04^{NS}	-0.05^{NS}	-0.03^{NS}	0.09^{NS}
YLD	-0.13^{**}	0.23^{NS}	-0.03^{NS}	-0.17^{NS}	-0.13^{NS}	-0.06^{NS}	-0.12^{NS}	-0.09^{NS}	0.05^{NS}
MFD	-0.26^{**}	-0.42^{NS}	0.24^{NS}	0.16^{NS}	0.12^{NS}	0.04^{NS}	-0.11^{NS}	-0.05^{NS}	0.01^{NS}
ON_r	0.28^{**}	-0.12^{NS}	-0.01^{NS}	-0.06^{NS}	-0.30^{NS}	-0.10^{NS}	0.09^{NS}	0.02^{NS}	0.11^{NS}
ON_m	0.28^{**}	0.28^{NS}	-0.03^{NS}	0.06^{NS}	0.06^{NS}	0.04^{NS}	0.05^{NS}	0.05^{NS}	0.16^{NS}
SL_r	-0.29^{**}	-0.15^{NS}	-0.26^{NS}	-0.32^{NS}	-0.08^{NS}	-0.12^{NS}	0.02^{NS}	-0.07^{NS}	-0.09^{NS}
SL_m	-0.27^{**}	-0.53^{*}	-0.28^{NS}	0.06^{NS}	-0.09^{NS}	-0.03^{NS}	-0.08^{NS}	-0.07^{NS}	-0.11^{NS}
TCN	0.20^{**}	0.43^{NS}	-0.36^{*}	0.05^{NS}	-0.07^{NS}	-0.04^{NS}	0.06^{NS}	0.01^{NS}	0.07^{NS}
CPC	0.24^{**}	0.50^{*}	-0.24^{NS}	0.03^{NS}	-0.02^{NS}	-0.03^{NS}	0.09^{NS}	0.03^{NS}	0.13^{NS}
CHR_r	0.07^{NS}	0.21^{NS}	-0.38^{NS}	0.37^{NS}	-0.09^{NS}	-0.10^{NS}	-0.03^{NS}	-0.08^{NS}	0.07^{NS}
CHR_m	0.12^{**}	0.44^{*}	-0.19^{NS}	0.10^{NS}	0.02^{NS}	-0.08^{NS}	-0.02^{NS}	-0.06^{NS}	0.07^{NS}
LUS	-0.26^{**}	-0.37^{NS}	-0.48^{**}	-0.01^{NS}	-0.21^{NS}	-0.09^{NS}	-0.03^{NS}	0.07^{NS}	0.01^{NS}
TIP	-0.13^{**}	0.59^{**}	0.14^{NS}	0.10^{NS}	0.13^{NS}	0.09^{NS}	-0.03^{NS}	0.03^{NS}	-0.02^{NS}
COT	0.05^{NS}	0.31^{NS}	0.05^{NS}	-0.25^{NS}	-0.11^{NS}	-0.06^{NS}	-0.09^{NS}	-0.08^{NS}	0.06^{NS}
SOU	0.07^{NS}	0.26^{NS}	0.01^{NS}	0.26^{NS}	0.16^{NS}	-0.02^{NS}	0.09^{NS}	0.03^{NS}	0.14^{NS}
HND	0.09^{*}	0.31^{NS}	0.11^{NS}	-0.07^{NS}	0.02^{NS}	-0.02^{NS}	0.06^{NS}	0.02^{NS}	-0.14^{NS}
GC_r	0.05^{NS}	0.30^{NS}	-0.09^{NS}	0.15^{NS}	-0.11^{NS}	-0.01^{NS}	-0.12^{NS}	-0.09^{NS}	-0.10^{NS}
GC_m	0.11^{*}	0.01^{NS}	0.21^{NS}	0.03^{NS}	0.12^{NS}	0.03^{NS}	-0.03^{NS}	0.00^{NS}	-0.10^{NS}
SC_m	0.06^{NS}	-0.22^{NS}	0.01^{NS}	0.03^{NS}	0.04^{NS}	-0.06^{NS}	-0.23^{**}	-0.15^{*}	0.07^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

* $p<0.05$
** $p<0.01$
NS   not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

LWT	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
GFW	0.55^{**}	0.33^{*}	0.52^{**}	0.43^{**}	0.60^{**}	0.33^{**}	0.31^{**}	0.43^{**}	0.50^{**}
CFW	0.52^{**}	0.12^{NS}	0.40^{*}	0.31^{NS}	0.53^{**}	0.22^{**}	0.27^{**}	0.36^{**}	0.45^{**}
YLD	0.07^{NS}	-0.00^{NS}	0.03^{NS}	-0.31^{NS}	-0.04^{NS}	-0.13^{NS}	-0.06^{NS}	-0.05^{NS}	0.01^{NS}
MFD	0.55^{**}	0.04^{NS}	0.31^{NS}	0.03^{NS}	0.38^{**}	0.08^{NS}	0.24^{**}	0.30^{**}	0.38^{**}
ON_r	-0.60^{**}	-0.66^{*}	-0.19^{NS}	0.21^{NS}	-0.47^{**}	-0.13^{NS}	0.04^{NS}	-0.13^{NS}	-0.33^{**}
ON_m	-0.51^{**}	-0.64^{*}	-0.03^{NS}	-0.04^{NS}	-0.29^{*}	0.07^{NS}	0.02^{NS}	-0.10^{NS}	-0.30^{**}
SL_r	0.45^{**}	0.38^{NS}	-0.03^{NS}	0.15^{NS}	0.26^{*}	0.02^{NS}	0.22^{*}	0.22^{**}	0.12^{NS}
SL_m	0.41^{**}	0.66^{**}	0.08^{NS}	0.03^{NS}	0.25^{*}	-0.17^{NS}	0.20^{*}	0.14^{*}	0.13^{NS}
TCN	-0.41^{**}	-0.34^{NS}	-0.09^{NS}	-0.08^{NS}	-0.30^{*}	0.01^{NS}	-0.01^{NS}	-0.14^{*}	-0.10^{NS}
CPC	-0.49^{**}	-0.48^{NS}	-0.14^{NS}	-0.13^{NS}	-0.38^{**}	0.09^{NS}	-0.10^{NS}	-0.12^{*}	-0.14^{NS}
CHR_r	-0.14^{*}	-0.62^{NS}	0.04^{NS}	-0.03^{NS}	0.04^{NS}	-0.06^{NS}	0.32^{**}	0.20^{**}	-0.25^{*}
CHR_m	-0.16^{**}	-0.29^{NS}	-0.31^{NS}	-0.23^{NS}	-0.30^{*}	-0.10^{NS}	0.13^{NS}	0.03^{NS}	-0.08^{NS}
LUS	0.44^{**}	0.57^{NS}	0.02^{NS}	0.12^{NS}	0.33^{**}	-0.06^{NS}	0.13^{NS}	0.12^{NS}	0.17^{NS}
TIP	-0.01^{NS}	-0.21^{NS}	-0.10^{NS}	-0.12^{NS}	-0.24^{*}	0.05^{NS}	0.06^{NS}	0.03^{NS}	-0.12^{NS}
COT	-0.05^{NS}	-0.70^{*}	0.06^{NS}	-0.07^{NS}	-0.02^{NS}	0.04^{NS}	0.16^{NS}	0.10^{NS}	-0.06^{NS}
SOU	-0.11^{*}	0.19^{NS}	0.08^{NS}	-0.12^{NS}	-0.01^{NS}	0.13^{NS}	-0.05^{NS}	0.03^{NS}	-0.17^{NS}
HND	-0.21^{**}	-0.39^{NS}	-0.32^{NS}	-0.04^{NS}	-0.29^{*}	-0.01^{NS}	0.11^{NS}	0.05^{NS}	-0.23^{*}
GC_r	-0.23^{**}	-0.56^{NS}	-0.15^{NS}	-0.12^{NS}	-0.24^{NS}	-0.14^{NS}	0.25^{*}	0.11^{NS}	-0.26^{*}
GC_m	-0.30^{**}	0.00^{NS}	-0.09^{NS}	-0.15^{NS}	-0.28^{*}	-0.11^{NS}	-0.01^{NS}	-0.04^{NS}	-0.26^{**}
SC_m	-0.24^{**}	0.22^{NS}	0.35^{NS}	-0.15^{NS}	-0.03^{NS}	-0.11^{NS}	0.16^{NS}	0.00^{NS}	-0.14^{NS}
n =	334-554	8-43	18-33	19-41	37-74	111-170	98-152	209-322	80-115

* $p<0.05$
** $p<0.01$
NS   not significant

TABLE 4.2: (continued)

TRAIT	GENOTYPE

GFW	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CFW	0.93^{**}	0.94^{**}	0.93^{**}	0.88^{**}	0.93^{**}	0.89^{**}	0.90^{**}	0.92^{**}	0.93^{**}
YLD	0.16^{**}	0.43^{NS}	-0.17^{NS}	-0.19^{NS}	-0.07^{NS}	0.07^{NS}	0.03^{NS}	0.09^{NS}	0.17^{NS}
MFD	0.52^{**}	0.29^{NS}	0.71^{**}	0.03^{NS}	0.55^{**}	0.34^{**}	0.34^{**}	0.48^{**}	0.48^{**}
ON_r	-0.49^{**}	-0.61^{*}	-0.32^{NS}	-0.28^{NS}	-0.62^{**}	-0.37^{**}	-0.25^{*}	-0.38^{**}	-0.51^{**}
ON_m	-0.49^{**}	0.01^{NS}	-0.08^{NS}	-0.07^{NS}	-0.34^{**}	-0.28^{**}	-0.27^{**}	-0.38^{**}	-0.47^{**}
SL_r	0.81^{**}	0.05^{NS}	-0.08^{NS}	0.26^{NS}	0.31^{*}	0.41^{**}	0.39^{**}	0.50^{**}	0.40^{**}
SL_m	0.45^{**}	0.02^{NS}	0.25^{NS}	0.24^{NS}	0.42^{**}	0.20^{*}	0.31^{**}	0.37^{**}	0.33^{**}
TCN	-0.43^{**}	-0.08^{NS}	-0.15^{NS}	-0.06^{NS}	-0.34^{**}	-0.19^{*}	-0.12^{NS}	-0.29^{**}	-0.29^{**}
CPC	-0.52^{**}	-0.05^{NS}	-0.21^{NS}	-0.20^{NS}	-0.46^{**}	-0.25^{**}	-0.27^{**}	-0.37^{**}	-0.39^{**}
CHR_r	0.11^{NS}	0.07^{NS}	-0.06^{NS}	0.17^{NS}	0.02^{NS}	0.21^{*}	0.31^{**}	0.36^{**}	-0.07^{NS}
CHR_m	-0.04^{NS}	-0.12^{NS}	-0.16^{NS}	0.00^{NS}	-0.11^{NS}	-0.04^{NS}	0.14^{NS}	0.08^{NS}	0.09^{NS}
LUS	0.40^{**}	-0.15^{NS}	-0.16^{NS}	0.01^{NS}	0.24^{NS}	0.29^{**}	0.25^{**}	0.33^{**}	0.26^{**}
TIP	-0.06^{NS}	0.23^{NS}	0.03^{NS}	-0.12^{NS}	-0.21^{NS}	0.06^{NS}	-0.08^{NS}	-0.02^{NS}	-0.11^{NS}
COT	-0.04^{NS}	-0.22^{NS}	-0.14^{NS}	-0.05^{NS}	-0.12^{NS}	0.02^{NS}	0.07^{NS}	0.05^{NS}	0.02^{NS}
SOU	-0.02^{NS}	0.06^{NS}	0.18^{NS}	-0.04^{NS}	0.08^{NS}	0.18^{*}	-0.03^{NS}	0.05^{NS}	-0.06^{NS}
HND	-0.17^{**}	-0.12^{NS}	-0.25^{NS}	0.01^{NS}	-0.24^{*}	-0.02^{NS}	0.00^{NS}	0.00^{NS}	-0.15^{NS}
GC_r	-0.15^{**}	-0.06^{NS}	-0.24^{NS}	-0.47^{*}	-0.41^{**}	-0.08^{NS}	0.08^{NS}	0.07^{NS}	-0.13^{NS}
GC_m	-0.19^{**}	0.22^{NS}	-0.23^{NS}	0.04^{NS}	-0.28^{*}	-0.07^{NS}	-0.11^{NS}	-0.06^{NS}	-0.06^{NS}
SC_m	-0.26^{**}	0.12^{NS}	0.00^{NS}	0.01^{NS}	-0.12^{NS}	-0.19^{*}	-0.14^{NS}	-0.17^{**}	-0.06^{NS}
n =	384-558	15-20	21-35	20-41	41-76	122-174	106-153	228-327	100-135

$*$ $p < 0.05$

$**$ $p < 0.01$

NS   not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

CFW	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
YLD	0.49^{**}	0.71^{**}	0.18^{NS}	0.28^{NS}	0.28^{*}	0.50^{**}	0.43^{**}	0.46^{**}	0.52^{**}
MFD	0.56^{**}	0.45^{*}	0.63^{**}	0.06^{NS}	0.53^{**}	0.38^{**}	0.35^{**}	0.50^{**}	0.44^{**}
QN_r	-0.50^{**}	-0.62^{*}	-0.26^{NS}	-0.39^{NS}	-0.62^{**}	-0.40^{**}	-0.25^{*}	-0.39^{**}	-0.48^{**}
QN_m	-0.53^{**}	0.10^{NS}	-0.09^{NS}	-0.16^{NS}	-0.40^{**}	-0.33^{**}	-0.28^{*}	-0.40^{**}	-0.49^{**}
SL_r	0.51^{**}	0.16^{NS}	0.01^{NS}	0.28^{NS}	0.38^{*}	0.33^{**}	0.38^{**}	0.46^{**}	0.45^{**}
SL_m	0.49^{**}	0.09^{NS}	0.27^{NS}	0.28^{NS}	0.48^{**}	0.23^{**}	0.31^{**}	0.39^{**}	0.36^{**}
TCN	-0.49^{**}	-0.21^{NS}	-0.13^{NS}	-0.05^{NS}	-0.34^{**}	-0.30^{**}	-0.22^{**}	-0.38^{**}	-0.29^{**}
CPC	-0.57^{**}	-0.16^{NS}	-0.21^{NS}	-0.19^{NS}	-0.48^{**}	-0.38^{**}	-0.37^{**}	-0.46^{**}	-0.42^{**}
CHR_r	-0.13^{*}	0.10^{NS}	0.14^{NS}	0.09^{NS}	0.11^{NS}	0.26^{**}	0.32^{**}	0.39^{**}	0.05^{NS}
CHR_m	-0.06^{NS}	-0.11^{NS}	0.00^{NS}	0.01^{NS}	-0.05^{NS}	-0.03^{NS}	-0.08^{NS}	0.05^{NS}	0.15^{NS}
LUS	0.39^{**}	-0.11^{NS}	-0.25^{NS}	0.05^{NS}	0.25^{*}	0.20^{*}	0.17^{*}	0.25^{**}	0.21^{*}
TIP	-0.09^{NS}	0.15^{NS}	-0.06^{NS}	-0.09^{NS}	-0.25^{*}	0.11^{NS}	-0.08^{NS}	0.00^{NS}	-0.13^{NS}
COT	-0.06^{NS}	-0.26^{NS}	-0.26^{NS}	0.08^{NS}	-0.13^{NS}	0.01^{NS}	0.06^{NS}	0.03^{NS}	0.09^{NS}
SOU	-0.02^{NS}	-0.03^{NS}	0.14^{NS}	0.01^{NS}	0.09^{NS}	0.12^{NS}	-0.06^{NS}	0.01^{NS}	-0.02^{NS}
HND	-0.17^{**}	-0.06^{NS}	-0.12^{NS}	0.10^{NS}	-0.16^{NS}	-0.07^{NS}	0.01^{NS}	-0.02^{NS}	-0.10^{NS}
GC_r	-0.08^{NS}	-0.15^{NS}	-0.01^{NS}	-0.53^{*}	-0.30^{NS}	0.01^{NS}	0.24^{*}	0.20^{**}	0.00^{NS}
GC_m	-0.13^{**}	0.18^{NS}	-0.16^{NS}	0.15^{NS}	-0.20^{NS}	0.02^{NS}	0.06^{NS}	0.05^{NS}	0.02^{NS}
SC_m	-0.24^{**}	0.02^{NS}	-0.10^{NS}	-0.01^{NS}	-0.19^{NS}	-0.16^{*}	-0.01^{NS}	-0.09^{NS}	0.01^{NS}
n =	354-542	15-20	20-34	20-44	40-78	110-167	94-147	204-314	95-130

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

YLD	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
ON_r	-0.22^{**}	-0.35^{NS}	0.05^{NS}	-0.29^{NS}	-0.18^{NS}	-0.13^{NS}	-0.04^{NS}	-0.11^{NS}	-0.07^{NS}
ON_m	-0.27^{**}	0.20^{NS}	-0.24^{NS}	-0.16^{NS}	-0.25^{*}	-0.16^{*}	-0.08^{NS}	-0.15^{**}	-0.23^{**}
SL_r	0.22^{**}	0.46^{NS}	0.21^{NS}	0.04^{NS}	0.21^{NS}	-0.02^{NS}	0.05^{NS}	0.05^{NS}	0.27^{**}
SL_m	0.27^{**}	0.18^{NS}	0.18^{NS}	0.05^{NS}	0.17^{NS}	0.18^{*}	0.09^{NS}	0.17^{**}	0.21^{*}
TCN	-0.28^{**}	-0.28^{NS}	-0.05^{NS}	-0.05^{NS}	-0.12^{NS}	-0.24^{**}	-0.19^{*}	-0.25^{**}	-0.11^{NS}
CPC	-0.32^{**}	-0.29^{NS}	-0.15^{NS}	-0.02^{NS}	-0.17^{NS}	-0.32^{**}	-0.24^{**}	-0.31^{**}	-0.21^{*}
CHR_r	0.10^{NS}	0.13^{NS}	0.56^{**}	-0.22^{NS}	0.33^{*}	0.12^{NS}	-0.02^{NS}	0.09^{NS}	0.30^{**}
CHR_m	-0.03^{NS}	-0.01^{NS}	0.41^{*}	-0.26^{NS}	-0.04^{NS}	0.04^{NS}	-0.06^{NS}	0.01^{NS}	0.20^{*}
LUS	0.08^{NS}	0.03^{NS}	-0.33^{*}	0.04^{NS}	-0.02^{NS}	-0.12^{NS}	-0.13^{NS}	-0.09^{NS}	-0.07^{NS}
TIP	-0.07^{NS}	-0.05^{NS}	-0.37^{*}	-0.01^{NS}	-0.20^{NS}	0.09^{NS}	-0.05^{NS}	0.03^{NS}	-0.02^{NS}
COT	-0.03^{NS}	-0.21^{NS}	-0.26^{NS}	0.07^{NS}	-0.10^{NS}	-0.04^{NS}	0.03^{NS}	-0.01^{NS}	0.20^{*}
SOU	-0.01^{NS}	-0.21^{NS}	0.08^{NS}	-0.04^{NS}	0.03^{NS}	-0.06^{NS}	-0.01^{NS}	-0.04^{NS}	0.04^{NS}
HND	-0.03^{NS}	0.12^{NS}	0.24^{NS}	-0.03^{NS}	0.03^{NS}	-0.08^{NS}	0.04^{NS}	-0.03^{NS}	0.16^{NS}
GC_r	0.20^{**}	-0.25^{NS}	0.64^{**}	-0.15^{NS}	0.33^{*}	0.27^{**}	0.32^{**}	0.30^{**}	0.35^{**}
GC_m	0.17^{**}	0.12^{NS}	0.45^{**}	0.30^{NS}	0.27^{*}	0.22^{**}	0.41^{**}	0.31^{**}	0.25^{**}
SC_m	-0.02^{NS}	-0.16^{NS}	-0.06^{NS}	-0.37^{*}	-0.26^{*}	0.08^{NS}	0.22^{**}	0.14^{*}	0.19^{*}
n =	365-550	15-21	20-37	20-44	40-81	110-171	94-146	204-317	96-131

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.2: (continued)

TRAIT	GENOTYPE								
MFD	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
QN_r	-0.78^{**}	-0.40^{NS}	-0.32^{NS}	-0.09^{NS}	-0.52^{**}	-0.51^{**}	-0.47^{**}	-0.52^{**}	-0.57^{**}
QN_m	-0.76^{**}	-0.06^{NS}	0.04^{NS}	-0.26^{NS}	-0.37^{**}	-0.47^{**}	-0.44^{**}	-0.54^{**}	-0.48^{**}
SL_r	0.64^{**}	0.33^{NS}	-0.15^{NS}	-0.19^{NS}	0.12^{NS}	0.20^{*}	0.28^{**}	0.37^{**}	0.12^{NS}
SL_m	0.62^{**}	0.32^{NS}	0.22^{NS}	0.02^{NS}	0.32^{**}	0.07^{NS}	0.11^{NS}	0.25^{**}	0.13^{NS}
TCN	-0.71^{**}	-0.56^{**}	-0.15^{NS}	-0.37^{*}	-0.45^{**}	-0.46^{**}	-0.50^{**}	-0.55^{**}	-0.34^{**}
CPC	-0.73^{**}	-0.50^{*}	-0.23^{NS}	-0.29^{NS}	-0.49^{**}	-0.43^{**}	-0.45^{**}	-0.52^{**}	-0.30^{**}
CHR_r	-0.23^{**}	0.01^{NS}	-0.28^{NS}	-0.21^{NS}	-0.21^{NS}	-0.07^{NS}	0.01^{NS}	0.13^{*}	-0.38^{**}
CHR_m	-0.32^{**}	-0.12^{NS}	-0.28^{NS}	-0.12^{NS}	-0.22^{*}	-0.08^{NS}	-0.00^{NS}	0.01^{NS}	-0.09^{NS}
LUS	0.63^{**}	0.08^{NS}	-0.09^{NS}	0.04^{NS}	0.25^{*}	0.17^{*}	0.13^{NS}	0.24^{**}	0.31^{**}
TIP	0.16^{**}	0.13^{NS}	0.16^{NS}	0.11^{NS}	-0.07^{NS}	0.22^{**}	0.02^{NS}	0.09^{NS}	-0.02^{NS}
COT	-0.19^{**}	-0.23^{NS}	0.06^{NS}	0.08^{NS}	0.00^{NS}	0.01^{NS}	-0.01^{NS}	0.01^{NS}	-0.09^{NS}
SOU	0.03^{NS}	-0.23^{NS}	0.04^{NS}	0.20^{NS}	0.15^{NS}	0.03^{NS}	0.06^{NS}	0.01^{NS}	-0.01^{NS}
HND	-0.39^{**}	-0.26^{NS}	-0.19^{NS}	-0.06^{NS}	-0.25^{*}	-0.24^{**}	-0.31^{**}	-0.22^{**}	-0.26^{**}
GC_r	-0.27^{**}	0.07^{NS}	-0.31^{NS}	0.15^{NS}	-0.24^{NS}	-0.20^{*}	-0.02^{NS}	-0.00^{NS}	0.00^{NS}
GC_m	-0.40^{**}	0.03^{NS}	-0.21^{NS}	-0.02^{NS}	-0.29^{**}	-0.19^{*}	-0.18^{*}	-0.14^{*}	-0.15^{NS}
SC_m	-0.43^{**}	0.10^{NS}	-0.13^{NS}	-0.34^{*}	-0.31^{**}	-0.15^{NS}	-0.13^{NS}	-0.15^{**}	-0.06^{NS}
n =	358-556	15-21	20-37	20-44	40-81	110-173	97-150	207-323	96-131

* $p<0.05$
** $p<0.01$
NS   not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

QN_r	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
QN_m	0.81^{**}	0.51^{*}	-0.20^{NS}	0.15^{NS}	0.46^{**}	0.54^{**}	0.62^{**}	0.61^{**}	0.62^{**}
SL_r	-0.61^{**}	-0.29^{NS}	0.15^{NS}	-0.10^{NS}	-0.33^{**}	-0.33^{**}	-0.39^{**}	-0.41^{**}	-0.34^{**}
SL_m	-0.62^{**}	-0.45^{NS}	-0.35^{NS}	0.02^{NS}	-0.51^{**}	-0.29^{**}	-0.26^{**}	-0.34^{**}	-0.24^{*}
TCN	0.73^{**}	0.44^{NS}	0.02^{NS}	0.08^{NS}	0.46^{**}	0.44^{**}	0.61^{**}	0.52^{**}	0.51^{**}
CPC	0.80^{**}	0.44^{NS}	0.21^{NS}	0.07^{NS}	-0.63^{**}	0.49^{**}	0.67^{**}	0.55^{**}	0.57^{**}
CHR_r	0.38^{**}	0.30^{NS}	0.25^{NS}	0.08^{NS}	-0.11^{NS}	0.19^{*}	0.29^{**}	0.15^{*}	0.43^{**}
CHR_m	0.37^{**}	0.33^{NS}	0.46^{*}	-0.30^{NS}	0.19^{NS}	0.16^{NS}	0.13^{NS}	0.11^{NS}	0.08^{NS}
LUS	-0.70^{**}	-0.17^{NS}	-0.32^{NS}	-0.04^{NS}	-0.51^{**}	-0.34^{**}	-0.46^{**}	-0.44^{**}	-0.53^{**}
TIP	0.30^{**}	0.01^{NS}	0.16^{NS}	-0.07^{NS}	0.24^{NS}	0.15^{NS}	0.30^{**}	0.23^{**}	0.23^{*}
COT	0.25^{**}	0.79^{**}	0.38^{NS}	0.37^{NS}	0.15^{NS}	0.15^{NS}	0.17^{NS}	0.16^{*}	0.16^{NS}
SOU	0.06^{NS}	-0.35^{NS}	0.08^{NS}	0.01^{NS}	-0.17^{NS}	0.05^{NS}	-0.19^{NS}	-0.04^{NS}	0.02^{NS}
HND	0.37^{**}	0.40^{NS}	0.22^{NS}	-0.39^{NS}	0.25^{NS}	0.11^{NS}	0.22^{*}	0.14^{*}	0.27^{**}
GC_r	0.42^{**}	0.27^{NS}	0.05^{NS}	0.43^{NS}	0.32^{NS}	0.33^{**}	0.22^{*}	0.23^{**}	0.28^{**}
GC_m	0.42^{**}	0.31^{NS}	0.32^{NS}	-0.29^{NS}	0.20^{NS}	0.11^{NS}	0.20^{NS}	0.11^{NS}	0.26^{*}
SC_m	0.40^{**}	0.16^{NS}	-0.25^{NS}	-0.36^{NS}	-0.08^{NS}	0.26^{**}	0.13^{NS}	0.18^{*}	0.26^{*}
n =	356–387	15–16	19–21	20	39–41	111–123	94–106	205–229	97–101

$*$ $p<0.05$
$**$ $p<0.01$
NS not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

QN_m	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
SL_r	-0.62^{**}	-0.25^{NS}	0.47^{*}	-0.23^{NS}	-0.22^{NS}	-0.31^{**}	-0.32^{**}	-0.40^{**}	-0.29^{**}
SL_m	-0.61^{**}	-0.30^{NS}	0.08^{NS}	0.00^{NS}	-0.25^{*}	-0.22^{**}	-0.26^{**}	-0.33^{**}	-0.29^{**}
TCN	0.75^{**}	0.44^{*}	0.36^{*}	0.34^{NS}	0.56^{**}	0.59^{**}	0.50^{**}	0.60^{**}	0.57^{**}
CPC	0.80^{**}	0.42^{NS}	0.33^{*}	0.27^{NS}	0.57^{**}	0.61^{**}	0.57^{**}	0.63^{**}	0.61^{**}
CHR_r	0.24^{**}	0.43^{NS}	-0.33^{NS}	0.04^{NS}	-0.16^{NS}	-0.09^{NS}	0.29^{**}	-0.03^{NS}	0.25^{*}
CHR_m	0.29^{**}	0.20^{NS}	-0.34^{*}	0.04^{NS}	-0.01^{NS}	0.20^{*}	0.06^{NS}	0.10^{NS}	0.07^{NS}
LUS	-0.75^{**}	-0.31^{NS}	0.10^{NS}	-0.53^{**}	-0.49^{**}	-0.53^{**}	-0.54^{**}	-0.56^{**}	-0.60^{**}
TIP	0.21^{**}	0.33^{NS}	0.01^{NS}	-0.06^{NS}	0.17^{NS}	0.03^{NS}	0.20^{*}	0.11^{NS}	0.20^{*}
COT	0.22^{**}	0.41^{NS}	-0.14^{NS}	0.03^{NS}	0.03^{NS}	0.15^{NS}	0.09^{NS}	0.11^{NS}	0.07^{NS}
SOU	-0.05^{NS}	-0.56^{**}	-0.03^{NS}	-0.11^{NS}	-0.11^{NS}	-0.04^{NS}	-0.11^{NS}	-0.05^{NS}	-0.14^{NS}
HND	0.39^{**}	0.34^{NS}	-0.03^{NS}	0.03^{NS}	0.17^{NS}	0.26^{**}	0.23^{**}	0.23^{**}	0.31^{**}
GC_r	0.36^{**}	0.30^{NS}	-0.32^{NS}	0.27^{NS}	0.10^{NS}	0.30^{**}	0.24^{*}	0.18^{**}	0.25^{*}
GC_m	0.42^{**}	-0.10^{NS}	-0.35^{*}	-0.01^{NS}	0.13^{NS}	0.27^{**}	0.21^{*}	0.21^{**}	0.27^{**}
SC_m	0.45^{**}	-0.12^{NS}	0.03^{NS}	0.16^{NS}	0.22^{*}	0.35^{**}	0.11^{NS}	0.24^{**}	0.22^{*}
n =	364-567	15-21	20-38	20-44	40-82	112-176	97-153	209-329	100-135

*   p<0.05
**   p<0.01
NS   not significant

TABLE 4.2: (continued)

| TRAIT | GENOTYPE | | | | | | | | |

SL_r	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
SL_m	0.86^{**}	0.45^{NS}	0.52^{*}	0.90^{**}	0.80^{**}	0.70^{**}	0.80^{**}	0.79^{**}	0.73^{**}
TCN	-0.48^{**}	-0.21^{NS}	0.42^{NS}	0.02^{NS}	-0.12^{NS}	-0.10^{NS}	-0.09^{NS}	-0.21^{**}	-0.06^{NS}
CPC	-0.66^{**}	-0.52^{*}	0.08^{NS}	-0.45^{*}	-0.46^{**}	-0.40^{**}	-0.51^{**}	-0.49^{**}	-0.43^{**}
CHR_r	-0.03^{NS}	-0.03^{NS}	0.29^{NS}	0.04^{NS}	0.17^{NS}	0.13^{NS}	0.10^{NS}	0.21^{**}	0.11^{NS}
CHR_m	-0.13^{*}	0.22^{NS}	0.16^{NS}	-0.07^{NS}	-0.05^{NS}	0.17^{NS}	0.15^{NS}	0.19^{**}	0.23^{*}
LUS	0.61^{**}	0.43^{NS}	-0.15^{NS}	0.50^{*}	0.42^{**}	0.35^{**}	0.42^{**}	0.44^{**}	0.11^{NS}
TIP	-0.32^{**}	0.11^{NS}	-0.25^{NS}	-0.02^{NS}	-0.22^{NS}	-0.00^{NS}	-0.32^{**}	-0.17^{*}	-0.17^{NS}
COT	-0.09^{NS}	-0.35^{NS}	-0.14^{NS}	0.26^{NS}	0.00^{NS}	0.05^{NS}	0.12^{NS}	0.08^{NS}	0.26^{**}
SOU	0.01^{NS}	0.48^{NS}	-0.39^{NS}	-0.07^{NS}	-0.07^{NS}	-0.01^{NS}	0.09^{NS}	0.01^{NS}	0.00^{NS}
HND	-0.12^{*}	-0.19^{NS}	0.28^{NS}	0.38^{NS}	0.12^{NS}	0.19^{*}	0.13^{NS}	0.17^{*}	0.08^{NS}
GC_r	-0.10^{NS}	0.23^{NS}	0.16^{NS}	-0.50^{*}	-0.22^{NS}	-0.04^{NS}	0.25^{**}	0.16^{*}	0.07^{NS}
GC_m	-0.15^{**}	0.07^{NS}	0.06^{NS}	-0.17^{NS}	-0.14^{NS}	0.10^{NS}	0.12^{NS}	0.15^{*}	0.10^{NS}
SC_m	-0.26^{**}	0.28^{NS}	0.14^{NS}	0.13^{NS}	0.06^{NS}	-0.11^{NS}	0.01^{NS}	-0.04^{NS}	0.02^{NS}
n =	356-396	14-15	19-21	20	39-41	112-123	94-106	206-229	97-101

*   p<0.05
** p<0.01
NS not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

SL_m	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
TCN	-0.45^{**}	-0.59^{**}	0.02^{NS}	-0.01^{NS}	-0.24^{NS}	0.02^{NS}	0.02^{NS}	-0.11^{NS}	0.01^{NS}
CPC	-0.71^{**}	-0.78^{**}	-0.43^{**}	-0.46^{**}	-0.59^{**}	-0.45^{**}	-0.52^{**}	-0.53^{**}	-0.51^{**}
CHR_r	-0.02^{NS}	-0.22^{NS}	0.07^{NS}	0.04^{NS}	0.06^{NS}	0.11^{NS}	0.14^{NS}	0.25^{**}	0.21^{*}
CHR_m	-0.17^{**}	-0.35^{NS}	0.04^{NS}	0.16^{NS}	0.05^{NS}	0.10^{NS}	0.11^{NS}	0.13^{*}	0.07^{NS}
LUS	0.60^{**}	0.71^{**}	-0.06^{NS}	0.09^{NS}	0.27^{*}	0.31^{**}	0.40^{**}	0.40^{**}	0.08^{NS}
TIP	-0.25^{**}	-0.31^{NS}	-0.14^{NS}	0.02^{NS}	-0.18^{NS}	0.03^{NS}	-0.32^{**}	-0.14^{*}	-0.11^{NS}
COT	-0.12^{**}	-0.78^{**}	-0.37^{*}	0.20^{NS}	-0.08^{NS}	0.07^{NS}	0.12^{NS}	0.10^{NS}	0.21^{*}
SOU	0.01^{NS}	0.16^{NS}	0.09^{NS}	-0.05^{NS}	0.04^{NS}	-0.07^{NS}	0.03^{NS}	-0.04^{NS}	0.03^{NS}
HND	-0.08^{NS}	-0.32^{NS}	0.05^{NS}	0.39^{*}	0.09^{NS}	0.23^{**}	0.19^{NS}	0.21^{**}	0.22^{*}
GC_r	-0.09^{NS}	-0.33^{NS}	0.34^{NS}	-0.50^{*}	-0.18^{NS}	0.05^{NS}	0.24^{*}	0.22^{**}	0.17^{NS}
GC_m	-0.19^{**}	-0.38^{NS}	-0.08^{NS}	0.11^{NS}	-0.15^{NS}	0.18^{*}	0.11^{NS}	0.15^{**}	0.13^{NS}
SC_m	-0.31^{**}	0.34^{NS}	0.07^{NS}	0.07^{NS}	-0.05^{NS}	-0.15^{NS}	0.08^{NS}	-0.05^{NS}	0.02^{NS}
n =	365-568	15-21	20-38	20-44	40-82	112-176	97-153	209-329	101-136

* $p<0.05$

** $p<0.01$

NS   not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

TCN	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CPC	0.91^{**}	0.89^{**}	0.88^{**}	0.86^{**}	0.91^{**}	0.86^{**}	0.81^{**}	0.87^{**}	0.82^{**}
CHR_r	0.27^{**}	0.28^{NS}	0.33^{NS}	-0.10^{NS}	0.11^{NS}	-0.02^{NS}	0.37^{**}	-0.01^{NS}	0.33^{**}
CHR_m	0.28^{**}	0.49^{*}	0.02^{NS}	-0.16^{NS}	-0.01^{NS}	0.13^{NS}	0.24^{**}	0.12^{*}	0.15^{NS}
LUS	-0.57^{**}	-0.52^{*}	0.35^{*}	-0.15^{NS}	-0.23^{*}	-0.26^{**}	-0.21^{**}	-0.29^{**}	-0.36^{**}
TIP	0.17^{**}	0.57^{**}	0.13^{NS}	-0.08^{NS}	0.19^{NS}	-0.08^{NS}	0.08^{NS}	-0.01^{NS}	0.12^{NS}
COT	0.21^{**}	0.61^{**}	0.02^{NS}	0.02^{NS}	0.08^{NS}	-0.03^{NS}	0.24^{**}	0.05^{NS}	0.16^{NS}
SOU	-0.03^{NS}	-0.04^{NS}	-0.13^{NS}	0.20^{NS}	-0.01^{NS}	-0.07^{NS}	0.07^{NS}	0.00^{NS}	-0.12^{NS}
HND	0.36^{**}	0.42^{NS}	0.09^{NS}	-0.02^{NS}	0.18^{NS}	0.23^{**}	0.26^{**}	0.22^{**}	0.21^{*}
GC_r	0.30^{**}	0.38^{NS}	0.10^{NS}	0.15^{NS}	0.24^{NS}	0.16^{NS}	0.09^{NS}	0.05^{NS}	0.17^{NS}
GC_m	0.36^{**}	0.29^{NS}	-0.04^{NS}	0.19^{NS}	0.28^{*}	0.17^{*}	0.12^{NS}	0.12^{*}	0.19^{*}
SC_m	0.40^{**}	-0.11^{NS}	0.34^{*}	0.22^{NS}	0.35^{**}	0.15^{NS}	0.16^{NS}	0.16^{**}	0.17^{NS}
n =	365-567	15-21	20-38	20-44	40-82	112-176	97-153	209-329	101-135

* $p < 0.05$

** $p < 0.01$

NS   not significant

TABLE 4.2: (continued)

TRAIT	GENOTYPE								
CPC	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CHR_r	0.20^{**}	0.21^{NS}	0.22^{NS}	-0.16^{NS}	0.03^{NS}	-0.10^{NS}	0.23^{*}	-0.12^{NS}	0.15^{NS}
CHR_m	0.24^{**}	0.45^{*}	-0.01^{NS}	-0.26^{NS}	-0.04^{NS}	0.08^{NS}	0.11^{NS}	0.05^{NS}	0.06^{NS}
LUS	-0.62^{**}	-0.63^{**}	0.39^{*}	-0.21^{NS}	-0.29^{**}	-0.36^{**}	-0.40^{**}	-0.40^{**}	-0.30^{**}
TIP	0.16^{**}	0.50^{*}	0.19^{NS}	-0.10^{NS}	0.23^{*}	-0.09^{NS}	0.21^{**}	0.02^{NS}	0.14^{NS}
COT	0.15^{**}	0.71^{**}	0.19^{NS}	-0.07^{NS}	0.12^{NS}	-0.09^{NS}	0.14^{NS}	-0.02^{NS}	0.00^{NS}
SOU	0.02^{NS}	-0.10^{NS}	-0.15^{NS}	0.25^{NS}	-0.01^{NS}	-0.02^{NS}	0.04^{NS}	0.02^{NS}	-0.10^{NS}
HND	0.26^{**}	0.29^{NS}	0.02^{NS}	-0.23^{NS}	0.10^{NS}	0.11^{NS}	0.08^{NS}	0.09^{NS}	0.02^{NS}
GC_r	0.27^{**}	0.17^{NS}	-0.18^{NS}	0.32^{*}	0.20^{NS}	0.13^{NS}	-0.06^{NS}	-0.03^{NS}	0.07^{NS}
GC_m	0.33^{**}	0.25^{NS}	-0.09^{NS}	0.09^{NS}	0.26^{*}	0.05^{NS}	0.04^{NS}	0.02^{NS}	0.07^{NS}
SC_m	0.41^{**}	-0.26^{NS}	0.24^{NS}	0.13^{NS}	0.28^{*}	0.21^{**}	0.09^{NS}	0.16^{**}	0.12^{NS}
n =	365-567	15-21	20-38	20-44	40-82	112-176	97-153	209-329	101-135

* $p<0.05$
** $p<0.01$
NS   not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

CHR_r	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CHR_m	0.44^{**}	0.45^{NS}	0.73^{**}	0.48^{*}	0.57^{**}	0.28^{**}	0.35^{**}	0.33^{**}	0.43^{**}
LUS	-0.17^{**}	-0.15^{NS}	-0.09^{NS}	0.03^{NS}	-0.01^{NS}	0.25^{**}	-0.04^{NS}	0.18^{**}	-0.37^{**}
TIP	0.14^{*}	-0.33	-0.12^{NS}	-0.24^{NS}	-0.16^{NS}	0.08^{NS}	0.09^{NS}	0.07^{NS}	0.19^{NS}
COT	0.34^{**}	0.51^{*}	0.09^{NS}	-0.11^{NS}	0.01^{NS}	0.27^{**}	0.43^{**}	0.33^{**}	0.41^{**}
SOU	0.08^{NS}	0.31^{NS}	-0.34^{NS}	-0.02^{NS}	-0.20^{NS}	0.19^{NS}	-0.03^{NS}	0.06^{NS}	0.02^{NS}
HND	0.32^{**}	0.73^{**}	0.21^{NS}	-0.22^{NS}	0.03^{NS}	0.18^{NS}	0.32^{**}	0.25^{**}	0.33^{**}
GC_r	0.45^{**}	0.59^{*}	0.48^{*}	0.26^{NS}	0.39^{*}	0.37^{**}	0.34^{**}	0.37^{**}	0.43^{**}
GC_m	0.38^{**}	0.22^{NS}	0.29^{NS}	0.25^{NS}	0.26^{NS}	0.14^{NS}	0.20^{NS}	0.20^{**}	0.47^{**}
SC_m	0.25^{**}	0.37^{NS}	0.09^{NS}	-0.30^{NS}	-0.07^{NS}	0.02^{NS}	0.25^{*}	0.13^{*}	0.29^{**}
n =	355-386	15-16	19-21	20	39-41	111-122	94-106	204-228	97-101

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.2: (continued)

CHR_m	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
LUS	-0.28^{**}	-0.23^{NS}	0.01^{NS}	0.01^{NS}	-0.06^{NS}	-0.03^{NS}	-0.06^{NS}	-0.02^{NS}	-0.16^{NS}
TIP	0.39^{**}	0.78^{**}	0.14^{NS}	0.27^{NS}	0.26^{*}	0.26^{**}	0.33^{**}	0.29^{**}	0.31^{**}
COT	0.46^{**}	0.52^{*}	0.13^{NS}	0.34^{*}	0.27^{*}	0.38^{**}	0.55^{**}	0.45^{**}	0.35^{**}
SOU	-0.07^{NS}	0.21^{NS}	0.02^{NS}	-0.04^{NS}	-0.03^{NS}	-0.02^{NS}	-0.00^{NS}	-0.02^{NS}	-0.07^{NS}
HND	0.45^{**}	0.34^{NS}	0.30^{NS}	0.44^{**}	0.41^{**}	0.52^{**}	0.35^{**}	0.45^{**}	0.24^{**}
GC_r	0.32^{**}	0.73^{**}	0.50^{*}	-0.10^{NS}	0.24^{NS}	0.27^{**}	0.05^{NS}	0.17^{*}	0.30^{**}
GC_m	0.44^{**}	0.43^{NS}	0.24^{NS}	0.19^{NS}	0.24^{*}	0.32^{**}	0.34^{**}	0.33^{**}	0.49^{**}
SC_m	0.29^{**}	0.01^{NS}	-0.23^{NS}	0.38^{*}	0.19^{NS}	0.14^{NS}	0.11^{NS}	0.12^{NS}	0.29^{**}
n =	368-569	15-21	20-38	20-44	40-82	115-177	97-153	212-330	101-136

TABLE 4.2: (continued)

TRAIT GENOTYPE

LUS	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
TIP	-0.34^{**}	-0.28^{NS}	-0.16^{NS}	-0.02^{NS}	-0.24^{*}	-0.22^{**}	-0.37^{**}	-0.29^{**}	-0.31^{**}
COT	-0.18^{**}	-0.47^{*}	0.12^{NS}	0.19^{NS}	0.07^{NS}	0.02^{NS}	-0.03^{NS}	0.01^{NS}	-0.16^{NS}
SOU	0.09^{*}	0.24^{NS}	-0.06^{NS}	0.04^{NS}	0.04^{NS}	0.17^{*}	0.11^{NS}	0.13^{*}	0.12^{NS}
HND	-0.33^{**}	0.22^{NS}	-0.16^{NS}	0.24^{NS}	-0.10^{NS}	-0.04^{NS}	-0.01^{NS}	-0.02^{NS}	-0.50^{**}
GC_r	-0.34^{**}	0.13^{NS}	-0.15^{NS}	-0.17^{NS}	-0.27^{NS}	-0.14^{NS}	-0.09^{NS}	-0.06^{NS}	-0.41^{**}
GC_m	-0.52^{**}	0.37^{NS}	-0.46^{**}	-0.28^{NS}	-0.50^{**}	-0.33^{**}	-0.24^{**}	-0.27^{**}	-0.49^{**}
SC_m	-0.42^{**}	0.30^{NS}	-0.06^{NS}	0.20^{NS}	-0.06^{NS}	-0.30^{**}	-0.10^{NS}	-0.21^{**}	-0.34^{**}
n =	366-568	15-21	20-38	20-44	40-82	113-176	97-153	210-329	101-136

* $p<0.05$
** $p<0.01$
NS   not significant

TABLE 4.2: (continued)

| TRAIT | GENOTYPE | | | | | | | | |

TIP	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
COT	0.28^{**}	0.39^{NS}	0.43^{**}	0.04^{NS}	0.23^{*}	0.21^{**}	0.26^{**}	0.24^{**}	0.13^{NS}
SOU	-0.19^{**}	0.13^{NS}	-0.01^{NS}	-0.09^{NS}	-0.08^{NS}	-0.02^{NS}	-0.12^{NS}	-0.06^{NS}	-0.20^{*}
HND	0.29^{**}	0.27^{NS}	0.10^{NS}	0.39^{**}	0.34^{**}	0.12^{NS}	0.17^{*}	0.14^{*}	0.39^{**}
GC_r	0.14^{**}	0.55^{*}	-0.08^{NS}	-0.35^{NS}	-0.11^{NS}	0.07^{NS}	0.03^{NS}	0.04^{NS}	0.22^{*}
GC_m	0.27^{**}	0.37^{NS}	0.13^{NS}	0.24^{NS}	0.30^{**}	0.18^{*}	0.17^{*}	0.17^{**}	0.36^{**}
SC_m	0.18^{**}	0.10^{NS}	0.20^{NS}	-0.01^{NS}	0.14^{NS}	0.08^{NS}	0.05^{NS}	0.07^{NS}	0.11^{NS}
n =	365-567	15-21	19-37	20-44	39-81	113-176	97-153	210-329	101-136

TABLE 4.2: (continued)

| TRAIT | GENOTYPE | | | | | | | | |

COT	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
SOU	-0.03^{NS}	-0.16^{NS}	0.03^{NS}	-0.01^{NS}	0.00^{NS}	0.10^{NS}	0.03^{NS}	0.07^{NS}	-0.14^{NS}
HND	0.44^{**}	0.52^{*}	0.29^{NS}	0.61^{**}	0.48^{**}	0.35^{**}	0.44^{**}	0.39^{**}	0.40^{**}
GC_r	0.19^{**}	0.55^{*}	0.12^{NS}	-0.32^{NS}	-0.02^{NS}	0.05^{NS}	0.16^{NS}	0.11^{NS}	0.25^{*}
GC_m	0.31^{**}	0.34^{NS}	0.36^{*}	0.12^{NS}	0.26^{*}	0.14^{NS}	0.31^{**}	0.22^{**}	0.34^{**}
SC_m	0.25^{**}	0.03^{NS}	0.16^{NS}	0.35^{*}	0.28^{*}	0.19^{*}	0.17^{NS}	0.18^{**}	0.13^{NS}
n =	365-567	15-21	19-37	20-44	39-81	113-176	97-153	210-329	101-136

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.2: (continued)

TRAIT   GENOTYPE

SOU	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
HND	-0.13^{**}	-0.01^{NS}	0.08^{NS}	-0.22^{NS}	-0.11^{NS}	-0.03^{NS}	-0.11^{NS}	-0.06^{NS}	-0.26^{**}
GC_r	0.04^{NS}	0.28^{NS}	0.03^{NS}	0.09^{NS}	-0.02^{NS}	0.04^{NS}	-0.24^{*}	-0.10^{NS}	0.07^{NS}
GC_m	-0.10^{*}	-0.02^{NS}	-0.01^{NS}	-0.10^{NS}	-0.09^{NS}	-0.03^{NS}	-0.12^{NS}	-0.07^{NS}	-0.24^{**}
SC_m	0.02^{NS}	0.26^{NS}	0.06^{NS}	0.06^{NS}	0.04^{NS}	0.11^{NS}	-0.06^{NS}	0.04^{NS}	0.02^{NS}
n =	366-568	15-21	20-38	20-44	40-82	113-176	97-153	210-329	101-136

TABLE 4.2: (continued)

TRAIT   GENOTYPE

HND	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
GC_r	0.36^{**}	0.46^{NS}	0.68^{**}	-0.56^{**}	0.27^{NS}	0.18^{NS}	0.23^{*}	0.21^{**}	0.39^{**}
GC_m	0.49^{**}	0.02^{NS}	0.54^{**}	0.18^{NS}	0.41^{**}	0.30^{**}	0.41^{**}	0.35^{**}	0.59^{**}
SC_m	0.30^{**}	0.16^{NS}	0.22^{NS}	0.31^{*}	0.33^{**}	0.08^{NS}	0.21^{**}	0.14^{*}	0.21^{*}
n =	537-569	15-21	20-38	20-44	40-82	144-177	97-153	211-330	101-136

* $p < 0.05$
** $p < 0.01$
NS   not significant

TABLE 4.2: (continued)

TRAIT	GENOTYPE								
GC_r	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
GC_m	0.46^{**}	0.28^{NS}	0.62^{**}	-0.17^{NS}	0.34^{*}	0.30^{**}	0.31^{**}	0.31^{**}	0.48^{**}
SC_m	0.49^{**}	0.56^{*}	0.31^{NS}	-0.19^{NS}	0.13^{NS}	0.41^{**}	0.52^{**}	0.46^{**}	0.52^{**}
n =	358-367	15	20	20	40	112-114	94-97	206-211	97-101

TABLE 4.2: (continued)

TRAIT	GENOTYPE								
GC_m	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
SC_m	0.43^{**}	0.07^{NS}	0.26^{NS}	-0.17^{NS}	0.10^{NS}	0.31^{**}	0.40^{**}	0.35^{**}	0.33^{**}
n =	537-569	20-21	34-38	40-44	74-82	167-177	145-153	313-330	130-136

* $p<0.05$
** $p<0.01$

TABLE 4.3 :   PHENOTYPIC CORRELATIONS FOR FLEECE AND FOLLICLE TRAITS USING DATA UNCORRECTED FOR FIXED EFFECTS

TRAIT   GENOTYPE

S/P	TOTAL	R	SFM	LM	SFM+LM	SFM×R	LM×R	SFMR+LMR	BX
ln S/P	0.97^{**}	0.99^{**}	0.97^{**}	0.99^{*}	0.98^{**}	0.99^{**}	0.99^{**}	0.99^{**}	0.98^{**}
n(P+S)	0.83^{**}	0.62^{**}	0.62^{**}	0.61^{**}	0.58^{**}	0.71^{**}	0.66^{**}	0.68^{**}	0.69^{**}
n(P+S)corr	0.79^{**}	0.45^{**}	0.57^{**}	0.55^{**}	0.54^{**}	0.53^{**}	0.50^{**}	0.52^{*}	0.57^{**}
nP	-0.18^{**}	-0.17^{NS}	-0.40^{*}	-0.19^{NS}	-0.27^{*}	-0.01^{NS}	-0.21^{**}	-0.10^{NS}	-0.05^{NS}
nP(corr)	-0.05^{NS}	-0.14^{NS}	-0.17^{NS}	-0.11^{NS}	-0.13^{NS}	-0.20^{**}	-0.22^{**}	-0.20^{**}	-0.05^{NS}
CF	-0.20^{**}	0.02^{NS}	0.21^{NS}	0.04^{NS}	0.10^{NS}	-0.21^{**}	0.07^{NS}	-0.14^{*}	-0.04^{NS}
LWT	-0.39^{**}	0.04^{NS}	-0.03^{NS}	-0.15^{NS}	-0.09^{NS}	-0.32^{**}	-0.24^{**}	-0.29^{**}	-0.14^{NS}
GFW	-0.21^{**}	-0.08^{NS}	0.07^{NS}	0.09^{NS}	0.04^{NS}	-0.07^{NS}	0.01^{NS}	-0.06^{NS}	-0.02^{NS}
CFW	-0.32^{**}	-0.05^{NS}	0.11^{NS}	0.08^{NS}	0.04^{NS}	-0.09^{NS}	0.01^{NS}	-0.07^{NS}	-0.00^{NS}
YLD	-0.17^{**}	0.07^{NS}	0.11^{NS}	0.14^{NS}	0.12^{NS}	-0.05^{NS}	0.00^{NS}	-0.04^{NS}	0.02^{NS}
MFD	-0.72^{**}	-0.36^{NS}	-0.19^{NS}	-0.16^{NS}	-0.15^{NS}	-0.50^{**}	-0.37^{**}	-0.43^{**}	-0.36^{**}
ON_r	0.65^{**}	0.40^{NS}	-0.52^{**}	-0.38^{NS}	-0.15^{NS}	0.18^{*}	0.19^{NS}	0.20^{**}	0.14^{NS}
ON_m	0.58^{**}	-0.05^{NS}	0.06^{NS}	-0.16^{NS}	-0.05^{NS}	0.19^{*}	0.04^{NS}	0.14^{*}	0.12^{NS}
SL_r	-0.43^{**}	-0.48^{NS}	0.34^{NS}	0.09^{NS}	-0.11^{NS}	-0.14^{NS}	-0.16^{NS}	-0.17^{*}	-0.01^{NS}
SL_m	-0.47^{**}	-0.52^{*}	-0.08^{NS}	-0.10^{NS}	-0.07^{NS}	-0.07^{NS}	-0.17^{*}	-0.14^{*}	-0.02^{NS}
TCN	0.52^{**}	-0.10^{NS}	0.14^{NS}	0.09^{NS}	0.09^{NS}	0.22^{**}	0.18^{*}	0.21^{**}	0.07^{NS}
CPC	0.59^{**}	0.10^{NS}	0.17^{NS}	0.18^{NS}	0.12^{NS}	0.21^{**}	0.23^{**}	0.22^{**}	0.07^{NS}
CHR_r	0.33^{**}	0.18^{NS}	0.10^{NS}	0.08^{NS}	0.10^{NS}	0.15^{NS}	0.15^{NS}	0.12^{NS}	0.17^{NS}
CHR_m	0.27^{**}	0.06^{NS}	0.10^{NS}	-0.31^{NS}	-0.15^{NS}	6.13^{NS}	0.18^{*}	0.14^{*}	0.15^{NS}
LUS	-0.50^{**}	-0.27^{NS}	0.11^{NS}	0.10^{NS}	0.10^{NS}	-0.06^{NS}	-0.01^{NS}	-0.05^{NS}	-0.10^{NS}
TIP	0.04^{NS}	-0.03^{NS}	0.21^{NS}	-0.26^{NS}	-0.04^{NS}	-0.13^{NS}	0.10^{NS}	-0.01^{NS}	-0.06^{NS}
COT	0.23^{**}	0.48^{*}	0.15^{NS}	-0.08^{NS}	0.03^{NS}	0.15^{NS}	-0.16^{*}	0.15^{**}	0.14^{NS}
SOU	0.02^{NS}	0.08^{NS}	-0.12^{NS}	-0.15^{NS}	-0.14^{NS}	-0.12^{NS}	-0.14^{NS}	-0.12^{*}	0.02^{NS}
HND	0.33^{**}	0.45^{*}	0.22^{NS}	-0.02^{NS}	0.08^{NS}	0.28^{**}	0.32^{**}	0.29^{**}	0.13^{NS}
GC_r	0.27^{**}	0.19^{NS}	0.21^{NS}	-0.03^{NS}	0.18^{NS}	-0.02^{NS}	-0.03^{NS}	-0.04^{NS}	-0.01^{NS}
GC_m	0.38^{**}	0.20^{NS}	0.15^{NS}	0.06^{NS}	0.09^{NS}	0.22^{**}	0.17^{*}	0.19^{**}	0.03^{NS}
SC_m	0.28^{**}	0.16^{NS}	0.38^{*}	0.01^{NS}	0.20^{NS}	0.05^{NS}	0.04^{NS}	0.04^{NS}	-0.01^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

* $p<0.05$
** $p<0.01$
NS   not significant

TABLE 4.3: (continued)

TRAIT   GENOTYPE

In S/P	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
n(P+S)	0.82^{**}	0.59^{**}	0.64^{NS}	0.63^{**}	0.60^{**}	0.69^{**}	0.67^{**}	0.67^{**}	0.69^{**}
n(P+S)corr	0.78^{**}	0.45^{**}	0.60^{**}	0.55^{**}	0.56^{**}	0.53^{**}	0.50^{**}	0.52^{**}	0.58^{**}
nP	-0.18^{**}	-0.20^{NS}	-0.36^{*}	-0.16^{NS}	-0.23^{*}	-0.03^{NS}	-0.22^{**}	-0.11^{NS}	-0.02^{NS}
nP(corr)	0.06^{NS}	-0.16^{NS}	-0.12^{NS}	-0.11^{NS}	-0.10^{NS}	-0.19^{*}	-0.23^{**}	-0.20^{**}	-0.03^{NS}
CF	0.22^{**}	0.04^{NS}	0.23^{NS}	0.03^{NS}	0.11^{NS}	0.19^{*}	-0.09^{NS}	-0.13^{*}	-0.03^{NS}
LWT	-0.38^{**}	0.03^{NS}	-0.05^{NS}	-0.18^{NS}	-0.10^{NS}	-0.33^{**}	-0.25^{**}	-0.30^{**}	-0.13^{NS}
GFW	-0.19^{**}	-0.06^{NS}	0.11^{NS}	0.08^{NS}	0.07^{NS}	-0.06^{NS}	0.02^{NS}	-0.06^{NS}	0.01^{NS}
CFW	-0.33^{**}	0.00^{NS}	0.13^{NS}	0.08^{NS}	0.06^{NS}	-0.07^{NS}	0.02^{NS}	-0.06^{NS}	0.03^{NS}
YLD	-0.18^{**}	0.10^{NS}	0.07^{NS}	0.12^{NS}	0.09^{NS}	-0.04^{NS}	0.02^{NS}	-0.02^{NS}	0.04^{NS}
MFD	-0.77^{**}	-0.35^{NS}	-0.13^{NS}	-0.21^{NS}	-0.14^{NS}	-0.48^{**}	-0.37^{**}	-0.43^{**}	-0.33^{**}
ON_r	0.66^{**}	0.40^{NS}	-0.48^{*}	-0.38^{NS}	-0.18^{NS}	0.20^{**}	0.21^{*}	0.22^{**}	0.11^{NS}
ON_m	0.60^{**}	-0.03^{NS}	0.11^{NS}	-0.15^{NS}	-0.03^{NS}	0.17^{*}	0.05^{NS}	0.14^{*}	0.09^{NS}
SL_r	-0.50^{**}	-0.49^{NS}	0.38^{NS}	0.11^{NS}	0.17^{NS}	-0.14^{NS}	-0.19^{NS}	-0.19^{**}	0.02^{NS}
SL_m	-0.52^{**}	-0.51^{*}	-0.06^{NS}	-0.04^{NS}	-0.03^{NS}	-0.06^{NS}	-0.20^{*}	-0.16^{*}	-0.00^{NS}
TCN	0.54^{**}	-0.11^{NS}	0.15^{NS}	0.08^{NS}	0.08^{NS}	0.20^{**}	0.18^{*}	0.20^{**}	0.08^{NS}
CPC	0.60^{**}	0.10^{NS}	0.16^{NS}	0.14^{NS}	0.09^{NS}	0.18^{*}	0.25^{**}	0.22^{**}	0.07^{NS}
CHR_r	0.31^{**}	0.19^{NS}	0.05^{NS}	0.09^{NS}	0.06^{NS}	0.17^{NS}	0.15^{NS}	0.12^{*}	0.18^{NS}
CHR_m	0.33^{**}	0.06^{NS}	0.08^{NS}	-0.24^{NS}	-0.10^{NS}	0.12^{NS}	0.19^{*}	0.13^{*}	0.19^{*}
LUS	-0.53^{**}	-0.25^{NS}	0.10^{NS}	0.12^{NS}	0.11^{NS}	-0.04^{NS}	-0.02^{NS}	-0.05^{NS}	-0.10^{NS}
TIP	0.11^{*}	-0.02^{NS}	0.21^{NS}	-0.25^{NS}	-0.04^{NS}	-0.13^{NS}	0.12^{NS}	0.00^{NS}	-0.05^{NS}
COT	0.27^{**}	0.46^{*}	0.18^{NS}	-0.05^{NS}	0.07^{NS}	0.13^{NS}	0.18^{*}	0.15^{*}	0.15^{NS}
SOU	-0.02^{NS}	0.06^{NS}	-0.11^{NS}	-0.19^{NS}	-0.15^{NS}	-0.11^{NS}	-0.14^{NS}	-0.11^{*}	0.00^{NS}
HND	0.38^{**}	0.45^{*}	0.23^{NS}	0.06^{NS}	0.13^{NS}	0.28^{**}	0.33^{**}	0.29^{**}	0.14^{NS}
GC_r	0.25^{**}	0.16^{NS}	0.13^{NS}	-0.03^{NS}	0.12^{NS}	-0.02^{NS}	-0.05^{NS}	-0.04^{NS}	0.01^{NS}
GC_m	0.40^{**}	0.22^{NS}	0.13^{NS}	0.08^{NS}	0.09^{NS}	0.21^{**}	0.17^{NS}	0.18^{**}	0.04^{NS}
SC_m	0.31^{NS}	0.16^{NS}	0.37^{*}	0.06^{NS}	0.23^{*}	0.06^{NS}	0.03^{NS}	0.05^{NS}	0.03^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

*	$p < 0.05$
**	$p < 0.01$
NS	not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
n(P+S)	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
n(P+S)corr	0.84^{**}	0.71^{**}	0.81^{**}	0.62^{**}	0.71^{**}	0.72^{**}	0.72^{**}	0.72^{**}	0.68^{**}
nP	0.36^{**}	0.65^{**}	0.45^{*}	0.65^{**}	0.62^{**}	0.68^{**}	0.53^{**}	0.62^{**}	0.68^{**}
nP(corr)	0.33^{**}	0.40^{**}	0.47^{*}	0.26^{NS}	0.39^{**}	0.25^{**}	0.23^{**}	0.25^{**}	0.33^{**}
CF	0.07^{NS}	-0.02^{NS}	0.15^{NS}	-0.23^{NS}	-0.13^{NS}	-0.33^{**}	-0.10^{NS}	-0.24^{**}	-0.24^{**}
LWT	-0.58^{**}	-0.26^{NS}	-0.57^{**}	-0.63^{**}	-0.47^{**}	-0.59^{**}	-0.55^{**}	-0.58^{**}	-0.46^{**}
GFW	-0.28^{**}	-0.36^{**}	-0.08^{NS}	-0.26^{NS}	0.00^{NS}	-0.16^{*}	-0.19^{*}	-0.21^{**}	-0.11^{NS}
CFW	-0.37^{**}	-0.18^{NS}	-0.05^{NS}	0.28^{NS}	0.01^{NS}	-0.21^{**}	-0.18^{*}	-0.23^{**}	-0.12^{NS}
YLD	-0.19^{**}	-0.00^{NS}	0.15^{NS}	0.00^{NS}	0.10^{NS}	-0.07^{NS}	-0.09^{NS}	-0.09^{NS}	-0.08^{NS}
MFD	-0.71^{**}	-0.22^{NS}	-0.35^{*}	-0.52^{**}	-0.21^{NS}	-0.56^{**}	-0.49^{**}	-0.54^{**}	-0.46^{**}
QN_r	0.60^{**}	0.49^{NS}	-0.31^{NS}	-0.40^{NS}	-0.31^{**}	0.20^{*}	0.34^{**}	0.28^{**}	0.18^{NS}
QN_m	0.48^{**}	0.36^{NS}	-0.10^{NS}	0.14^{NS}	0.15^{NS}	0.10^{NS}	0.15^{*}	-0.15^{NS}	-0.08^{NS}
SL_r	-0.43^{**}	-0.23^{NS}	0.25^{NS}	0.17^{NS}	0.26^{NS}	-0.17^{NS}	-0.30^{**}	-0.26^{**}	0.00^{**}
SL_m	-0.36^{**}	-0.15^{NS}	0.09^{NS}	0.24^{NS}	0.29^{**}	0.06^{NS}	-0.10^{NS}	-0.05^{NS}	0.10^{NS}
TCN	0.48^{**}	0.21^{NS}	-0.16^{NS}	0.01^{NS}	-0.22^{*}	0.35^{**}	0.32^{**}	0.36^{**}	0.03^{NS}
CPC	0.48^{**}	0.20^{NS}	-0.17^{NS}	-0.10^{NS}	-0.30^{**}	0.26^{**}	0.30^{**}	0.30^{**}	-0.05^{NS}
CHR_r	0.32^{**}	0.48^{*}	0.17^{NS}	0.39^{NS}	0.24^{NS}	0.21^{*}	0.15^{NS}	0.14^{*}	0.17^{*}
CHR_m	0.33^{**}	-0.05^{NS}	0.18^{NS}	0.05^{NS}	0.06^{NS}	0.31^{**}	0.18^{*}	0.24^{**}	0.20^{*}
LUS	-0.44^{**}	-0.03^{NS}	-0.04^{NS}	-0.16^{NS}	0.07^{NS}	-0.04^{NS}	-0.10^{NS}	-0.09^{NS}	-0.01^{NS}
TIP	-0.00^{NS}	-0.09^{NS}	0.01^{NS}	-0.26^{NS}	-0.24^{*}	-0.16^{*}	-0.01^{NS}	-0.09^{NS}	-0.01^{NS}
COT	0.25^{**}	0.48^{*}	0.20^{NS}	0.14^{NS}	0.13^{NS}	0.17^{*}	0.18^{*}	0.16^{**}	0.18^{NS}
SOU	-0.09^{*}	0.16^{NS}	-0.33^{*}	-0.50^{**}	-0.41^{**}	-0.21^{**}	-0.15^{NS}	-0.18^{**}	-0.11^{NS}
HND	0.44^{**}	0.52^{*}	0.44^{*}	0.39^{**}	0.32^{**}	0.44^{**}	0.39^{**}	0.41^{**}	0.26^{**}
GC_r	0.25^{**}	0.14^{NS}	0.30^{NS}	-0.21^{NS}	0.08^{NS}	0.09^{NS}	0.01^{NS}	0.03^{NS}	-0.02^{NS}
GC_m	0.36^{**}	-0.14^{NS}	0.32^{NS}	0.25^{NS}	0.14^{NS}	0.31^{**}	0.08^{NS}	0.21^{**}	0.03^{NS}
SC_m	0.25^{**}	0.23^{NS}	0.28^{NS}	-0.10^{NS}	0.03^{NS}	0.09^{NS}	0.03^{NS}	0.06^{NS}	0.01^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

*   p<0.05
**   p<0.01
NS   not significant

TABLE 4.3: (continued)

TRAIT   GENOTYPE

n(P+S)corr	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
nP	0.17^{**}	0.47^{**}	0.27^{NS}	0.24^{NS}	0.30^{**}	0.49^{**}	0.36^{**}	0.43^{**}	0.38^{**}
nP(corr)	0.61^{**}	0.80^{**}	0.70^{**}	0.75^{**}	0.74^{**}	0.71^{**}	0.70^{**}	0.70^{**}	0.77^{**}
CF	0.52^{**}	0.64^{**}	0.67^{**}	0.58^{**}	0.57^{**}	0.37^{**}	0.57^{**}	0.47^{**}	0.51^{**}
LWT	-0.46^{**}	-0.34^{*}	-0.70^{**}	-0.23^{NS}	-0.33^{**}	-0.45^{**}	-0.37^{**}	-0.43^{**}	-0.20^{*}
GFW	-0.26^{**}	-0.39^{**}	-0.03^{NS}	-0.12^{NS}	0.03^{NS}	-0.15^{*}	-0.18^{*}	-0.20^{**}	-0.05^{NS}
CFW	-0.35^{**}	-0.25^{NS}	-0.04^{NS}	-0.11^{NS}	0.05^{NS}	-0.17^{*}	-0.19^{*}	-0.22^{**}	-0.03^{NS}
YLD	-0.19^{**}	-0.33^{NS}	-0.05^{NS}	-0.06^{NS}	-0.02^{NS}	-0.03^{NS}	-0.09^{NS}	-0.07^{NS}	0.00^{NS}
MFD	-0.68^{**}	-0.40^{NS}	-0.23^{NS}	-0.25^{NS}	-0.09^{NS}	-0.46^{**}	-0.41^{**}	-0.45^{**}	-0.35^{**}
QN_r	0.57^{**}	0.32^{NS}	-0.18^{NS}	-0.32^{NS}	-0.41^{**}	0.15^{*}	0.30^{*}	0.24^{**}	0.24^{*}
QN_m	0.53^{**}	0.41^{NS}	-0.06^{NS}	0.11^{NS}	-0.09^{NS}	0.17^{*}	0.11^{NS}	0.18^{**}	0.08^{NS}
SL_r	-0.46^{**}	-0.24^{NS}	0.00^{NS}	-0.08^{NS}	0.16^{NS}	-0.26^{**}	-0.32^{**}	0.31^{**}	-0.12^{NS}
SL_m	-0.44^{**}	-0.60^{**}	-0.03^{NS}	0.06^{NS}	0.12^{NS}	-0.04^{NS}	-0.23^{**}	-0.17^{*}	-0.08^{NS}
TCN	0.44^{**}	0.48^{*}	-0.22^{NS}	0.07^{NS}	-0.17^{NS}	-0.24^{**}	0.17^{*}	0.23^{**}	-0.03^{NS}
CPC	0.51^{**}	0.57^{**}	-0.18^{NS}	0.06^{NS}	-0.19^{NS}	0.20^{*}	0.26^{**}	0.24^{**}	0.03^{NS}
CHR_r	0.26^{**}	0.50^{*}	-0.06^{NS}	0.46^{*}	0.12^{NS}	0.13^{NS}	0.03^{NS}	0.05^{NS}	0.11^{NS}
CHR_m	0.28^{**}	0.36^{NS}	0.10^{NS}	0.03^{NS}	0.03^{NS}	0.20^{**}	0.12^{NS}	0.14^{*}	0.14^{NS}
LUS	-0.48^{**}	-0.34^{NS}	-0.27^{NS}	-0.11^{NS}	-0.04^{NS}	-0.11^{NS}	-0.06^{NS}	-0.11^{NS}	-0.01^{NS}
TIP	0.03^{NS}	0.41^{NS}	0.06^{NS}	0.03^{NS}	-0.07^{NS}	-0.10^{NS}	-0.00^{NS}	-0.05^{NS}	-0.04^{NS}
COT	0.18^{**}	0.67^{**}	0.23^{NS}	-0.22^{NS}	-0.04^{NS}	0.07^{NS}	0.09^{NS}	0.08^{NS}	0.10^{NS}
SOU	0.03^{NS}	0.22^{NS}	-0.28^{NS}	-0.12^{NS}	-0.18^{NS}	-0.13^{NS}	-0.02^{NS}	-0.07^{NS}	0.09^{NS}
HND	0.31^{**}	0.49^{*}	0.45^{**}	0.07^{NS}	0.16^{NS}	0.30^{**}	0.29^{**}	0.29^{**}	0.01^{NS}
GC_r	0.17^{**}	0.40^{NS}	0.11^{NS}	-0.12^{NS}	-0.08^{NS}	0.08^{NS}	-0.11^{NS}	-0.04^{NS}	-0.14^{NS}
GC_m	0.32^{**}	-0.02^{NS}	0.34^{*}	0.12^{NS}	0.12^{NS}	0.25^{**}	0.10^{NS}	0.17^{**}	-0.11^{NS}
SC_m	0.24^{**}	-0.03^{NS}	0.15^{NS}	-0.05^{NS}	0.02^{NS}	0.07^{NS}	-0.06^{NS}	0.01^{NS}	0.04^{NS}
n =	385–637	15–52	21–39	20–45	41–84	122–194	106–170	228–364	101–137

* $p<0.05$
** $p<0.01$
NS   not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
nP	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
nP(corr)	0.54^{**}	0.66^{**}	0.72^{**}	0.43^{**}	0.58^{**}	0.59^{**}	0.59^{**}	0.59^{**}	0.54^{**}
CF	-0.20^{**}	-0.01^{NS}	-0.10^{NS}	-0.33^{NS}	-0.26^{*}	-0.24^{**}	-0.04^{NS}	-0.18^{*}	-0.25^{**}
LWT	-0.40^{**}	-0.44^{**}	-0.56^{**}	-0.69^{**}	-0.48^{**}	-0.54^{**}	-0.43^{**}	-0.49^{**}	-0.46^{**}
GFW	-0.17^{**}	-0.42^{**}	-0.16^{NS}	-0.42^{**}	-0.05^{NS}	-0.17^{*}	-0.26^{**}	-0.21^{**}	-0.12^{NS}
CFW	-0.17^{**}	-0.19^{NS}	-0.17^{NS}	-0.44^{**}	-0.04^{NS}	-0.20^{**}	-0.25^{**}	-0.23^{**}	-0.15^{NS}
YLD	-0.06^{NS}	-0.08^{NS}	0.06^{NS}	-0.09^{NS}	0.04^{NS}	-0.03^{NS}	-0.13^{NS}	-0.08^{NS}	-0.12^{NS}
MFD	-0.11^{*}	-0.02^{NS}	-0.22^{NS}	-0.45^{**}	-0.10^{NS}	-0.30^{**}	-0.25^{**}	-0.28^{**}	-0.27^{**}
QN_r	-0.10^{*}	0.27^{NS}	0.26^{NS}	-0.12^{NS}	-0.24^{NS}	0.03^{NS}	0.13^{NS}	0.07^{NS}	0.10^{NS}
QN_m	-0.07^{NS}	0.42^{NS}	-0.19^{NS}	0.26^{NS}	-0.14^{NS}	-0.04^{NS}	0.10^{NS}	0.04^{NS}	-0.21^{*}
SL_r	0.04^{NS}	0.13^{NS}	-0.10^{NS}	0.10^{NS}	0.20^{NS}	-0.03^{NS}	-0.14^{NS}	-0.08^{NS}	0.02^{NS}
SL_m	0.14^{*}	0.15^{NS}	0.23^{NS}	0.34^{*}	0.39^{**}	0.17^{*}	0.10^{NS}	0.11^{NS}	0.16^{NS}
TCN	0.03^{NS}	0.33^{NS}	-0.35^{*}	-0.08^{NS}	-0.34^{**}	0.27^{**}	0.22^{**}	0.26^{**}	-0.03^{NS}
CPC	-0.07^{NS}	0.18^{NS}	-0.40^{*}	-0.29	-0.46^{**}	0.15^{NS}	0.11^{NS}	0.15^{*}	-0.13^{NS}
CHR_r	0.00^{NS}	0.46^{NS}	0.11^{NS}	0.40^{NS}	0.20^{NS}	0.07^{NS}	-0.01^{NS}	0.02^{NS}	0.06^{NS}
CHR_m	0.14^{**}	-0.06^{NS}	0.10^{NS}	0.32^{*}	0.20^{NS}	0.31^{**}	0.01^{NS}	0.19^{**}	0.12^{NS}
LUS	0.03^{NS}	0.09^{NS}	-0.16^{NS}	-0.24^{NS}	0.00^{NS}	-0.01^{NS}	-0.08^{NS}	-0.05^{NS}	0.07^{NS}
TIP	-0.08^{NS}	-0.04^{NS}	-0.20^{NS}	-0.05^{NS}	-0.20^{NS}	-0.07^{NS}	-0.19^{*}	-0.12^{*}	0.03^{NS}
COT	0.07^{NS}	0.18^{NS}	0.05^{NS}	0.24^{NS}	0.12^{NS}	0.08^{NS}	0.05^{NS}	0.06^{NS}	0.08^{NS}
SOU	-0.16^{**}	0.12^{NS}	-0.24^{NS}	-0.47^{**}	-0.35^{**}	-0.19^{*}	0.02^{NS}	-0.10^{NS}	-0.16^{NS}
HND	0.23^{**}	0.21^{NS}	0.30^{NS}	0.46^{**}	0.30^{**}	0.36^{**}	0.13^{NS}	0.27^{**}	0.20^{*}
GC_r	-0.02^{NS}	0.02^{NS}	0.18^{NS}	-0.27^{NS}	-0.09^{NS}	0.14^{NS}	0.02^{NS}	0.07^{NS}	-0.02^{NS}
GC_m	-0.02^{NS}	-0.25^{NS}	0.21^{NS}	0.23^{NS}	0.09^{NS}	0.23^{**}	-0.10^{NS}	-0.09^{NS}	-0.01^{NS}
SC_m	-0.01^{NS}	0.06^{NS}	-0.08^{NS}	-0.17^{NS}	-0.16^{NS}	0.07^{NS}	-0.04^{NS}	0.02^{NS}	0.00^{NS}
n =	385–637	15–52	21–39	20–45	41–84	122–194	106–170	228–364	101–137

*   p<0.05
**   p<0.01
NS   not significant

TABLE 4.3: (continued)

| TRAIT | GENOTYPE | | | | | | | | |

nP(corr)	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CF	0.67^{**}	0.70^{**}	0.59^{**}	0.69^{**}	0.61^{**}	0.59^{**}	0.72^{**}	0.66^{**}	0.64^{**}
LWT	-0.29^{**}	-0.46^{**}	-0.77^{**}	-0.17^{NS}	-0.33^{**}	-0.25^{**}	-0.21^{**}	-0.24^{**}	-0.15^{NS}
GFW	-0.20^{**}	-0.42^{**}	-0.11^{NS}	-0.22^{NS}	-0.01^{NS}	-0.13^{NS}	-0.22^{**}	-0.19^{**}	-0.05^{NS}
CFW	-0.13^{**}	-0.11^{NS}	0.02^{NS}	0.11^{NS}	0.03^{NS}	0.00^{NS}	-0.09^{NS}	0.05^{NS}	0.12^{NS}
YLD	-0.11^{*}	-0.39^{NS}	-0.13^{NS}	-0.16^{NS}	-0.10^{NS}	-0.01^{NS}	-0.13^{NS}	-0.07^{NS}	0.00^{NS}
MFD	-0.25^{**}	-0.29^{NS}	-0.13^{NS}	-0.13^{NS}	0.02^{NS}	-0.12^{NS}	-0.19^{*}	-0.16^{**}	-0.16^{NS}
QN_r	0.16^{**}	0.08^{NS}	0.23^{NS}	0.02^{NS}	-0.34^{**}	0.03^{NS}	0.18^{NS}	0.11^{NS}	0.19^{NS}
QN_m	0.17^{**}	0.48^{*}	-0.10^{NS}	0.24^{NS}	-0.07^{NS}	0.06^{NS}	0.08^{NS}	0.09^{NS}	0.02^{NS}
SL_r	-0.25^{**}	0.09^{NS}	-0.26^{NS}	-0.23^{NS}	0.10^{NS}	-0.18^{*}	-0.22^{*}	-0.20^{**}	-0.14^{NS}
SL_m	-0.17^{**}	-0.37^{NS}	0.06^{NS}	0.11^{NS}	0.18^{NS}	0.01^{NS}	-0.12^{NS}	-0.07^{NS}	-0.09^{NS}
TCN	0.12^{**}	0.60^{**}	-0.37^{*}	-0.04^{NS}	-0.29^{*}	0.11^{NS}	0.06^{NS}	0.10^{NS}	-0.07^{NS}
CPC	0.13^{**}	0.58^{**}	-0.36^{*}	-0.10^{NS}	-0.33^{**}	0.08^{NS}	0.12^{NS}	0.10^{NS}	0.00^{NS}
CHR_r	0.03^{NS}	0.42^{NS}	-0.18^{NS}	0.51^{*}	0.07^{NS}	0.02^{NS}	-0.09^{NS}	-0.05^{NS}	0.03^{NS}
CHR_m	0.14^{**}	0.34^{NS}	0.02^{NS}	0.25^{NS}	0.15^{NS}	0.13^{NS}	-0.04^{NS}	0.05^{NS}	0.06^{NS}
LUS	-0.17^{**}	-0.24^{NS}	-0.40^{*}	-0.16^{NS}	-0.10^{NS}	-0.09^{NS}	-0.04^{NS}	-0.08^{NS}	0.04^{NS}
TIP	0.04^{NS}	0.44^{*}	-0.12^{NS}	0.18^{NS}	-0.02^{NS}	0.01^{NS}	-0.13^{NS}	-0.06^{NS}	0.01^{NS}
COT	0.05^{NS}	0.44^{*}	0.11^{NS}	-0.23^{NS}	-0.09^{NS}	-0.03^{NS}	-0.03^{NS}	-0.03^{NS}	0.00^{NS}
SOU	0.02^{NS}	0.21^{NS}	-0.25^{NS}	0.01^{NS}	-0.10^{NS}	-0.06^{NS}	0.12^{NS}	0.03^{NS}	0.07^{NS}
HND	0.12^{**}	0.31^{NS}	0.39^{*}	0.05^{NS}	0.13^{NS}	0.12^{NS}	0.07^{NS}	0.09^{NS}	-0.08^{NS}
GC_r	-0.01^{NS}	0.29^{NS}	-0.05^{NS}	-0.08^{NS}	-0.19^{NS}	0.12^{NS}	-0.12^{NS}	-0.02^{NS}	-0.12^{NS}
GC_m	0.06^{NS}	-0.13^{NS}	0.27^{NS}	0.06^{NS}	0.06^{NS}	0.11^{NS}	-0.04^{NS}	0.03^{NS}	-0.16^{NS}
SC_m	0.05^{NS}	-0.13^{NS}	-0.14^{NS}	-0.06^{NS}	-0.12^{NS}	0.04^{NS}	-0.13^{NS}	-0.04^{NS}	0.05^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

*   p<0.05
**   p<0.01
NS   not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								

CF	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
LWT	0.00^{NS}	-0.18^{NS}	-0.42^{*}	0.33^{*}	0.06^{NS}	0.21^{**}	0.06^{NS}	0.15^{*}	0.21^{*}
GFW	-0.09^{*}	-0.13^{NS}	0.13^{NS}	0.06^{NS}	0.00^{NS}	0.00^{NS}	-0.05^{NS}	-0.04^{NS}	0.07^{NS}
YLD	-0.10^{*}	-0.34^{NS}	-0.30^{NS}	-0.07^{NS}	-0.16^{NS}	0.00^{NS}	0.07^{NS}	-0.03^{NS}	0.13^{NS}
MFD	-0.22^{**}	-0.37^{NS}	0.04^{NS}	0.28^{NS}	0.11^{NS}	0.13^{NS}	-0.07^{NS}	0.04^{NS}	0.08^{NS}
QN_r	0.28^{**}	-0.13^{NS}	0.07^{NS}	0.07^{NS}	-0.28^{NS}	-0.04^{NS}	0.08^{NS}	0.08^{NS}	0.13^{NS}
QN_m	0.27^{**}	0.24^{NS}	0.10^{NS}	0.04^{NS}	0.08^{NS}	0.10^{NS}	0.01^{NS}	0.08^{NS}	0.22^{*}
SL_r	-0.33^{**}	-0.04^{NS}	-0.30^{NS}	-0.37^{NS}	-0.07^{NS}	-0.19^{*}	-0.09^{NS}	-0.18^{*}	0.14^{NS}
SL_m	-0.31^{**}	-0.51^{*}	-0.19^{NS}	-0.11^{NS}	-0.15^{NS}	-0.15^{NS}	0.15^{NS}	-0.20^{*}	-0.20^{*}
TCN	0.13^{**}	-0.42^{NS}	-0.20^{NS}	-0.02^{NS}	-0.03^{NS}	-0.15^{NS}	-0.08^{NS}	-0.11^{NS}	-0.01^{NS}
CPC	0.21^{**}	0.49^{*}	-0.09^{NS}	0.07^{NS}	0.05^{NS}	-0.07^{NS}	0.02^{NS}	0.00^{NS}	0.13^{NS}
CHR_r	0.04^{NS}	0.23^{NS}	-0.37^{NS}	0.22^{NS}	-0.14^{NS}	-0.05^{NS}	-0.09^{NS}	-0.10^{NS}	0.04^{NS}
CHR_m	0.05^{NS}	0.50^{*}	-0.12^{NS}	-0.02^{NS}	-0.04^{NS}	-0.16^{*}	-0.08^{NS}	-0.12^{*}	-0.02^{NS}
LUS	-0.23^{**}	-0.27^{NS}	-0.37^{*}	0.02^{NS}	-0.14^{NS}	-0.08^{NS}	-0.01^{NS}	-0.07^{NS}	-0.03^{NS}
TIP	0.12^{**}	0.64^{**}	0.05^{NS}	0.21^{NS}	0.17^{NS}	0.06^{NS}	-0.03^{NS}	0.04^{NS}	-0.03^{NS}
COT	0.01^{NS}	0.36^{NS}	0.10^{NS}	-0.39^{*}	-0.20^{NS}	-0.12^{NS}	-0.09^{NS}	-0.10^{NS}	-0.06^{NS}
SOU	0.16^{**}	0.21^{NS}	-0.02^{NS}	0.42^{**}	0.27^{*}	0.12^{NS}	0.13^{NS}	0.10^{*}	0.23^{**}
HND	-0.04^{NS}	0.24^{NS}	0.23^{NS}	-0.31^{*}	-0.13^{NS}	-0.19^{*}	-0.02^{NS}	-0.13^{*}	-0.26^{**}
GC_r	0.03^{NS}	0.38^{NS}	-0.21^{NS}	0.09^{NS}	-0.20^{NS}	0.03^{NS}	-0.15^{NS}	-0.09^{NS}	-0.11^{NS}
GC_m	0.05^{NS}	0.08^{NS}	0.09^{NS}	-0.12^{NS}	-0.02^{NS}	-0.08^{NS}	0.01^{NS}	-0.03^{NS}	-0.16^{NS}
SC_m	0.04^{NS}	-0.17^{NS}	-0.15^{NS}	0.05^{NS}	-0.02^{NS}	-0.05^{NS}	-0.19^{*}	-0.07^{NS}	0.05^{NS}
n =	385-637	15-52	21-39	20-45	41-84	122-194	106-170	228-364	101-137

$*$ $p < 0.05$
$**$ $p < 0.01$
NS   not significant

TABLE 4.3: (continued)

| TRAIT | GENOTYPE | | | | | | | | |

LWT	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
GFW	0.48^{**}	0.72^{**}	0.24^{NS}	0.51^{**}	0.46^{**}	0.26^{**}	0.40^{**}	0.38^{**}	0.41^{**}
CFW	0.52^{**}	0.21^{NS}	0.34^{NS}	0.52^{*}	0.49^{**}	0.28^{**}	0.46^{**}	0.40^{**}	0.46^{**}
YLD	0.26^{**}	0.05^{NS}	0.15^{NS}	0.14^{NS}	0.18^{NS}	0.12^{NS}	0.22^{*}	0.18^{**}	0.22^{*}
MFD	0.52^{**}	0.01^{NS}	0.33^{NS}	0.33^{*}	0.41^{**}	0.30^{**}	0.34^{**}	0.36^{**}	0.26^{**}
QN_r	-0.55^{**}	-0.65^{NS}	-0.28^{NS}	0.05^{NS}	-0.53^{**}	-0.25^{**}	0.01^{NS}	-0.19^{**}	-0.36^{**}
QN_m	-0.30^{**}	-0.60^{*}	0.37^{*}	-0.05^{NS}	-0.04^{NS}	0.07^{NS}	0.02^{NS}	-0.02^{NS}	0.15^{NS}
SL_r	0.51^{**}	0.45^{**}	0.05^{NS}	0.25^{NS}	0.37^{*}	0.26^{**}	0.41^{**}	0.39^{**}	0.26^{*}
SL_m	0.26^{**}	0.70^{*}	-0.11^{NS}	-0.14^{NS}	0.01^{NS}	-0.18^{*}	0.21^{*}	0.07^{NS}	-0.06^{NS}
TCN	-0.35^{**}	-0.21^{NS}	0.35^{*}	0.22^{NS}	0.09^{NS}	-0.23^{**}	-0.18^{*}	-0.25^{**}	-0.02^{NS}
CPC	-0.35^{**}	-0.37^{NS}	0.39^{*}	0.27^{NS}	0.07^{NS}	-0.10^{NS}	-0.27^{**}	-0.21^{**}	0.01^{NS}
CHR_r	-0.07^{NS}	-0.62^{NS}	0.09^{NS}	-0.08^{NS}	0.04^{NS}	-0.08^{NS}	0.39^{**}	0.21^{**}	-0.10^{NS}
CHR_m	-0.28^{**}	-0.41^{NS}	-0.15^{NS}	-0.46^{**}	-0.35^{**}	-0.25^{**}	-0.12^{NS}	-0.17^{**}	-0.18^{NS}
LUS	0.36^{**}	0.47^{NS}	0.24^{NS}	0.10^{NS}	0.27^{*}	0.00^{NS}	0.24^{**}	0.15^{**}	-0.03^{NS}
TIP	-0.03^{NS}	-0.29^{NS}	0.02^{NS}	0.02^{NS}	-0.07^{NS}	0.07^{NS}	0.04^{NS}	0.04^{NS}	-0.18^{NS}
COT	-0.19^{**}	-0.74^{**}	-0.43^{*}	-0.34^{*}	-0.36^{**}	-0.03^{NS}	-0.07^{NS}	-0.05^{NS}	-0.28^{**}
SOU	0.17^{**}	0.11^{NS}	0.65^{**}	0.73^{**}	0.66^{**}	0.29^{**}	0.11^{NS}	0.19^{**}	0.21^{*}
HND	-0.46^{**}	-0.54^{NS}	-0.56^{**}	-0.62^{**}	-0.62^{**}	-0.38^{**}	-0.29^{**}	-0.32^{**}	-0.45^{**}
GC_r	-0.17^{**}	-0.79^{*}	-0.03^{NS}	-0.22^{NS}	-0.20^{NS}	-0.17^{NS}	0.30^{**}	0.12^{NS}	-0.22^{*}
GC_m	-0.35^{**}	-0.17^{NS}	-0.57^{**}	-0.10^{NS}	-0.37^{**}	-0.34^{**}	-0.02^{NS}	-0.18^{**}	-0.26^{**}
SC_m	-0.12^{**}	-0.04^{NS}	-0.20^{NS}	0.01^{NS}	-0.11^{NS}	-0.10^{NS}	0.21^{*}	0.04^{NS}	-0.09^{NS}
n =	334-554	8-43	18-33	19-41	37-74	111-170	98-152	209-322	80-115

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.3: (continued)

TRAIT   GENOTYPE

GFW	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CFW	0.94^{**}	0.93^{**}	0.93^{**}	0.90^{**}	0.94^{**}	0.91^{**}	0.94^{**}	0.93^{**}	0.93^{**}
YLD	0.19^{**}	0.40^{NS}	-0.11^{NS}	-0.02^{NS}	0.02^{NS}	0.06^{NS}	0.11^{NS}	0.12^{*}	0.16^{NS}
MFD	0.53^{**}	0.39^{NS}	0.66^{**}	0.02^{NS}	0.51^{**}	0.32^{**}	0.39^{**}	0.44^{**}	0.42^{**}
QN_r	-0.50^{**}	-0.68^{**}	-0.50^{*}	-0.24^{NS}	-0.69^{**}	-0.44^{**}	-0.29^{**}	-0.43^{**}	-0.52^{**}
QN_m	-0.49^{**}	0.01^{NS}	-0.28^{NS}	-0.04^{NS}	-0.39^{**}	-0.31^{**}	-0.26^{**}	-0.37^{**}	-0.36^{**}
SL_r	0.61^{**}	-0.10^{NS}	0.08^{NS}	0.31^{NS}	0.42^{**}	0.60^{**}	0.58^{**}	0.65^{**}	0.48^{**}
SL_m	0.53^{**}	0.05^{NS}	0.29^{NS}	0.15^{NS}	0.40^{**}	0.33^{**}	0.46^{**}	0.48^{**}	0.37^{**}
TCN	-0.37^{**}	-0.21^{NS}	0.00^{NS}	0.14^{NS}	-0.22^{*}	-0.16^{*}	-0.03^{NS}	-0.18^{**}	-0.14^{NS}
CPC	-0.51^{**}	-0.13^{NS}	-0.13^{NS}	0.03^{NS}	-0.37^{**}	-0.31^{**}	-0.32^{**}	-0.40^{**}	-0.36^{**}
CH_r	0.14^{**}	0.14^{NS}	0.03^{NS}	0.22^{NS}	0.07^{NS}	0.09^{NS}	0.40^{**}	0.35^{**}	0.01^{NS}
CH_m	-0.06^{NS}	-0.13^{NS}	0.02^{NS}	-0.16^{NS}	-0.10^{NS}	0.01^{NS}	0.08^{NS}	0.09^{NS}	0.05^{NS}
LUS	0.44^{**}	-0.15^{NS}	0.07^{NS}	0.04^{NS}	0.31^{**}	0.30^{**}	0.29^{**}	0.35^{**}	0.24^{**}
TIP	-0.08^{NS}	0.11^{NS}	0.08^{NS}	-0.25^{NS}	-0.24^{*}	0.14^{NS}	-0.03^{NS}	0.03^{NS}	-0.15^{NS}
COT	-0.05^{NS}	-0.14^{NS}	0.03^{NS}	-0.15^{NS}	-0.08^{NS}	0.08^{NS}	0.03^{NS}	0.06^{NS}	-0.04^{NS}
SOU	-0.04^{NS}	0.01^{NS}	0.09^{NS}	0.10^{NS}	0.07^{NS}	0.11^{NS}	-0.10^{NS}	-0.03^{NS}	-0.02^{NS}
HND	-0.15^{**}	-0.16^{NS}	-0.05^{NS}	-0.13^{NS}	-0.16^{NS}	0.07^{NS}	-0.08^{NS}	0.02^{NS}	-0.14^{NS}
GC_r	-0.11^{*}	-0.16^{NS}	-0.06^{NS}	-0.26^{NS}	-0.26^{NS}	-0.15^{NS}	0.19^{NS}	0.10^{NS}	-0.15^{NS}
GC_m	-0.19^{**}	0.12^{NS}	-0.09^{NS}	0.02^{NS}	-0.19^{NS}	-0.10^{NS}	-0.07^{NS}	-0.05^{NS}	-0.03^{NS}
SC_m	-0.21^{**}	-0.02^{NS}	0.19^{NS}	0.04^{NS}	0.05^{NS}	-0.15^{NS}	-0.10^{NS}	-0.12^{**}	-0.05^{NS}
n =	384-558	15-20	21-35	20-41	41-76	122-174	106-153	228-327	100-135

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.3: (continued)

TRAIT   GENOTYPE

CFW	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
YLD	0.50^{**}	0.70^{**}	0.26^{NS}	0.42^{**}	0.37^{**}	0.48^{**}	-0.45^{**}	0.46^{**}	0.51^{**}
MFD	0.58^{**}	0.53^{*}	0.56^{**}	0.10^{NS}	0.50^{**}	0.38^{**}	0.41^{**}	0.47^{**}	0.41^{**}
QN_r	-0.52^{**}	-0.66^{**}	-0.42^{NS}	-0.36^{NS}	-0.67^{**}	-0.35^{**}	-0.28^{**}	-0.38^{**}	-0.49^{**}
QN_m	-0.52^{**}	0.09^{NS}	-0.28^{NS}	-0.10^{NS}	-0.41^{**}	-0.34^{**}	-0.27^{**}	-0.40^{**}	-0.36^{**}
SL_r	0.60^{**}	0.00^{NS}	0.17^{NS}	0.40^{NS}	0.49^{**}	0.48^{**}	0.52^{**}	0.57^{**}	0.50^{**}
SL_m	0.55^{**}	0.11^{NS}	0.34^{NS}	0.22^{NS}	0.47^{**}	0.33^{**}	0.42^{**}	0.46^{**}	0.35^{**}
TCN	-0.43^{**}	-0.32^{NS}	0.05^{NS}	0.16^{NS}	-0.21^{NS}	0.27^{**}	-0.15^{NS}	-0.28^{**}	-0.18^{*}
CPC	-0.56^{**}	-0.26^{NS}	-0.11^{NS}	-0.03^{NS}	-0.38^{**}	-0.42^{**}	-0.41^{**}	-0.48^{**}	-0.38^{**}
CHR_r	0.16^{**}	0.16^{NS}	0.27^{NS}	0.24^{NS}	0.21^{NS}	0.20^{*}	0.42^{**}	0.41^{**}	0.09^{NS}
CHR_m	-0.11^{*}	-0.11^{NS}	0.13^{NS}	-0.16^{NS}	-0.07^{NS}	-0.02^{NS}	0.02^{NS}	0.04^{NS}	0.07^{NS}
LUS	0.44^{**}	-0.13^{NS}	0.05^{NS}	0.07^{NS}	0.32^{**}	0.23^{**}	0.24^{**}	0.30^{**}	0.18^{*}
TIP	-0.09^{*}	0.09^{NS}	-0.03^{NS}	-0.19^{NS}	-0.27^{*}	0.19^{*}	-0.01^{NS}	0.06^{NS}	-0.16^{NS}
COT	-0.09^{*}	-0.19^{NS}	-0.10^{NS}	-0.11^{NS}	-0.11^{NS}	0.03^{NS}	0.00^{NS}	0.02^{NS}	0.00^{NS}
SOU	-0.02^{NS}	-0.09^{NS}	0.10^{NS}	0.16^{NS}	0.09^{NS}	0.08^{NS}	-0.11^{NS}	-0.05^{NS}	0.04^{NS}
HND	-0.20^{**}	-0.08^{NS}	0.00^{NS}	-0.10^{NS}	-0.13^{NS}	-0.03^{NS}	-0.11^{NS}	-0.05^{NS}	-0.12^{NS}
GC_r	-0.05^{NS}	-0.21^{NS}	0.24^{NS}	-0.26^{NS}	-0.09^{NS}	-0.02^{NS}	0.28^{*}	0.21^{**}	-0.04^{NS}
GC_m	-0.15^{**}	0.14^{NS}	-0.04^{NS}	0.13^{NS}	-0.12^{NS}	-0.05^{NS}	0.05^{NS}	0.02^{NS}	0.03^{NS}
SC_m	-0.18^{**}	-0.07^{NS}	0.15^{NS}	-0.00^{NS}	0.01^{NS}	-0.11^{NS}	0.03^{NS}	-0.04^{NS}	0.03^{NS}
n =	354-542	15-20	20-34	20-44	40-78	110-167	94-147	204-314	95-130

* $p < 0.05$
** $p < 0.01$
NS not significant

TABLE 4.3: (continued)

TRAIT   GENOTYPE

YLD	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
MFD	0.30^{**}	0.58^{*}	-0.34^{*}	-0.20^{NS}	0.03^{NS}	0.20^{**}	0.15^{NS}	0.20^{**}	0.11^{NS}
QN_m	-0.27^{**}	0.13^{NS}	-0.14^{NS}	-0.16^{NS}	-0.21^{NS}	-0.16^{*}	-0.10^{NS}	-0.17^{**}	-0.11^{NS}
QN_r	-0.26^{**}	-0.27^{NS}	-0.02^{NS}	-0.42^{NS}	-0.24^{NS}	-0.14^{NS}	-0.05^{NS}	-0.13^{NS}	-0.06^{NS}
SL_r	0.22^{**}	0.26^{NS}	0.22^{NS}	0.30^{NS}	0.31^{NS}	0.00^{NS}	0.02^{NS}	0.05^{NS}	0.20^{NS}
SL_m	0.24^{**}	0.20^{NS}	0.25^{NS}	0.08^{NS}	0.21^{NS}	0.11^{NS}	0.04^{NS}	0.11^{*}	0.07^{NS}
TCN	-0.31^{**}	-0.45^{*}	-0.09^{NS}	0.04^{NS}	-0.04^{NS}	-0.31^{**}	-0.30^{**}	-0.32^{**}	-0.12^{NS}
CPC	-0.33^{**}	-0.43^{NS}	-0.05^{NS}	0.03^{NS}	-0.11^{NS}	-0.35^{**}	-0.32^{**}	-0.35^{**}	-0.15^{NS}
CHR_r	0.07^{NS}	0.13^{NS}	0.62^{**}	0.04^{NS}	0.44^{**}	0.09^{NS}	-0.00^{NS}	0.08^{NS}	0.25^{*}
CHR_m	-0.10^{*}	-0.06^{NS}	0.43^{**}	-0.25^{NS}	-0.03^{NS}	0.01^{NS}	-0.13^{NS}	-0.03^{NS}	0.09^{NS}
LUS	0.14^{**}	0.04^{NS}	-0.18^{NS}	0.07^{NS}	0.04^{NS}	-0.07^{NS}	-0.03^{NS}	-0.03^{NS}	-0.11^{NS}
TIP	-0.06^{NS}	-0.06^{NS}	-0.31^{NS}	-0.01^{NS}	-0.18^{NS}	0.12^{NS}	0.02^{NS}	0.07^{NS}	-0.06^{NS}
COT	-0.11^{*}	-0.22^{NS}	-0.25^{NS}	-0.03^{NS}	-0.14^{NS}	-0.06^{NS}	-0.07^{NS}	-0.06^{NS}	0.08^{NS}
SOU	0.03^{NS}	-0.29^{NS}	0.12^{NS}	0.11^{NS}	0.11^{NS}	-0.05^{NS}	-0.01^{NS}	-0.04^{NS}	0.16^{NS}
HND	-0.14^{**}	0.11^{NS}	0.16^{NS}	-0.13^{NS}	-0.04^{NS}	-0.13^{NS}	-0.15^{NS}	-0.13^{*}	0.05^{NS}
GC_r	0.20^{**}	-0.24^{NS}	0.71^{**}	-0.07^{NS}	0.42^{**}	0.25^{**}	0.31^{**}	0.29^{**}	0.36^{**}
GC_m	0.10^{*}	0.17^{NS}	0.32^{NS}	0.30^{*}	0.24^{*}	0.16^{*}	0.35^{**}	0.24^{**}	0.22^{*}
SC_m	0.04^{NS}	-0.06^{NS}	-0.05^{NS}	-0.32^{*}	-0.20^{NS}	0.14^{NS}	0.28^{**}	0.20^{**}	0.23^{**}
n =	365-550	15-21	20-37	20-44	40-81	110-171	94-146	204-317	96-131

*   p<0.05
**   p<0.01
NS   not significant

TABLE 4.3: (continued)

TRAIT   GENOTYPE

MFD	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
QN_m	-0.75^{**}	0.07^{NS}	0.02^{NS}	-0.37^{*}	-0.41^{**}	-0.40^{**}	-0.48^{**}	-0.50^{**}	-0.42^{**}
QN_r	-0.81^{**}	-0.35^{NS}	-0.43^{NS}	-0.14^{NS}	-0.60^{**}	-0.50^{**}	-0.53^{**}	-0.56^{**}	-0.57^{**}
SL_r	0.62^{**}	0.29^{NS}	-0.11^{NS}	-0.15^{NS}	0.19^{NS}	0.18^{*}	0.32^{**}	0.35^{**}	0.07^{NS}
SL_m	0.56^{**}	0.28^{NS}	0.12^{NS}	-0.19^{NS}	0.20^{NS}	0.01^{NS}	0.13^{NS}	0.18^{*}	0.03^{NS}
TCN	-0.71^{**}	-0.46^{*}	0.02^{NS}	-0.26^{NS}	-0.36^{**}	-0.52^{**}	-0.52^{**}	-0.55^{**}	-0.36^{**}
CPC	-0.73^{**}	-0.48^{*}	-0.03^{NS}	-0.10^{NS}	-0.37^{**}	-0.47^{**}	-0.52^{**}	-0.54^{**}	-0.30^{**}
CHR_r	-0.25^{**}	0.03^{NS}	-0.26^{NS}	-0.30^{NS}	-0.23^{NS}	-0.08^{NS}	-0.06^{NS}	0.11^{NS}	-0.40^{**}
CHR_m	-0.33^{**}	-0.02^{NS}	-0.29^{NS}	-0.27^{NS}	-0.27^{*}	-0.15^{*}	-0.05^{NS}	-0.06^{NS}	-0.09^{NS}
LUS	0.65^{**}	-0.06^{NS}	0.17^{NS}	0.15^{NS}	0.37^{**}	0.19^{*}	0.19^{*}	0.25^{**}	0.31^{**}
TIP	-0.14^{**}	-0.07^{NS}	0.09^{NS}	0.05^{NS}	-0.12^{NS}	0.24^{**}	0.03^{NS}	0.12^{*}	-0.05^{NS}
COT	-0.22^{**}	-0.12^{NS}	0.07^{NS}	-0.05^{NS}	-0.03^{NS}	-0.07^{NS}	-0.03^{NS}	-0.03^{NS}	-0.13^{NS}
SOU	0.02^{NS}	-0.23^{NS}	0.07^{NS}	0.46^{**}	0.24^{*}	0.10^{NS}	0.08^{NS}	0.06^{NS}	-0.01^{NS}
HND	-0.41^{**}	-0.20^{NS}	-0.25^{NS}	-0.34^{*}	-0.35^{**}	-0.34^{**}	-0.35^{**}	-0.31^{**}	-0.26^{**}
GC_r	-0.27^{**}	0.09^{NS}	-0.28^{NS}	0.05^{NS}	-0.27^{NS}	-0.20^{*}	0.01^{NS}	-0.01^{NS}	0.00^{NS}
GC_m	-0.42^{**}	0.08^{NS}	-0.36^{*}	-0.14^{NS}	-0.36^{**}	-0.28^{**}	-0.14^{NS}	-0.18^{**}	-0.13^{NS}
SC_m	-0.33^{**}	0.02^{NS}	0.03^{NS}	-0.16^{NS}	-0.11^{NS}	-0.13^{NS}	-0.05^{NS}	-0.09^{NS}	0.02^{NS}
n =	358-556	15-21	20-37	20-44	40-81	110-173	97-150	207-323	96-131

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
QN_r	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
QN_m	0.18^{**}	0.50^{*}	0.17^{NS}	0.30^{NS}	0.55^{**}	0.47^{**}	0.63^{**}	0.57^{**}	0.61^{**}
SL_r	-0.60^{**}	-0.31^{NS}	-0.13^{NS}	-0.10^{NS}	-0.47^{**}	-0.41^{**}	-0.39^{**}	-0.45^{**}	-0.33^{**}
SL_m	-0.60^{**}	-0.45^{NS}	-0.41^{NS}	0.00^{NS}	-0.53^{**}	-0.29^{**}	-0.29^{**}	-0.36^{**}	-0.22^{**}
TCN	0.72^{**}	0.31^{NS}	0.04^{NS}	0.02^{NS}	0.46^{**}	0.45^{**}	0.61^{**}	0.52^{**}	0.48^{**}
CPC	0.80^{**}	0.39^{NS}	0.26^{NS}	0.01^{NS}	0.65^{**}	0.52^{**}	0.71^{**}	0.58^{**}	0.58^{**}
CHR_r	0.37^{**}	0.26^{NS}	0.24^{NS}	0.05^{NS}	0.12^{NS}	0.22^{**}	0.20^{NS}	0.12^{NS}	0.43^{**}
CHR_m	0.33^{**}	0.32^{NS}	0.30^{NS}	-0.26^{NS}	0.15^{NS}	0.12^{NS}	0.14^{NS}	0.09^{NS}	0.08^{NS}
LUS	-0.72^{**}	-0.12^{NS}	-0.55^{*}	-0.18^{NS}	-0.57^{**}	-0.32^{**}	-0.45^{**}	-0.43^{**}	-0.53^{**}
TIP	0.27^{**}	-0.01^{NS}	0.09^{NS}	0.01^{NS}	0.23^{NS}	0.09^{NS}	0.27^{**}	0.19^{**}	0.25^{*}
COT	0.23^{**}	0.70^{**}	0.23^{NS}	-0.28^{NS}	0.10^{NS}	0.16^{*}	0.18^{NS}	0.16^{*}	0.13^{NS}
SOU	0.16^{**}	-0.31^{NS}	0.37^{NS}	0.01^{NS}	0.04^{NS}	0.03^{NS}	-0.17^{NS}	-0.04^{NS}	0.04^{NS}
HND	0.31^{**}	0.38^{NS}	0.05^{NS}	-0.47^{*}	0.17^{NS}	0.06^{NS}	0.28^{**}	0.13^{NS}	0.26^{**}
GC_r	0.40^{**}	0.26^{NS}	0.00^{NS}	0.31^{NS}	0.26^{NS}	0.37^{**}	0.14^{NS}	0.20^{**}	0.30^{**}
GC_m	0.38^{**}	0.38^{NS}	0.19^{NS}	-0.25^{NS}	0.11^{NS}	0.12^{NS}	0.18^{NS}	0.10^{NS}	0.23^{*}
SC_m	0.25^{**}	0.17^{NS}	-0.52^{*}	-0.32^{NS}	-0.30^{NS}	0.26^{**}	0.18^{NS}	0.20^{**}	0.15^{NS}
n =	356-387	15-16	19-21	20	39-41	111-123	94-106	205-229	97-101

* p<0.05
** p<0.01
NS not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
QN_m	TOTAL	R	SFM	LM	SFM+LM	SFM×R	LM×R	SFMR+LMR	BX
SL_r	-0.59^{**}	-0.34^{NS}	0.01^{NS}	-0.23^{NS}	-0.37^{*}	-0.29^{**}	-0.28^{**}	-0.37^{**}	-0.23^{*}
SL_m	-0.58^{**}	-0.20^{NS}	-0.27^{NS}	0.08^{NS}	-0.30^{**}	-0.25^{**}	-0.23^{**}	-0.33^{**}	-0.26^{**}
TCN	0.72^{**}	0.37^{NS}	0.27^{NS}	0.39^{*}	0.54^{**}	0.48^{**}	0.50^{**}	0.52^{**}	0.51^{**}
CPC	0.79^{**}	0.35^{NS}	0.37^{*}	0.28^{NS}	0.56^{**}	0.56^{**}	0.56^{**}	0.61^{**}	0.59^{**}
CHR_r	0.25^{**}	0.38^{NS}	0.44^{NS}	0.13^{NS}	-0.15^{NS}	0.02^{NS}	0.19^{NS}	-0.04^{NS}	0.30^{**}
CHR_m	0.24^{**}	0.14^{NS}	-0.39^{*}	0.05^{NS}	-0.03^{NS}	0.13^{NS}	0.05^{NS}	0.06^{NS}	-0.05^{NS}
LUS	-0.77^{**}	-0.20^{NS}	-0.21^{NS}	-0.72^{**}	-0.62^{**}	-0.60^{**}	-0.48^{**}	-0.58^{**}	-0.64^{**}
TIP	0.18^{**}	0.21^{NS}	0.08^{NS}	0.08^{NS}	0.24^{*}	-0.03^{NS}	0.15^{NS}	0.05^{NS}	0.22^{*}
COT	0.19^{**}	0.39^{NS}	-0.40^{*}	-0.01^{NS}	-0.11^{NS}	0.16^{*}	0.07^{NS}	0.10^{NS}	-0.06^{NS}
SOU	0.08^{NS}	-0.45^{*}	0.35^{*}	0.10^{NS}	0.18^{NS}	0.09^{NS}	-0.13^{NS}	0.03^{NS}	0.08^{NS}
HND	0.29^{**}	0.28^{NS}	-0.31^{NS}	-0.01^{NS}	-0.01^{NS}	0.10^{NS}	0.23^{**}	0.13^{*}	0.10^{NS}
CG_r	0.34^{**}	0.29^{NS}	-0.33^{NS}	0.11^{NS}	0.04^{NS}	0.30^{**}	0.19^{*}	0.15^{*}	0.54^{*}
GC_m	0.37^{**}	-0.10^{NS}	-0.50^{*}	0.05^{NS}	0.02^{NS}	0.22^{**}	0.20^{*}	0.18^{**}	0.15^{NS}
SC_m	0.29^{**}	0.04^{NS}	-0.39^{*}	-0.29^{*}	-0.21^{NS}	0.19^{*}	0.15^{NS}	0.17^{**}	0.04^{NS}
n =	364-567	15-21	20-38	20-44	40-82	112-176	97-153	209-329	100-135

* p<0.05

** p<0.01

NS not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
SL_r	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
SL_m	0.88^{**}	0.37^{NS}	0.55^{*}	0.89^{**}	0.79^{**}	0.78^{**}	0.85^{**}	0.84^{**}	0.78^{**}
TCN	-0.36^{**}	-0.11^{NS}	0.47^{*}	0.33^{NS}	-0.01^{NS}	-0.02^{NS}	0.10^{NS}	-0.05^{NS}	0.10^{NS}
CPC	-0.63^{**}	-0.26^{NS}	0.00^{NS}	-0.12^{NS}	-0.41^{**}	-0.41^{**}	-0.48^{**}	-0.48^{**}	-0.38^{**}
CHR_r	0.02^{NS}	-0.12^{NS}	0.36^{NS}	-0.01^{NS}	0.17^{NS}	0.08^{NS}	0.22^{*}	0.24^{**}	0.19^{NS}
CHR_m	-0.09^{NS}	0.23^{NS}	0.31^{NS}	-0.32^{NS}	-0.10^{NS}	0.26^{**}	0.13^{NS}	0.22^{**}	0.23^{*}
LUS	0.60^{**}	0.45^{NS}	0.05^{NS}	0.48^{*}	0.44^{**}	0.37^{**}	0.39^{**}	0.44^{**}	0.13^{NS}
TIP	-0.29^{**}	0.08^{NS}	-0.05^{NS}	-0.45^{*}	-0.35^{*}	0.11^{NS}	-0.26^{**}	-0.10^{NS}	-0.16^{NS}
COT	-0.06^{NS}	-0.31^{NS}	0.01^{NS}	0.18^{NS}	0.04^{NS}	0.12^{NS}	0.13^{NS}	0.12^{NS}	0.22^{*}
SOU	-0.06^{NS}	0.47^{NS}	-0.34^{NS}	-0.21^{NS}	-0.17^{NS}	-0.03^{NS}	0.02^{NS}	-0.03^{NS}	-0.04^{NS}
HND	-0.07^{NS}	-0.32^{NS}	0.46^{*}	0.38^{NS}	0.19^{NS}	0.28^{**}	0.08^{NS}	0.20^{**}	0.12^{NS}
CG_r	-0.07^{NS}	0.07^{NS}	0.32^{NS}	-0.18^{NS}	-0.04^{NS}	-0.11^{NS}	0.32^{**}	0.18^{*}	0.02^{NS}
CG_m	-0.13^{*}	-0.07^{NS}	0.30^{NS}	-0.08^{NS}	0.04^{NS}	0.06^{NS}	0.13^{NS}	0.14^{*}	0.10^{NS}
SC_m	-0.18^{**}	0.18^{NS}	0.24^{NS}	0.29^{NS}	0.24^{NS}	-0.07^{NS}	0.00^{NS}	-0.02^{NS}	-0.02^{NS}
n =	356–396	14–15	19–21	20	39–41	112–123	94–106	206–229	97–101

$*$ $p < 0.05$

$**$ $p < 0.01$

NS   not significant

TABLE 4.3: (continued)

TRAIT   GENOTYPE

SL_m	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
TCN	-0.33^{**}	-0.39^{NS}	-0.02^{NS}	-0.15^{NS}	-0.19^{NS}	0.14^{NS}	0.14^{NS}	0.04^{NS}	0.19^{*}
CPC	-0.66^{**}	-0.68^{**}	-0.57^{**}	-0.38^{*}	-0.61^{**}	-0.38^{**}	-0.48^{**}	-0.47^{**}	-0.43^{**}
CHR_r	0.04^{NS}	-0.20^{NS}	0.19^{NS}	0.02^{NS}	0.10^{NS}	0.12^{NS}	0.26^{*}	0.30^{**}	0.29^{**}
CHR_m	-0.11^{*}	-0.38^{NS}	0.25^{NS}	0.15^{NS}	0.12^{NS}	0.22^{**}	0.10^{NS}	0.19^{**}	0.14^{NS}
LUS	0.57^{**}	0.62^{**}	-0.11^{NS}	-0.01^{NS}	0.17^{NS}	0.32^{**}	0.38^{**}	0.39^{**}	0.10^{NS}
TIP	-0.23^{**}	-0.37^{NS}	-0.03^{NS}	-0.27^{NS}	-0.28^{*}	0.09^{NS}	-0.29^{**}	-0.10^{NS}	-0.09^{NS}
COT	-0.08^{NS}	-0.73^{**}	-0.14^{NS}	0.28^{NS}	0.05^{NS}	0.17^{*}	0.11^{NS}	0.15^{*}	0.24^{**}
SOU	-0.07^{NS}	0.15^{NS}	-0.09^{NS}	-0.27^{NS}	-0.17^{NS}	-0.14^{NS}	-0.02^{NS}	-0.10^{NS}	-0.10^{NS}
HND	0.00^{NS}	-0.33^{NS}	0.34^{*}	0.46^{**}	0.28^{*}	0.36^{**}	0.13^{NS}	0.26^{**}	0.32^{**}
GC_r	-0.05^{NS}	-0.50^{NS}	0.52^{*}	-0.17^{NS}	0.09^{NS}	0.02^{NS}	0.34^{**}	0.26^{**}	0.10^{NS}
GC_m	-0.14^{*}	-0.45^{*}	0.33^{*}	0.21^{NS}	0.08^{NS}	0.19^{*}	0.09^{NS}	0.16^{*}	0.16^{NS}
SC_m	-0.25^{**}	0.20^{NS}	0.19^{NS}	0.05^{NS}	0.05^{NS}	-0.12^{NS}	0.01^{NS}	-0.06^{NS}	-0.08^{NS}
n =	365–568	15–21	20–38	20–44	40–82	112–176	97–153	209–329	101–136

* $p < 0.05$
** $p < 0.01$
NS   not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
TCN	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CPC	0.89^{**}	0.93^{**}	0.83^{**}	0.83^{**}	0.88^{**}	0.84^{**}	0.79^{**}	0.83^{**}	0.77^{**}
CH_r	0.32^{**}	0.23^{NS}	0.26^{NS}	0.02^{NS}	0.12^{NS}	0.00^{NS}	0.40^{**}	0.07^{NS}	0.40^{**}
CH_m	0.30^{**}	0.30^{NS}	-0.02^{NS}	-0.16^{NS}	-0.04^{NS}	0.23^{**}	0.26^{**}	0.21^{**}	0.16^{NS}
LUS	-0.56^{**}	-0.39^{NS}	0.15^{NS}	-0.16^{NS}	-0.28^{*}	-0.25^{**}	-0.22^{**}	-0.28^{**}	-0.33^{**}
TIP	0.14^{**}	0.38^{NS}	0.29^{NS}	-0.21^{NS}	0.19^{NS}	-0.07^{NS}	0.04^{NS}	-0.02^{NS}	0.14^{NS}
COT	0.22^{**}	0.44^{*}	-0.08^{NS}	0.00^{NS}	0.01^{NS}	0.08^{NS}	0.28^{**}	0.14^{*}	0.15^{NS}
SOU	-0.03^{NS}	-0.02^{NS}	0.02^{NS}	0.06^{NS}	0.04^{NS}	-0.13^{NS}	-0.04^{NS}	-0.08^{NS}	-0.13^{NS}
HND	0.38^{**}	0.29^{NS}	-0.04^{NS}	-0.02^{NS}	0.08^{NS}	0.37^{**}	0.34^{**}	0.34^{**}	0.22^{*}
CG_r	0.31^{**}	0.22^{NS}	0.05^{NS}	0.28^{NS}	0.26^{NS}	0.14^{NS}	0.19^{NS}	0.10^{NS}	0.15^{NS}
CG_m	0.37^{**}	0.07^{NS}	-0.03^{NS}	0.14^{NS}	0.23^{*}	0.24^{**}	0.11^{NS}	0.17^{**}	0.16^{NS}
SC_m	0.30^{**}	-0.08^{NS}	0.27^{NS}	0.14^{NS}	0.23^{*}	0.09^{NS}	0.09^{NS}	0.09^{NS}	0.03^{NS}
n =	365-567	15-21	20-38	20-44	40-82	112-176	97-153	209-329	101-135

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.3: (continued)

<u>TRAIT</u>   <u>GENOTYPE</u>

CPC	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CHR_r	0.21^{**}	0.22^{NS}	0.09^{NS}	-0.04^{NS}	0.03^{NS}	-0.09^{NS}	0.16^{NS}	-0.13^{NS}	0.17^{NS}
CHR_m	0.22^{**}	0.36^{NS}	-0.17^{NS}	-0.29^{NS}	-0.12^{NS}	0.11^{NS}	0.16^{*}	0.07^{NS}	0.03^{NS}
LUS	-0.63^{**}	-0.54^{*}	0.22^{NS}	-0.14^{NS}	-0.28^{*}	-0.39^{**}	-0.41^{**}	-0.43^{**}	-0.32^{**}
TIP	0.14^{**}	0.43^{NS}	0.27^{NS}	-0.12^{NS}	0.56^{*}	-0.11^{NS}	0.19^{*}	0.00^{NS}	0.16^{NS}
COT	0.15^{**}	0.59^{**}	0.01^{NS}	-0.13^{NS}	0.01^{NS}	-0.04^{NS}	0.18^{*}	0.02^{NS}	-0.04^{NS}
SOU	0.05^{NS}	-0.08^{NS}	0.09^{NS}	0.23^{NS}	0.12^{NS}	-0.04^{NS}	-0.03^{NS}	-0.01^{NS}	-0.05^{NS}
HND	0.24^{**}	0.30^{NS}	-0.25^{NS}	-0.29^{NS}	-0.08^{NS}	0.16^{*}	0.20^{*}	0.15	-0.02^{NS}
GC_r	0.26^{**}	0.27^{NS}	-0.30^{NS}	0.34^{*}	0.15^{NS}	0.12^{NS}	-0.08^{NS}	-0.04^{NS}	0.09^{NS}
GC_m	0.31^{**}	0.19^{NS}	-0.25^{NS}	-0.00^{NS}	0.12^{NS}	0.10^{NS}	0.05^{NS}	0.05^{NS}	0.04^{NS}
SC_m	0.32^{**}	-0.20^{NS}	0.15^{NS}	0.10^{NS}	0.17^{NS}	0.14^{NS}	0.09^{NS}	0.12^{*}	0.05^{NS}
n =	365-567	15-21	20-38	20-44	40-82	112-176	97-153	209-329	101-135

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.3: (continued)

TRAIT   GENOTYPE

CHR_r	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
CHR_m	0.41**	0.39NS	0.81**	0.50*	0.63**	0.26**	0.35**	0.32**	0.40**
LUS	-0.18**	-0.11NS	-0.03NS	-0.05NS	-0.03NS	0.16NS	0.06NS	0.20**	-0.39**
TIP	0.11*	0.30NS	-0.12NS	-0.26NS	-0.16NS	0.08NS	0.08NS	0.07NS	0.17NS
COT	0.34**	0.50*	0.13NS	-0.11NS	0.04NS	0.29**	0.42**	0.34**	0.38**
SOU	0.13*	0.36NS	-0.30NS	-0.29NS	-0.29NS	0.28**	-0.11NS	0.06NS	0.06NS
HND	0.30**	0.68**	0.30NS	-0.12NS	0.14NS	0.13NS	0.33**	0.23**	0.34**
GC_r	0.45**	0.57*	0.52	0.27NS	0.43**	0.34**	0.37**	0.38**	0.41**
GC_m	0.36**	0.18NS	0.40*	0.37NS	0.38*	0.10NS	0.22*	0.19**	0.44**
SC_m	0.16**	0.24NS	0.10NS	-0.06NS	0.05NS	-0.04NS	0.25*	0.11*	0.11NS
n =	355-386	15-16	19-21	20	39-41	111-122	94-106	204-228	97-101

* $p < 0.05$
** $p < 0.01$
NS   not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
CHR_m	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
LUS	-0.26^{**}	-0.11^{NS}	-0.13^{NS}	-0.07^{NS}	-0.12^{NS}	0.00^{NS}	-0.07^{NS}	0.00^{NS}	-0.08^{NS}
TIP	0.37^{**}	0.81^{**}	0.12^{NS}	0.18^{NS}	0.19^{NS}	0.25^{**}	0.32^{**}	0.27^{**}	0.31^{**}
COT	0.49^{**}	0.50^{*}	0.16^{NS}	0.36^{*}	0.29^{**}	0.42^{**}	0.57^{**}	0.48^{**}	0.41^{**}
SOU	-0.15^{**}	0.14^{NS}	-0.04^{NS}	-0.21^{NS}	-0.15^{NS}	-0.10^{NS}	-0.11^{NS}	-0.11^{NS}	-0.20^{*}
HND	0.51^{**}	0.24^{NS}	0.27^{NS}	0.49^{**}	0.43^{**}	0.58^{**}	0.42^{**}	0.52^{**}	0.32^{**}
GC_r	0.30^{**}	0.75^{**}	0.45^{*}	-0.06^{NS}	0.23^{NS}	0.35^{**}	0.09^{NS}	0.18^{*}	0.29^{**}
GC_m	0.47^{**}	0.47^{*}	0.39^{*}	0.29^{NS}	0.33^{**}	0.38^{**}	0.35^{**}	0.37^{**}	0.49^{**}
SC_m	0.26^{**}	0.00^{NS}	-0.07^{NS}	0.34^{*}	0.18^{NS}	0.19^{*}	0.09^{NS}	0.14^{*}	0.26^{**}
n =	368-569	15-21	20-38	20-44	40-82	115-177	97-153	212-330	101-136

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
LUS	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
TIP	-0.29^{**}	-0.13^{NS}	-0.17^{NS}	-0.13^{NS}	-0.28^{*}	-0.16^{*}	-0.30^{**}	-0.22^{**}	-0.33^{**}
COT	-0.18^{**}	-0.40^{NS}	0.11^{NS}	0.07^{NS}	0.04^{NS}	0.02^{NS}	-0.04^{NS}	0.00^{NS}	-0.04^{NS}
SOU	-0.00^{NS}	0.19^{NS}	-0.22^{NS}	-0.04^{NS}	-0.11^{NS}	0.08^{NS}	0.11^{NS}	0.07^{NS}	-0.02^{NS}
HND	-0.29^{**}	-0.17^{NS}	-0.16^{NS}	0.09^{NS}	-0.11^{NS}	0.01^{NS}	-0.07^{NS}	-0.01^{NS}	-0.35^{**}
GC_r	-0.31^{**}	-0.13^{NS}	0.00^{NS}	-0.01^{NS}	-0.12^{NS}	-0.16^{*}	-0.02^{NS}	-0.02^{NS}	-0.40^{**}
GC_m	-0.49^{**}	-0.33^{NS}	-0.30^{NS}	-0.30^{*}	-0.41^{**}	-0.32^{**}	-0.22^{**}	-0.26^{**}	-0.41^{**}
SC_m	-0.26^{**}	0.21^{NS}	0.42^{**}	0.49^{**}	0.34^{**}	-0.18^{*}	-0.06^{NS}	-0.13^{*}	-0.17^{*}
n =	366-568	15-21	20-38	20-44	40-82	113-176	97-153	210-329	101-136

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								

TIP	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
COT	0.25^{**}	0.34^{NS}	0.41^{*}	-0.07^{NS}	0.16^{NS}	0.22^{**}	0.24^{**}	0.23^{**}	0.08^{NS}
SOU	-0.19^{**}	0.03^{NS}	0.03^{NS}	0.06^{NS}	0.04^{NS}	-0.04^{NS}	-0.21^{**}	-0.11^{NS}	-0.23^{**}
HND	0.25^{**}	0.21^{NS}	0.05^{NS}	0.16^{NS}	0.17^{NS}	0.11^{NS}	0.14^{NS}	0.12^{*}	0.35^{**}
GC_r	0.13^{*}	0.60^{*}	-0.15^{NS}	-0.32^{NS}	-0.13^{NS}	0.10^{NS}	0.02^{NS}	0.05^{NS}	0.22^{*}
GC_m	0.25^{**}	0.38^{NS}	0.11^{NS}	0.17^{NS}	0.24^{*}	0.18^{*}	0.16^{*}	0.17^{**}	0.34^{**}
SC_m	0.16^{**}	-0.10^{NS}	0.20^{NS}	-0.17^{NS}	0.04^{NS}	0.11^{NS}	0.14^{NS}	0.12^{*}	0.06^{NS}
n =	365-567	15-21	19-37	20-44	39-81	113-176	97-153	210-329	101-136

TABLE 4.3: (continued)

TRAIT	GENOTYPE								

COT	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
SOU	-0.09^{*}	-0.05^{NS}	-0.25^{NS}	-0.19^{NS}	-0.22^{*}	0.04^{NS}	-0.03^{NS}	0.01^{NS}	-0.21^{*}
HND	0.48^{**}	0.48^{*}	0.42^{*}	0.66^{**}	0.56^{**}	0.40^{**}	0.47^{**}	0.43^{**}	0.48^{**}
GC_r	0.19^{**}	0.59^{*}	0.08^{NS}	-0.34^{NS}	-0.05^{NS}	0.06^{NS}	0.17^{NS}	-0.12^{NS}	0.23^{**}
GC_m	0.35^{**}	0.39^{NS}	0.48^{**}	0.21^{NS}	0.34^{*}	0.20^{**}	0.31^{**}	0.25^{**}	0.37^{**}
SC_m	0.22^{**}	0.17^{NS}	0.33^{*}	0.18^{NS}	0.26^{*}	0.19^{*}	0.13^{NS}	0.16^{**}	0.11^{NS}
n =	365-567	15-21	19-37	20-44	39-81	113-176	97-153	210-329	101-136

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
SOU	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
HND	-0.28^{**}	0.04^{NS}	-0.31^{NS}	-0.56^{**}	-0.45^{**}	-0.24^{**}	-0.21^{*}	-0.23^{**}	-0.36^{**}
GC_r	0.05^{NS}	0.35^{NS}	0.00^{NS}	-0.17^{NS}	-0.09^{NS}	0.08^{NS}	-0.25^{**}	-0.10^{NS}	0.04^{NS}
GC_m	-0.15^{**}	-0.07^{NS}	-0.35^{*}	-0.24^{NS}	-0.27^{*}	-0.14^{NS}	-0.12^{NS}	-0.13^{*}	-0.26^{**}
SC_m	-0.06^{NS}	0.41^{NS}	-0.45^{**}	-0.06^{NS}	-0.25^{*}	0.01^{NS}	-0.10^{NS}	-0.03^{NS}	-0.06^{NS}
n =	366-568	15-21	20-38	20-44	40-82	113-176	97-153	210-329	101-136

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
HND	TOTAL	R	SFM	LM	SFM+LM	SFMxR	LMxR	SFMR+LMR	BX
GC_r	0.35^{**}	0.46^{NS}	0.68^{**}	-0.53^{*}	0.31^{*}	0.14^{NS}	0.26^{**}	0.20^{**}	0.42^{**}
GC_m	0.52^{**}	-0.01^{NS}	0.75^{**}	0.32^{*}	0.52^{**}	0.42^{**}	0.36^{**}	0.40^{**}	0.58^{**}
SC_m	0.26^{**}	0.27^{NS}	0.35^{*}	0.18^{NS}	0.27^{*}	0.15^{NS}	0.10^{NS}	0.13^{*}	0.17^{NS}
n =	537-569	15-21	20-38	20-44	40-82	144-177	97-153	211-330	101-136

* $p<0.05$
** $p<0.01$
NS not significant

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
GC_r	TOTAL	R	SFM	LM	SFM+LM	SFM×R	LM×R	SFMR+LMR	BX
GC_m	0.45^{**}	0.33^{NS}	0.71^{**}	-0.12^{NS}	0.39^{*}	0.29^{**}	0.29^{**}	0.30^{**}	0.49^{**}
SC_m	0.43^{**}	0.51^{NS}	0.18^{NS}	0.03^{NS}	0.12^{NS}	0.38^{**}	0.49^{**}	0.44^{**}	0.46^{**}
n =	358–367	15	20	20	40	112–114	94–97	206–211	97–101

TABLE 4.3: (continued)

TRAIT	GENOTYPE								
GC_m	TOTAL	R	SFM	LM	SFM+LM	SFM×R	LM×R	SFMR+LMR	BX
SC_m	0.38^{**}	0.13^{NS}	0.28^{NS}	0.17^{NS}	-0.09^{NS}	0.32^{**}	0.36^{**}	0.33^{**}	0.33^{**}
n =	537–569	20–21	34–38	40–44	74–82	167–177	145–153	313–330	130–136

* $p<0.05$
** $p<0.01$
NS not significant

There was a low negative correlation (-0.16 to -0.35^{**}), between S/P and primary density for all genotypes. This pattern also held for primary density corrected for skin shrinkage. There was no consistent pattern for CF and S/P. The low negative correlation in the total data set indicates less skin shrinkage in the higher S/P groups perhaps due to the reduced connective tissue in these skin types (Carter and Clarke, 1957a).

It appeared that as liveweight increased, S/P decreased slightly. The correlation was significant ($p<0.01$) in the total data set only.

S/P was poorly correlated with CFW and GFW in all groups except the SFM where the S/P x GFW correlation was 0.33^{**}.

In the total data set S/P and MFD were negatively correlated (-0.69^{**}), reflecting the higher S/P and finer diameter associated with Merino ancestry. Within parental genotypes the correlation was lower and it was significant only in the combined Merino data.

For the total data set, QN_r and QN_m had correlations of similar magnitude but opposite sign to those with mean fibre diameter. The within genotype correlations were inconsistent and the significant negative correlation of S/P and QN_r in the Superfine Merinos is difficult to explain.

There were negative correlations between S/P and both SL_r and SL_m, the lowest in the total and SFM data sets.

The correlation between S/P and TCN was moderate, positive and significant ($p<0.01$) in the total data set but was low and generally non-significant within genotypes. The correlations of S/P with CHR_r and CHR_m tended to be low and positive but were often non-significant.

There was a moderately high negative significant correlation between LUS and S/P for the total data set, reflecting the greater lustre associated with Romney genes but the correlation was not significant within genotypes.

Greasy colour, as assessed on both the Ruakura and Massey scales, was positively and significantly associated with S/P in the total data set, probably as a result of the whiteness of Merino wool. Within genotypes the correlations were usually low positive and non-significant.

As expected, the highest, most significant correlations were between S/P and total follicle density. The other traits most highly correlated with S/P were: MFD, LWT, CFW, QN, and SL.

4.2.2.2 ln S/P

The level and sign of the correlations between ln S/P and fleece and follicle characteristics were similar to those discussed between S/P and these traits. There was a slightly higher correlation between ln S/P and fibre diameter.

4.2.2.3 Total Density

With the exception of the total data set, the correlations between $n(P+S)corr$ and $n(P+S)$ were moderate, ranging from 0.53^{**} to 0.74^{**}. The correlation in the total data set between these two traits (0.41^{**}) was surprisingly low. Other evidence cast considerable doubt on the usefulness of using CF applied to individual observations. Individual correction factors often seemed to be acting as random variables.

Correlations between nP and $n(P+S)$ ranged from 0.22^{**} to 0.59^{**}, the lowest correlation occuring in the total data set. Since nP is a component of $n(P+S)$ the degree of association might be expected. However $n(P+S)$ was more closely associated with another component S/P which seemed a more important determinant, particularly when variation between breeds was involved. The lower correlations with nP may reflect greater errors in determining nP. Carter and Clarke (1957a) rechecked their data because of doubts about their classification of primary follicles in the Merino. Their original classification of follicles as primaries or secondaries was confirmed.

The Tokanui Merino flocks, especially the crossbreds, have become larger framed animals (J.L. Dobbie, personal communication). As liveweight increases the skin expands and total density is expected to decrease; hence the negative correlations with liveweight across genotypes (the highest being -0.48^{**} in the total data set).

There was a negative correlation between GFW and $n(P+S)$ in the total data set. Within most genotypes the correlation was low, negative and non-significant. However in Romneys the correlation of $n(P+S)$ with GFW was moderate and positive. In view of the fact that follicle and fibre number is a component of fleece weight this negative association is rather surprising but it is perhaps due to the association between liveweight and wool growth.

The correlation between MFD and total follicle density ranged from -0.27^{NS} to -0.69^{**} across groups, indicating that as the number of follicles increased, average fibre diameter decreased. The relationships between n(P+S) and MFD were very similar but often slightly stronger than those between S/P and MFD.

The correlations between total follicle density and QN_r, QN_m for the total data set were 0.57^{**} and 0.67^{**} respectively. This positive relationship held for most genetic groups but was far lower.

SL_r and SL_m tended to decrease as total density increased, reflecting the smaller fibres produced when density is high. However, the correlations were not significant within genotypes.

TCN increased with total follicle density, the association being stronger across genotypes and within crossbred genotypes. Both CHR_r and CHR_m increased with n(P+S). Denser fibres should give a better defined staple crimp.

4.2.2.4 Total Follicle Density (corrected for skin shrinkage)

With the exception of the shrinkage correction factor (CF), the relationships between n(P+S)corr and follicle and fleece characterisitics were weaker than those beween these traits and uncorrected total follicle density.

4.2.2.5 Primary Follicle Density

There was a low negative correlation between primary density and both liveweight and fleeceweight for all genotypes. For most genotypes, the low negative correlation between primary density and mean fibre diameter was non-significant, the exceptions being the BX (-0.26^{**}) and (SFMR+LMR) (-0.18^{*}) genotypes.

Mixed results were noted for the correlations between both QN_r, QN_m and nP (see Tables 4.2 - 4.3). Both measures of staple length (SL_r and SL_m) were positively correlated with primary density. The correlations between primary density and the other traits measured were low and mainly non-significant.

4.2.2.6 Primary Follicle Density (corrected for skin shrinkage)

MFD and LWT were more highly correlated with nP(corr) than with uncorrected primary density. This suggests that the CF is more strongly influenced by these factors. All other correlations resembled those between uncorrected primary follicle density and the various fleece and follicle traits.

4.2.2.7 Skin Shrinkage Correction Factor (CF)

CF was negatively correlated; -0.28^{**}, with both QN_r and QN_m. SL_r and SL_m were each positively correlated with the skin shrinkage coefficient; (total data set, 0.29^{**}, 0.27^{**}).

LUS had low positive correlations with CF in all genotypes but these were significant in the SFM (0.48^{**}) and total data (0.26^{**}) sets only.

As the correlations between CF and other traits were low and often non-significant they will not be discussed.

4.2.2.8 Liveweight

There were moderately high, positive correlations between LWT and both GFW and CFW. Those between GFW and LWT ranged from 0.31^{**} to 0.60^{**}.

The correlations between QN_r, QN_m and LWT for the total data set were -0.60^{**} and -0.51^{**} respectively. They ranged from 0.00 to -0.66^{*} between the genotype groups. This supports the general conclusion that animals with higher quality numbers have lower liveweights e.g., Merinos.

There was a correlation of 0.55^{**} between fibre diameter and LWT in the total data set. The relationship between these traits in the other groups was also positive, suggesting that fibre diameter increases with increasing liveweight.

In the total data set both SL_r, SL_m and LWT were positively correlated at 0.41^{**} and 0.45^{**}. This was expected as GFW, of which staple length is a major component, was positively correlated with liveweight.

The only significant correlation between LWT and TCN (-0.41**) was in the total data set.

Although LUS and LWT were positively correlated in most data sets, the correlations were only significant in the total and SFM+LM combined genotypes (p<0.01).

LWT was negatively correlated with GC_r, GC_m and SC_m, in the total data set, at similar levels. Although often non-significant, the correlations between LWT x GC_r and LWT x GC_m, were similar across genotypes.

4.2.2.9 Fleeceweight

For the most part, GFW and both QN_r and QN_m were moderately negatively correlated (p<0.01; see Tables 4.2 - 4.3).

Both SL_r and SL_m were positively correlated with GFW. In the crossbreds the correlations ranged from 0.20 to 0.50 (p<0.01).

The negative correlation between TCN and GFW suggests that more highly crimped fleeces have lower weights.

With the exception of the R and SFM genotype groups, there was a consistent positive correlation between LUS and GFW, with values of 0.29** and 0.25** for the SFMxR and LMxR groups.

The correlations between GFW and the 3 colour grades were consistently negative and often not significant.

Fibre diameter and fleeceweight were moderately correlated: 0.34** (SFMR); 0.34** (LMxR); 0.48** (BX); 0.52** (Total); 0.71** (LM).

The results indicate that SL, MFD and LUS all increase with increasing GFW while QN and TCN decline.

4.2.2.10 Clean Fleeceweight

The correlations between CFW and the various traits were similar to those for GFW.

4.2.2.11 Yield

There were negative correlations between YLD and QN_r in most groups, with the only significant correlation occurring in the total data set (-0.22^{**}). This negative trend also occurred with QN_m. Several of the within genotype correlations were significant.

SL_r and SL_m were both positively correlated with YLD. SL_m showed a more consistent relationship across genotypes.

For most data sets, GC_r was positively correlated with YLD ($p<0.01$), the exceptions being the Romneys (-0.25^{NS}) and Local Merinos (-0.15^{NS}). The relationship between SC_m and YLD was less consistent and often non-significantly negative.

The only genotype in which YLD was not positively correlated with MFD was the Superfine Merino group (-0.31^{NS}).

4.2.2.12 Mean Fibre Diameter

MFD was negatively correlated with both QN_r and QN_m. The values ranged from 0.04 to 0.78, but were greater and more significant ($p<0.01$), in the numerically larger groups.

The relationships between SL_r, SL_m and MFD were mainly positive, with the exception of the non-significant negative correlations between SL_r and MFD in the Merino genotypes.

The MFD x TCN correlations were negative ($p<0.05$ or $p<0.01$). The correlation was non significant in the SFM data set.

There was a tendency for both CHR_r and CHR_m to be negatively correlated with MFD, but the correlations were mainly low and non-significant.

MFD and LUS were positively correlated, the most significant correlations being those in the total (0.63^{**}); SFMR+LMR (0.24^{*}) and BX (0.31^{**}) data sets.

All three colour grades were negatively correlated with MFD, (i.e., finer fleeces were whiter), the level and significance of the correlation varying between genotypes.

4.2.2.13 Quality Number

There was generally a positive relationship (p<0.01) between QN_r and QN_m. The only exception being the SFM and LM groups, where the correlations were negative or low positive and non-significant.

For most classes, the correlations between both SL_r, SL_m and QN_r, QN_m were negative (p<0.01). In the crossbreds the correlations (QN_mxSL_r; QN_mxSL_m), ranged from -0.22^{**} to -0.40^{**}. The correlations between QN_r and TCN ranged from 0.02^{NS} to 0.73^{**} across groups. TCN and QN_m were positively correlated; the only non-significant correlation occurred in the LM group.

The QN_r x CHR_m, QN_r x CHR_r, QN_m x CHR_r and QN_m x CHR_m correlations varied with the data set, being highest in the total and lowest in the SFM. This may indicate a difference in QN assessment depending on fleece type and assessor.

The relationship between QN_r and LUS was generally negative and significant at p<0.01 in the groups with larger numbers of animals. The only exceptions to this pattern for QN_m were the Romneys and Superfine Merinos.

There were positive correlations between QN_r and all three estimates of fleece colour for all data sets except the SFM and SFM+LM. A similar pattern was noted between QN_m and the colour grades.

4.2.2.14 Staple Length

The correlations between SL_r and SL_m ranged from 0.52^{*} to 0.90^{**}, the lower estimates coming from data sets where there were few observations.

With the exception of the SFM and LM groups, the correlation between TCN and SL_r was negative. In contrast, the relationship between SL_m and TCN was not consistent: -0.45^{**} and -0.59^{**} in the total and the Romney data sets, while the SFMxR, LMxR and BX groups had correlations ranging from 0.01 to 0.02.

There were moderately high, positive correlations between LUS and both SI_r and SL_m. The correlations between SL_r and each of GC_r, GC_m and SC_m, were low and varied between data sets. With the exception of the correlation between SC_m and SL_m in the total data set (-0.31**), most of the correlations between SL_m and each of GC_r, GC_m, and SC_m were low and non-significant.

4.2.2.15 Total Crimp Number

There was generally a low positive correlation between TCN and both CHR_r and CHR_m. LUS and TCN were negatively correlated in all genotypes with the correlations ranging from -0.15^{NS} to -0.57**. The correlations between each of the colour grades and TCN were low to moderately positive, and generally non-significant.

4.2.2.16 Character Grade

CHR_r and CHR_m were only moderately correlated. The correlation between LUS and CHR_r varied between data sets being negative in all except the LM, SFMxR, and SFMR+LMR groups. CHR_m and LUS were negatively correlated. For most data sets the correlations were low and non-significant.

Both character grades generally had modest positive correlations with HND. There was a consistent pattern of low to moderate positive correlation between both CHR_r, CHR_m and all of the colour grades for all data sets. Many of the correlations were significant (see Tables 4.2 - 4.3).

4.2.2.17 Lustre Grade

The relationships between lustre and the three colour grades tended to be negative apart from non-significant positive correlations in the small Romney group.

4.2.2.18 Greasy Colour

The correlations between GC_r and GC_m were low and positive. This indicates high between operator variation in subjective assessment of colour.

The correlation between GC_m and SC_m varied widely from (-0.17^{NS} (LM) to 0.43^{**} (Total)) between data sets. This suggests that there may be differences in the accuracy of predicting scoured colour from greasy colour depending on the fleece type. SC_m tended to be slightly more highly correlated with GC_r than GC_m.

4.2.3 Discussion

The correlations between S/P and n(P+S) in this study were higher than those of Ross, Cockrem and Wickham (unpublished) 0.53; Nay and Hayman (1969) 0.46^{***}; and Jackson et al (1975) 0.48^{**}. The values for the crossbreds (0.63^{**} to 0.69^{**}) were similar to those obtained for Corriedales (0.807^{**}), Polwarths (0.702^{**}), and Australian Merinos (0.635^{*}) by Arbiza et al, (1966). Steinhagen et al (1984; 1986) reported higher correlations between S/P and n(P+S) of 0.98^{**} and 0.97^{**}. Secondary follicle numbers are important in determining follicle density.

Both Gregory (1982b) and Steinhagen et al (1986) reported negative correlations between S/P and nP (-0.46; -0.49^{***}). The relationship between these traits in this study was much lower.

LWT x S/P correlations were low in the present study. Similar results have been reported (-0.05), by Nay and Hayman (1969) and (0.00), by Gregory (1982b). The major justification of using S/P rather than n(P+S) in follicle population studies is that it is less affected by short-term environmental factors.

The poor correlations between S/P and both GFW and CFW noted in this study are supported by Nay and Hayman (1969), Jackson et al (1975), and Gregory (1982 b) who obtained correlations of 0.010 and 0.14, 0.17 and 0.15, and 0.14 respectively.

Studies using Merinos (Nay and Hayman, 1969; Jackson et al, 1975; Gregory, 1982b) reported negative correlations between S/P and MFD (-0.39^{***}, -0.25^{**} and -0.23^{***} respectively). These were lower than those obtained in the present project but indicate that as S/P increases MFD decreases, more follicles producing finer fibres.

The low relationship between QN and S/P found in this study was supported by Gregory (1982b) who obtained a correlation of 0.03 between these traits.

The negative correlations obtained in the present study between S/P and SL were similar to those of Jackson et al (1975); (-0.14^{**}) and Steinhagen et al (1986); (-0.68^{*}).

The low positive (often non-significant) correlations observed between S/P and both TCN and CHR were similar to those found by Jackson et al (1975) and Gregory (1982b).

The correlations between n(P+S) and nP in this study resembled those of Steinhagen et al(1984); 0.34 and Gregory (1982b); 0.55. nP contributes significantly to n(P+S).

The correlations between n(P+S) and both GFW and CFW in the current work were in line with those of other authors (Nay and Hayman, 1969; Jackson et al, 1975; and Gregory, 1982b). Only Steinhagen et al (1984), who studied very few animals, reported a lower correlation (-0.84[**]) between CFW and n(P+S).

The range of correlations between n(P+S) and MFD noted in the present study agrees with that reported by other workers: -0.34 (Nay and Hayman, 1969); -0.39 (Jackson et al, 1975); -0.65 (Steinhagen et al, 1986).

The low negative correlations of both GFW and CFW with nP have also been observed by Gregory (1982b; GFW x nP, -0.13[**]; CFW x nP, -0.08[**]). Gregory (1982b) also found a low negative correlation between MFD and nP: -0.12[**]. It appears that in breeds with Merino ancestry, nP has little influence on fleeceweight and fibre diameter. The negative relationship probably reflects the fact that adverse environments tend to lower fleece weight and body size, the body size change inducing higher nP.

The positive correlations between LWT and both GFW;CFW are in line with those reported by Morley, (1955); Nay and Hayman (1969); Rae (1982) and Gregory (1982b). These indicate a concomitant increase between both GFW, CFW and LWT and that heavier animals produce more wool. Liveweight seems to have a lesser effect on nP than on n(P+S) but an alternative explanation is that n(P+S) can be estimated more reliably and thus there is a smaller proportion of uncontrolled variation.

Nay and Hayman (1969) reported a correlation between SL and LWT of 0.31[**], while those of Morley (1951; 1955) and Sumner (1969) ranged from 0.10 to 0.12 and 0.09 to 0.17. The current relationships are higher, suggesting that heavier sheep produce longer fleeces.

Both Nay and Hayman (1969) and Sumner (1969) reported low positive correlations between LWT and MFD. The present correlations, although positive, were much higher, indicating that fibre diameter increases concurrently with liveweight.

The moderate positive correlations between both GFW; CFW and MFD recorded by Sumner (1969) and Mullaney et al (1970) agree with the increase in MFD with increasing fleeceweight reported in the present study. The negative correlations noted between GFW and QN were in accord with those of Mullaney et al (1970) and Gregory (1982b).

The positive correlations between SL and GFW and CFW agree with the results of Nay and Hayman (1969); Sumner (1969); Mullaney et al (1970) and Gregory (1982b).

The low variable nature of the within-group correlations between MFD and SL agree with those of Nay and Hayman (1969) and Mullaney et al (1970). The stronger correlation in the total data set is probably a reflection of the longer staples of the coarser woolled Romneys and crossbreds. As also noted by Mullaney et al (1970), the relationship between QN and SL, although negative, was stronger.

Both CHR_r and CHR_m tended to be positively correlated with SL_r, but at low levels. This pattern was noted for CHR_r and CHR_m and SL_m with the exception of the R and total data sets, where these traits were positively correlated.

4.3 GENETIC CORRELATIONS

4.3.1 Method of Analysis

Genetic correlations were estimated from a data file in which dam (P) and daughter (O) records had been matched together. Covariances from a product-moment correlation programme were used to derive the genetic correlations as:

$$r_{gxy} = \frac{\text{cov } P_x O_y + \text{cov } P_y O_x}{2\sqrt{\text{cov } P_x O_x * \text{cov } P_y O_y}}$$

The standard errors of the genetic correlations were calculated using the method of Falconer (1981) adapted from Reeve(1955) and Robertson(1959):

$$\text{S.E.} \approx \frac{1 - r_g^2}{\sqrt{2}} \sqrt{\left[\frac{\sigma h_x \sigma h_y}{h^2_x h^2_y} \right]}$$

Covariances for various genotypes were pooled in different ways to produce a series of estimates (Turner and Young, 1969; Becker, 1984).

4.3.2 Results

Genetic correlations, some using data corrected for age, year sampled and birth/rearing rank and others uncorrected for these fixed effects, are given in Tables 4.4 - 4.5. The combined genotypes for both data sets have also been adjusted for genotype. Estimates from data sets with very few dam/daughter pairs have not been tabulated.

TABLE 4.4: Genetic correlations calculated for fleece and follice traits using daughter/dam pairs corrected for age, year sampled and birth/rearing rank

Trait	Genotype	Total[1]	SFMxR	LMxR	SFMR+LMR[1]
S/P					
ln S/P		0.97±0.024	0.97±0.051	1.00±0.000	0.99±0.013
n(P+S)		0.73±0.185	0.54±0.366	0.78±0.163	0.73±0.183
n(P+S)corr		a	0.95±0.079	>1.00	>1.00
nP		-0.08±0.300	0.11±0.472	0.20±0.493	0.24±0.400
nP(corr)		a	0.52±0.775	a	a
LWT		-0.23±0.481	0.39±0.427	0.38±0.634	0.30±0.393
GFW		-0.17±0.394	0.13±0.578	>1.00	0.61±0.362
CFW		0.10±0.370	a	>1.00	>1.00
YLD		a	>1.00	0.86±0.200	>1.00
MFD		-0.28±0.343	>1.00	-0.70±0.265	0.15±0.514
QN_m		0.75±0.224	0.36±0.577	0.40±0.392	0.35±0.257
SL_m		-0.56±0.198	>1.00	-0.02±0.413	-0.68±0.184
TCN		-0.21±0.467	-0.41±0.462	>1.00	0.41±0.303
CPC		0.11±0.425	0.85±0.207	>1.00	0.89±0.109
n=		140-200	53-71	31-51	26-122
ln S/P					
n(P+S)		0.80±0.118	0.45±0.370	0.78±0.330	0.73±0.160
n(P+S)corr		a	0.87±0.177	>1.00	>1.00
nP		-0.03±0.284	0.01±0.430	0.19±0.432	0.23±0.352
nP(corr)		a	0.43±0.138	a	a
LWT		0.13±0.470	0.50±0.340	0.29±0.591	0.32±0.340
GFW		0.11±0.377	0.22±0.503	>1.00	0.54±0.358
CFW		0.05±0.350	0.73±0.267	>1.00	>1.00
YLD		a	>1.00	0.78±0.261	>1.00
MFD		-0.25±0.328	>1.00	-0.54±0.454	0.08±0.458
QN_m		a	0.22±0.567	0.41±0.338	0.32±0.493
SL_m		-0.61±0.170	<-1.00	-0.12±0.355	-0.53±0.215
TCN		0.06±0.458	-0.43±0.408	>1.00	0.32±0.343
CPC		0.47±0.349	0.30±0.609	>1.00	0.70±0.234
n=		140-200	53-71	31-51	85-122

[1] Data combined and corrected for genotype

TABLE 4.4:   continued

Trait	Genotype	Total[1]	SFMxR	LMxR	SFMR+LMR[1]
n(P+S)					
n(P+S)corr		>1.00	>1.00	>1.00	>1.00
nP		0.68±0.123	0.89±0.054	0.79±0.111	0.84±0.071
nP(corr)		a	1.00	a	a
LWT		-0.37±0.333	-0.11±0.271	0.51±0.314	0.06±0.245
GFW		-0.13±0.303	0.24±0.301	>1.00	0.71±0.163
CFW		0.27±0.263	>1.00	>1.00	>1.00
YLD		0.45±0.286	0.80±0.164	0.77±0.178	0.77±0.143
MFD		-0.57±0.191	0.19±0.478	-0.43±0.242	-0.21±0.287
QN_m		-0.01±0.389	-0.04±0.360	-0.09±0.265	-0.11±0.251
SL_m		-0.08±0.218	0.34±0.226	0.47±0.283	0.03±0.195
TCN		-0.02±0.371	0.36±0.263	0.64±0.214	0.37±0.215
CPC		0.05±0.361	0.68±0.218	0.11±0.628	0.39±0.254
n=		140-200	53-71	31-51	84-122
n(P+S)corr					
nP		>1.00	>1.00	0.20±0.489	0.71±0.182
nP(corr)		a	0.84±0.267	a	a
LWT		a	-0.29±0.393	0.80±0.264	0.18±0.361
GFW		a	0.43±0.782	>1.00	>1.00
CFW		a	0.90±0.103	>1.00	>1.00
YLD		a	>1.00	>1.00	>1.00
MFD		a	-0.57±0.525	-0.02±0.327	-0.32±0.408
QN_m		a	0.41±0.470	-0.07±0.460	0.19±0.370
SL_m		a	-0.06±0.399	0.43±0.334	0.11±0.292
TCN		a	0.11±0.468	0.43±0.513	0.14±0.369
CPC		a	0.26±0.592	0.04±0.537	0.15±0.443
n=		138-200	53-71	31-51	84-122
nP					
nP(corr)		>1.00	>1.00	a	a
LWT		-0.23±0.318	-0.37±0.219	0.64±0.309	-0.11±0.264
GFW		0.30±0.244	0.23±0.281	>1.00	0.71±0.177
CFW		0.58±0.164	0.43±0.262	>1.00	0.83±0.117
YLD		0.38±0.267	0.09±0.417	0.82±0.177	0.37±0.389
MFD		-0.48±0.190	-0.30±0.418	-0.31±0.332	-0.37±0.281
QN_m		-0.57±0.229	-0.01±0.334	-0.35±0.289	-0.23±0.261
SL_m		0.51±0.141	0.36±0.206	0.83±0.091	0.59±0.138
TCN		-0.03±0.323	0.52±0.204	-0.05±0.447	0.28±0.249
CPC		-0.31±0.285	0.36±0.327	-0.67±0.211	-0.12±0.320
n=		140-200	43-71	31-51	84-122

[1] Data combined and corrected for genotype

TABLE 4.4: continued

Trait	Genotype	Total[1]	SFMxR	LMxR	SFMR+LMR[1]
LWT					
GFW		-0.12±0.445	0.26±0.291	-0.44±1.020	0.00±0.000
CFW		-0.05±0.415	0.06±0.337	-0.37±1.100	-0.11±0.379
YLD		0.07±0.524	-0.04±0.443	0.27±0.722	0.00±0.000
MFD		0.04±0.414	-0.09±0.480	-0.25±0.496	-0.23±0.314
QN_m		0.39±0.483	0.49±0.298	0.55±0.056	0.55±0.195
SL_m		-0.42±0.264	-0.39±0.212	-0.04±0.420	-0.33±0.192
TCN		0.74±0.246	0.30±0.269	>1.00	0.45±0.219
CPC		0.62±0.327	0.73±0.185	0.54±0.391	0.65±0.191
n=		105-133	47-53	22-31	61-78
GFW					
CFW		0.96±0.026	0.99±0.008	0.97±0.127	0.98±0.200
YLD		0.58±0.278	0.75±0.224	>1.00	0.80±0.186
MFD		0.28±0.305	-0.19±0.545	0.06±0.988	-0.09±0.439
QN_m		-0.56±0.312	-0.08±0.408	-0.97±0.053	-0.45±0.298
SL_m		0.58±0.170	0.39±0.247	0.59±0.513	0.46±0.227
TCN		-0.58±0.288	-0.25±0.323	<-1.00	-0.53±0.264
CPC		-0.82±0.139	-0.57±0.312	<-1.00	-0.84±0.130
n=		138-149	53-55	32-38	85-92
CFW					
YLD		0.79±0.145	0.85±0.150	>1.00	0.93±0.074
MFD		0.46±0.240	-0.37±0.528	0.81±0.308	0.12±0.460
QN_m		-0.56±0.288	-0.06±0.610	<-1.00	-0.63±0.238
SL_m		0.57±0.159	0.38±0.270	>1.00	0.39±0.257
TCN		-0.79±0.150	-0.23±0.353	<-1.00	-0.68±0.208
CPC		-0.89±0.123	-0.49±0.380	<-1.00	-0.96±0.037
n=		136-138	53-54	31-32	84-85
YLD					
MFD		0.25±0.361	-0.28±0.740	0.53±0.393	0.13±0.464
QN_m		0.00±0.000	0.39±0.495	<-1.00	-0.21±0.381
SL_m		0.38±0.225	0.18±0.400	0.83±0.135	0.33±0.273
TCN		-0.40±0.424	-0.08±0.486	<-1.00	-0.33±0.349
CPC		-0.44±0.397	-0.14±0.644	<-1.00	-0.54±0.333
n=		147-149	59	31-32	90-91

[1] Data combined and corrected for genotype

TABLE 4.4: continued

Trait	Genotype	Total[1]	SFMxR	LMxR	SFMR+LMR[1]
MFD					
QN_m		-0.90±0.079	-0.67±0.351	-0.51±0.247	-0.57±0.230
SL_m		0.29±0.216	0.73±0.211	-0.32±0.265	0.12±0.259
TCN		-0.92±0.061	<-1.00	<-1.00	<-1.00
CPC		-0.91±0.067	<-1.00	-0.93±0.052	<-1.00
n=		150-151	60	33	93
QN_m					
SL_m		-0.70±0.165	-0.20±0.260	-0.51±0.196	-0.37±0.191
TCN		>1.00	0.94±0.045	0.51±0.301	0.77±0.115
CPC		>1.00	>1.00	0.81±0.120	>1.00
n=		158	60	38	98
SL_m					
TCN		0.21±0.295	0.49±0.209	0.12±0.355	0.33±0.194
CPC		-0.63±0.182	-0.23±0.349	-0.84±0.091	-0.49±0.609
n=		159	60	38	98
TCN					
CPC		0.62±0.314	0.74±0.197	0.52±0.345	0.68±0.179
n=		159	60	38	98

[1] Data combined and corrected for genotype

TABLE 4.5: Genetic correlations for fleece and follicle traits calculated with daughter/dam pairs uncorrected for fixed effects

Trait	Genotype	Total[1]	SFMxR	LMxR	SFMR+LMR[1]
S/P					
ln S/P		0.93±0.057	>1.00	>1.00	>1.00
n(P+S)		0.56±0.192	0.89±0.203	0.75±0.281	0.80±0.201
n(P+S)corr		>1.00	>1.00	>1.00	>1.00
nP		0.18±0.295	0.98±0.033	0.21±0.721	0.58±0.383
nP(corr)		a	1.00	a	a
LWT		a	0.04±a	0.38±1.098	a
GFW		-0.27±0.863	-0.98±0.042	a	0.19±0.936
CFW		0.93±0.125	a	>1.00	a
YLD		>1.00	a	a	a
MFD		-0.52±0.233	a	a	a
QN$_m$		>1.00	a	>1.00	a
SL$_m$		-0.06±0.353	a	>1.00	a
TCN		0.34±0.410	a	>1.00	a
CPC		0.12±0.465	a	>1.00	a
n=		140-200	53-71	31-51	26-122
ln S/P					
n(P+S)		0.59±0.169	0.55±0.449	0.74±0.228	0.67±0.224
n(P+S)corr		>1.00	>1.00	>1.00	>1.00
nP		0.14±0.337	0.48±0.423	0.21±0.566	0.39±0.356
nP(corr)		a	>1.00	a	a
LWT		a	0.83±a	0.25±a	a
GFW		0.37±0.526	-0.41±0.576	a	0.45±0.563
CFW		>1.00	>1.00	>1.00	>1.00
YLD		>1.00	a	a	a
MFD		-0.50±0.222	a	-0.96±0.045	-0.30±0.443
QN$_m$		>1.00	a	>1.00	>1.00
SL$_m$		0.04±0.328	a	0.79±0.314	0.07±0.460
TCN		0.58±0.285	a	>1.00	>1.00
CPC		0.34±0.386	a	>1.00	1.00±a
n=		140-200	53-71	31-51	85-122

[1] Data combined and corrected for genotype

TABLE 4.5: continued

Trait	Genotype	Total[1]	SFMxR	LMxR	SFMR+LMR[1]
n(P+S)					
n(P+S)corr		>1.00	>1.00	>1.00	>1.00
nP		0.86±0.049	>1.00	0.84±0.094	0.95±0.022
nP(corr)		a	>1.00	a	a
LWT		a	0.03±a	0.23±0.516	a
GFW		0.88±0.091	0.03±0.348	a	0.94±0.044
CFW		>1.00	>1.00	a	>1.00
YLD		>1.00	>1.00	>1.00	>1.00
MFD		-0.67±0.108	-0.30±0.374	-0.46±0.242	-0.41±0.216
QN_m		0.74±0.168	0.18±0.488	0.43±0.237	0.32±0.265
SL_m		0.49±0.159	0.07±0.282	0.98±0.018	0.31±0.223
TCN		0.61±0.178	0.55±0.233	0.99±0.075	0.64±0.149
CPC		0.19±0.278	0.59±0.264	0.24±0.292	0.44±0.221
n=		140-200	53-71	31-51	84-122
n(P+S)corr					
nP		0.70±0.181	>1.00	0.32±0.636	0.88±0.074
nP(corr)		a	>1.00	a	a
LWT		a	a	0.23±1.140	a
GFW		>1.00	0.10±0.410	a	>1.00
CFW		a	0.92±0.088	a	>1.00
YLD		>1.00	>1.00	>1.00	>1.00
MFD		-0.94±0.043	-0.66±0.276	-0.59±0.443	-0.60±0.243
QN_m		0.85±0.196	-0.23±0.568	>1.00	0.07±0.428
SL_m		>1.00	0.10±0.324	>1.00	0.62±0.222
TCN		0.86±0.140	0.28±0.367	>1.00	0.56±0.252
CPC		0.10±0.542	0.20±0.461	0.33±0.610	0.20±0.385
n=		140-200	53-71	31-51	84-122
nP					
nP(corr)		a	>1.00	a	0.88±a
LWT		a	a	0.38±0.547	a
GFW		>1.00	0.51±0.220	a	>1.00
CFW		>1.00	0.72±0.198	a	>1.00
YLD		>1.00	0.45±0.587	>1.00	>1.00
MFD		-0.62±0.131	-0.53±0.252	-0.30±0.356	-0.49±0.204
QN_m		-0.45±0.325	0.11±0.425	-0.14±0.335	-0.01±0.355
SL_m		0.67±0.131	0.36±0.210	>1.00	0.59±0.166
TCN		0.26±0.289	0.66±0.161	-0.14±0.433	0.39±0.220
CPC		-0.11±0.312	0.51±0.255	-0.62±0.224	0.08±0.281
n=		140-200	43-71	31-51	84-122

[1] Data combined and corrected for genotype

TABLE 4.5:   continued

Trait	Genotype	Total[1]	SFMxR	LMxR	SFMR+LMR[1]
LWT					
GFW		a	-0.71±a	-1.00	-1.00
CFW		a	a	-1.00	-1.00
YLD		a	a	a	
MFD		a	a	-0.13±0.603	
QN_m		a	a	0.34±0.650	
SL_m		a	a	a	
TCN		a	a	0.56±0.740	
CPC		a	a	0.27±0.701	
n=		105-133	47-53	22-31	61-78
GFW					
CFW		>1.00	0.99±0.010	<-1.00	0.96±0.088
YLD		-0.51±1.803	0.37±0.801	a	0.10±1.188
MFD		0.19±0.443	-0.01±0.442	0.06±a	-0.10±0.446
QN_m		-1.39±0.743	-0.17±0.526	<-1.00	-0.47±0.398
SL_m		0.68±0.275	0.63±0.184	>1.00	0.63±0.258
TCN		-0.25±0.626	-0.14±0.353	<-1.00	-0.17±0.424
CPC		-0.71±0.337	-0.70±0.222	<-1.00	-0.69±0.249
n=		138-149	53-55	32-38	85-92
CFW					
YLD		<-1.00	0.40±1.079	a	-0.30±1.874
MFD		0.90±0.123	-0.02±0.617	a	0.40±0.650
QN_m		-0.82±0.404	-0.15±0.733	a	<-1.00
SL_m		>1.00	0.72±0.203	a	>1.00
TCN		<-1.00	-0.31±0.450	a	<-1.00
CPC		<-1.00	-0.93±0.081	a	<-1.00
n=		136-138	53-54	31-32	84-85
YLD					
MFD		0.31±1.067	-0.34±0.969	0.85±0.383	0.07±0.823
QN_m		>1.00	>1.00	a	0.00±a
SL_m		a	-0.13±0.742	a	0.64±0.463
TCN		a	0.05±0.889	a	-0.64±0.473
CPC		a	0.23±1.02	a	-0.81±0.300
n=		147-149	59	31-32	90-91

[1] Datacombined and corrected for genotype

TABLE 4.5: continued

Trait	Genotype	Total[1]	SFMxR	LMxR	SFMR+LMR[1]
MFD					
QN_m		<-1.00	-0.93±0.087	-0.95±0.031	-0.94±0.041
SL_m		0.18±0.240	0.46±0.284	-0.49±0.387	0.14±0.289
TCN		-0.92±0.050	-0.96±0.033	<-1.00	-0.98±0.020
CPC		-0.84±0.097	<-1.00	-0.87±0.085	<-1.00
n=		150-151	60	33	93
QN_m					
SL_m		-0.50±0.354	-0.31±0.398	-0.35±0.423	-0.32±0.300
TCN		>1.00	>1.00	>1.00	>1.00
CPC		>1.00	>1.00	0.85±0.092	>1.00
n=		158	60	38	98
SL_m					
TCN		0.20±0.346	0.47±0.228	-0.47±0.486	0.25±0.268
CPC		-0.54±0.259	-0.24±0.216	-0.97±0.030	-0.47±0.327
n=		159	60	38	98
TCN					
CPC		0.71±0.237	0.74±0.189	0.81±0.147	0.75±0.139
n=		159	60	38	98

[1] Data combined and corrected for genotype

4.3.2.1   S/P

There were high positive correlations between S/P and n(P+S) for all data sets for both models, (0.54 to 0.89); the correlations being greater in the uncorrected model. This confirms that the genes controlling S/P also affect n(P+S). A similar pattern was observed for log transformed S/P although the correlations were slightly lower (0.45 to 0.80).

The relationship between S/P and nP was less consistent; ranging from -0.08 to 0.24 for the data sets corrected for fixed effects (CFE), to 0.18 to 0.98 for the data sets uncorrected for fixed effects (UFE). If the 0.98 estimate is ignored this suggests S/P and nP are influenced by different genetic factors.

With the exception of the total data set corrected for fixed effects, the correlations between LWT and S/P were negligible to low (0.04 to 0.39). A similar pattern was seen in ln S/P x LWT correlations.

The correlations between S/P and GFW in the total data sets for both models, were negative (-0.27, -0.23 (CFE) while those using the SFMR+LMR data sets were positive (0.19 and 0.61 (CFE)). The correlations between GFW and ln S/P were more consistent and i.e., 0.88, 0.11 [total, total(CFE)]; 0.94, 0.54 [SFMR+LMR, SFMR+LMR(CFE)]. Most correlations between S/P and CFW were > 1.0 or inestimable and will not be discussed.

The correlations between MFD and both S/P and ln S/P ranged from -0.25 to -0.96, indicating that the genes increasing S/P make MFD finer. The correlations of QN with S/P and ln S/P suggest a similar effect.

The relationships of both S/P and ln S/P with TCN were low. The correlations of S/P and ln S/P with CPC were consistently positive ranging from 0.11 to 1.00.

In the larger combined genotypes there were negative correlations of both S/P and ln S/P with SL. The data corrected for fixed effects gave consistently better results.

4.3.2.2 Total Density

The correlations between n(P+S) and nP were consistently high and positive (0.68 to 1.00).

For the uncorrected model with the larger data sets (Total; SFMR+LMR), the correlations between n(P+S) and GFW were 0.88 and 0.94. These contrasted with those for the same data sets for the corrected model (-0.13 and 0.71).

With the exception of the SFMxR genotype in the corrected model, all correlations between n(P+S) and MFD were moderately negative (-0.30 to -0.67). The correlations between SL and n(P+S) for both models and all data sets were inconsistent and ranged from: 0.08 to 0.98. From the relationship noted between n(P+S) and MFD where n(P+S) decreased with increasing MFD, one would have expected a similar result between n(P+S) and SL. The low numbers of SL observations may explain the current results.

Both TCN and CPC were generally positively correlated with n(P+S). When all data sets were corrected for fixed effects the correlations between these traits were less consistent and in one case a slightly negative correlation was obtained.

4.3.2.3 Primary Density

The correlations of GFW and CFW with nP for both models were mainly positive (see Tables 4.4 - 4.5). The nP x MFD correlations were consistently negative (-0.30 to -0.62). This pattern is similar to that noted with the phenotypic correlations. SL_m and nP were positively correlated within and across data sets for both models.

4.3.2.4 Liveweight

The dramatic improvement in the correlations between LWT and other fleece characteristics when data were corrected for fixed effects, indicates the effect that environmental factors have on LWT.

Both LWT x GFW and LWT x CFW correlations were variable ranging from: -0.44 to 0.26. There was a non-significant trend for a decrease in MFD as LWT increased.

When data were corrected for fixed effects, the correlations between LWT and QN_m were moderately positive (0.39 to 0.55). The correlations between LWT and SL_m were negative (-0.39 to -0.59) in contrast to the phenotypic correlations which were positive. This suggests that environmental factors can override the negative genetic relationship between these traits.

There was a consistent pattern of negative correlation of both TCN and CPC with LWT, suggesting that genes for greater liveweight are associated with less well crimped fleeces. (see Tables 4.4 - 4.5).

4.3.2.5 Fleeceweight

The correlations between GFW and MFD were variable; more consistently positive correlations were obtained between CFW and MFD (see Tables 4.4 - 4.5). Both GFW and CFW were positively correlated with SL_m for all data sets in both models (0.38 to 1.00).

The relationships between both GFW and CFW with both TCN and CPC, for the uncorrected and corrected data sets, were consistently negative indicating that the genes controlling fleeceweight act in an opposite manner on crimp frequency.

4.3.2.6 Fibre Diameter

As expected the relationship between QN_m with MFD was negative (-0.19 to -1.00). The correlations between MFD and SL tended to be positive but varied between data sets (see Tables 4.4 - 4.5). For all the data sets, the correlations between MFD and both TCN and CPC were moderately negative (-0.23 to -1.00).

4.3.2.7 Quality Number

The correlations between SL_m and QN_m tended to be negative. The correlations between QN and both TCN and CPC were variable.

4.3.2.8 Staple Length

There was a trend for SL_m to be positively correlated with TCN but negatively correlated with CPC. TCN and CPC were positively correlated.

4.3.3 Discussion

Low numbers of daughter/dam pairs limit the accuracy of the genetic correlations calculated in this study. This is reflected in the large number of correlations outside the -1.0 to 1.0 range. The standard errors of the present correlations are also relatively high.

The high positive correlations between S/P and n(P+S) were greater than those of Abouhief (1980), lower than that of Gregory (1982b) (1.00), but close to those of Jackson et al (1975) and Mortimer (1987).

Earlier workers (Carter and Clarke, 1957a, b), have indicated that between-breed variation in follicle density is largely due to the S/P ratio. The current genetic correlations nP x n(P+S) suggest that within Merino x Romney sheep the number of follicle groups per unit area is just as important genetically. The significant positive relationship between n(P+S) and nP agreed with the findings of Abouhief (1980) and Gregory (1982b). These results indicate that the genes controlling nP also affect n(P+S).

Rendel and Nay (1978) selected up and down for both S/P and nP. They found that the high S/P lines had low nP and vice versa. They suggested that the two traits were inter-related. The current genetic correlations are at variance but the phenotypic correlations are in line, with those reported. This may reflect genetic differences between the flocks studied (Merinos vs. crossbreds) and/or fewer animals examined over a shorter time.

The inverse relationships noted between S/P and both MFD and SL agreed with the S/P x MFD; S/P x SL correlations of: -0.45^{**}; -0.27^{**} (Jackson et al, 1975) and -0.20^{*}; -0.17 (Gregory, 1982b). Rendel and Nay (1978) reported similar results. Within the current genotype range, sheep with higher S/P ratios should have finer shorter fleeces. Genes which increase S/P appear to decrease MFD and SL.

From the correlations between ln S/P x GFW and those between S/P and both MFD and SL in the crossbreds, genetic increases in the progeny's GFW appear to be due to increases in follicle numbers.

Heydenrych et al (1975, cited by Heydenrych et al, 1984) and Heydenrych et al (1984); obtained realized genetic correlations of 0.37 and 0.34 between S/P and CFW. A larger increase in CFW was obtained through selection for CFW rather than selection for S/P.

The authors of the
study suggested that plane of nutrition also interacted with genetic factors controlling CFW, such that sheep with high S/P ratios expressed their genetic potential for wool production only under adequate nutritional conditions.

The n(P+S) x GFW correlation for the Total(CFE) data set (-0.13) was in line with that of Jackson et al (1975) (-0.12). The high positive correlations between n(P+S) and GFW, for the crossbred combined genotypes, contrast with that of Jackson et al (1975) -0.12 and were slightly greater than that of Gregory (1982b) 0.24[*]. This may indicate genotype differences between Merino x Romneys and Merinos and/or problems of low numbers of dam/daughter pairs in the present work.

The moderate negative correlations between n(P+S) and MFD are as expected and most are only slightly lower than those of Jackson et al (1975) -0.66[**] and Gregory (1982b) -0.56[***].

For n(P+S) x SL, the low number of observations for SL gave an inconsistent pattern of relationship. Jackson et al (1975) obtained a correlation of -0.20[**] and Gregory (1982b) -0.28[*]. One would expect the genetic factors influencing n(P+S) to act antagonistically towards both MFD and SL. This suggests that the genes controlling increases in follicle numbers also affect follicle output.

The positive correlation between SL_m and nP was in line with that reported by Rendel and Nay (1978). This suggests that different genetic factors may influence the follicle output of primaries rather than the total follicle population.

Rendel and Nay (1978) found that low nP and low S/P lines produced the heaviest fleeces. Within the low nP lines, the best wool producers had high S/P ratios. The present positive correlations between nP and both GFW and CFW agree with their results. They contrast with those of Gregory (1982b) who reported low non-significant negative correlations between nP and both GFW and CFW. Rendel and Nay (1978) suggested that selection for nP and S/P in combination would lead to increased GFW whereas selection for one or the other would not.

Since the relationships of both S/P and In S/P with CPC were consistently positive and significant, it seems that the genes controlling S/P also influence CPC. Jackson et al (1975) also noted a positive genetic correlation (0.22[**]) between these traits.

The pattern of relationship between QN and n(P+S) was not consistent. n(P+S) x QN correlations were positive when the data were uncorrected for fixed effects and negative in the corrected data. Gregory (1982b) obtained a correlation of -0.08 between QN and n(P+S).

The variability of the LWT x GFW and LWT x CFW correlations coincides with those reported by Morley (1951; 1955) -0.11 to 0.24. Gregory (1982b) reported correlations of -0.03 (LWT x GFW) and -0.04 (LWT x CFW). In a recent review, Williams (1987), suggested that the genetic correlation between LWT and GFW was 0.00, e.g., factors controlling LWT acted independently of GFW. This conclusion is in contrast with the results of J.L. Dobbie, (personal communication), who obtained LWT x GFW and LWT x CFW genetic correlations of 0.70 and 0.66 respectively, using Merino flocks from which the present study animals were obtained.

The positive correlations observed for GFW and CFW with SL were in line with, but slightly higher than, those of Mullaney et al (1970). The present CFW x MFD correlations agree with this study. The genetic correlations between GFW and CFW with MFD of 0.52 and -0.16 reported by J.L. Dobbie (personal communication) for the Tokanui Merino flocks, contrast markedly with the present results. It seems that the genetic factors influencing fleeceweight may do so with concomitant increases in MFD and SL.

The moderate negative correlations of GFW and CFW with TCN and CPC agree with the findings of Mullaney et al (1970). Similar patterns were noted in both studies between MFD and TCN and CPC. The results indicate that the genes controlling GFW act in the opposite manner on MFD; TCN and CPC.

It seems that the genes affecting QN and MFD also affect TCN, and CPC. For most data sets the correlations were moderately positive, indicating some common genetic pathways between the two traits. The genetic correlations between MFD x QN were negative but lower than those of MFD with TCN and CPC. These results contrast with those of Gregory (1982b) who found negative correlations between CPC and both QN and MFD.

The present QN x SL correlations tended to be negative but were in line with the moderately to highly negative correlations reported by Mullaney et al (1970) and Lewer et al (1983).

The results of the present study suggest that in these flocks there may have been some selection for crimp. This could have occurred through indirect selection of sheep for fleeces of good character grade.

The present genetic correlations suggest that sheep with genes for high S/P will produce progeny with finer, shorter, well crimped fleeces. The main increase in fleeceweight in these sheep is through increases in follicle numbers (primary and secondary) and not in output per follicle.

The genes controlling CFW may act through or on MFD, SL and CPC, such that genetic increases in MFD and SL and decreases in CPC will be associated with increased CFW. At the follicle level, and by a separate pathway to that above, the genes controlling CFW may act to increase follicle output of longer, straighter, coarser fibres.

Genetic correlations can be highly changeable, both between environments within breeds and between breeds within environments. Due to the methods used to calculate genetic correlations, a low h^2 estimate for one trait tends to inflate the genetic correlations between this characteristic and others. Given the low heritability estimates obtained for some traits under discussion (see Tables 4.6 - 4.7) this could explain some of the variability associated with the present genetic correlation estimates. Genetic correlations may also alter under selection (Turner and Young, 1969). For the above reasons, and due to the low numbers of daughter/dam pairs in the present study, the genetic correlations should be treated with caution.

4.4 HERITABILITIES

4.4.1 Method of Analysis

The heritabilities of several follicle traits and fibre diameter were calculated using dam/daughter regression. Two data sets were used: 1. Uncorrected data and 2. Data corrected for age, year sampled and birth/rearing rank.

Only the Total, SFMR+LMR, SFMxR and LMxR data sets had sufficient numbers of daughter/dam pairs for the results to be given any credence. The first two classes have been pooled and corrected for genotype. The heritability estimates are shown in Tables 4.6 to 4.7.

TABLE 4.6: Estimates of heritability based on daughter/dam regressions using data corrected for age, year sampled and birth/rearing rank

Trait	Total*	S.E.	n	SFMxR	S.E.	n	LMxR	S.E.	n	SFMR+LMR*	S.E.	n
S/P	0.24	0.155	200	0.24	0.322	71	0.27	0.278	51	0.22	0.213	122
ln S/P	0.24	0.137	200	0.26	0.282	71	0.33	0.258	51	0.25	0.186	122
n(P+S)	0.48	0.179	200	0.99	0.393	71	1.00	0.337	51	0.84	0.265	122
n(P+S)corr	0.00	0.165	200	0.24	0.234	71	0.29	0.293	51	0.25	0.181	122
nP	0.51	0.144	200	0.74	0.252	71	0.62	0.318	51	0.54	0.201	122
nP(corr)	0.00	0.143	200	0.12	0.202	71	0.00	0.289	51	0.00	0.167	122
CF	0.00	0.165	200	0.00	0.246	71	0.00	0.389	51	0.00	0.207	122
LWT	0.20	0.160	140	0.59	0.223	53	0.39	0.416	31	0.52	0.200	84
GFW	0.29	0.148	184	0.53	0.273	65	0.09	0.270	47	0.28	0.192	112
CFW	0.37	0.160	138	0.47	0.284	53	0.11	0.337	32	0.28	0.214	85
YLD	0.26	0.179	148	0.33	0.343	59	0.34	0.387	32	0.33	0.257	91
MFD	0.40	0.172	153	0.25	0.310	61	0.68	0.357	34	0.41	0.234	95
QN_m	0.18	0.146	158	0.38	0.249	60	0.43	0.182	38	0.40	0.163	98
SL_m	0.54	0.139	159	0.72	0.237	60	0.80	0.265	38	0.73	0.176	98
TCN	0.20	0.148	159	0.56	0.258	60	0.40	0.313	38	0.51	0.200	98
CPC	0.25	0.176	159	0.38	0.314	60	0.60	0.343	38	0.42	0.238	98
CHR_m	0.00	0.145	160	0.00	0.252	61	0.17	0.356	38	0.00	0.204	99
LUS	0.16	0.115	159	0.00	0.187	60	0.31	0.164	38	0.14	0.126	98
TIP	0.21	0.149	159	0.02	0.248	60	0.57	0.304	38	0.26	0.192	98
COT	0.08	0.134	159	0.30	0.246	60	0.00	0.252	38	0.19	0.180	98
SOU	0.05	0.134	159	0.30	0.203	60	0.00	0.255	38	0.14	0.158	98
HND	0.00	0.135	160	0.17	0.195	61	0.46	0.334	38	0.22	0.173	99
GC_m	0.06	0.169	160	0.00	0.276	61	0.88	0.266	38	0.15	0.204	99
SC_m	0.09	0.190	147	0.38	0.319	60	0.10	0.400	30	0.25	0.245	90

*Data have been combined and adjusted for genotype

TABLE 4.7: Estimates of heritability based on daughter/dam regressions using uncorrected data

Trait	Total*	S.E.	n	SFMxR	S.E.	n	LMxR	S.E.	n	SFMR+LMR*	S.E.	n
S/P	0.24	0.155	200	0.08	0.334	71	0.14	0.300	51	0.11	0.224	122
ln S/P	0.26	0.144	200	0.16	0.290	71	0.20	0.264	51	0.18	0.194	122
n(P+S)	0.88	0.213	200	1.00	0.458	71	1.00	0.386	51	1.00	0.307	122
n(P+S)corr	0.20	0.174	200	0.38	0.246	71	0.16	0.302	51	0.29	0.190	122
nP	0.55	0.159	200	0.82	0.293	71	0.61	0.324	51	0.64	0.209	122
nP(corr)	0.00	0.141	200	0.05	0.202	71	0.00	0.293	51	0.00	0.168	122
CF	0.00	0.166	200	0.00	0.209	71	0.00	0.313	51	0.00	0.205	122
LWT	0.00	0.191	140	0.00	0.285	53	0.27	0.415	31	0.00	0.232	84
GFW	0.12	0.161	183	0.61	0.323	65	0.00	0.275	47	0.24	0.222	111
CFW	0.06	0.159	139	0.28	0.284	54	0.68	0.333	34	0.08	0.218	86
YLD	0.02	0.177	148	0.10	0.325	59	0.05	0.389	32	0.08	0.249	91
MFD	0.53	0.167	153	0.41	0.303	61	0.68	0.333	34	0.51	0.224	95
QN_m	0.11	0.126	158	0.21	0.233	60	0.46	0.202	38	0.29	0.164	98
SL_m	0.38	0.148	159	0.72	0.252	60	0.27	0.286	38	0.48	0.190	98
TCN	0.23	0.153	157	0.54	0.264	60	0.45	0.330	38	0.50	0.206	98
CPC	0.25	0.172	158	0.45	0.321	60	0.66	0.328	38	0.49	0.240	98
CHR_m	0.00	0.145	160	0.00	0.230	61	0.30	0.335	38	0.00	0.188	99
LUS	0.08	0.108	159	0.06	0.184	60	0.24	0.180	38	0.14	0.130	98
TIP	0.14	0.138	159	0.04	0.252	60	0.32	0.313	38	0.17	0.194	98
COT	0.12	0.150	159	0.43	0.242	60	0.00	0.262	38	0.28	0.181	98
SOU	0.00	0.135	159	0.23	0.219	60	0.00	0.224	38	0.06	0.158	98
HND	0.07	0.159	160	0.30	0.215	61	0.46	0.420	38	0.30	0.196	99
GC_m	0.17	0.171	160	0.00	0.280	61	0.85	0.252	38	0.21	0.202	99
SC_m	0.11	0.182	148	0.31	0.310	60	0.00	0.393	38	0.09	0.241	90

*Data have been combined and adjusted for genotype

Heritabilities were estimated by the daughter/dam regression method. The equation used to derive the heritability estimates was:

$$h^2 = \frac{2cov_{DO}}{\sigma^2_D}$$

Where: D = Dam; O = Offspring

cov_{DO} = the covariance of dam and offspring
values for each trait

σ^2_D = the variance of the dam
records for that trait

Only estimates obtained using data sets with a minimum of 50 daughter-dam pairs have been reported.

4.4.2 Results

Tables 4.6 - 4.7 contain heritability estimates using data corrected and uncorrected for fixed effects. As a consequence of the low numbers of daughter/dam pairs in all data sets, the estimates of h^2 have high standard errors.

Heritability estimates of S/P ranged from 0.08 to 0.24 and (0.22 to 0.27)CFE) across genotypes, with the most reasonable estimates obtained using SFMxR and LMxR group data sets corrected for fixed effects. The ln S/P estimates ranged from 0.16 to 0.26. For the data sets corrected for fixed effects, the estimates of h^2 using ln S/P were more consistent than those for S/P.

In contrast, both total and primary follicle density had high h^2 estimates for both data sets: 0.48 to 1.00. The estimates for h^2 of nP were lower than those for n(P+S): (0.51 to 0.82) vs. (0.48 to 1.00).

Using follicle densities corrected for skin shrinkage gave drastically reduced heritability estimates (0.00 to 0.29). The h^2 estimates for the shrinkage correction factor were 0.00, indicating that the variation in skin shrinkage does not have a genetic basis within broad genetic groupings or, the correction factors may have been too inaccurate to reveal it. Application of correction factors had many of the consequences to be expected if data items were multiplied by a random variable.

The heritability estimates for LWT were moderately high in the crossbreds ranging from 0.39 to 0.52. With the exception of the LMxR data (CFE), the h^2 estimates for both GFW and CFW were moderate. For these 3 traits data correction for fixed effects gave much higher h^2 estimates.

The components of fleeceweight, showed moderate h^2 estimates, with those for SL_m ranging from 0.54 to 0.80 (CFE) and 0.27 to 0.72 (UFE). The estimates of h^2 for MFD ranged from 0.25 to 0.68; being lower when data corrected for fixed effects were used.

4.4.3 Discussion

Some of the reported h^2 estimates for S/P, obtained using Merinos range from 0.26 to 0.62 (Schinckel, 1958b; Jackson et al, 1975; Heydenrych et al, 1975; 1977; Gregory, 1982a; Mortimer, 1987). Abouhief (1980), using Western cross-breds (U.S.A.), reported h^2 estimates of 0.55 to 0.81. The present results are closer to that reported by Gregory (1982a) (0.26).

Compared with the present estimates, the levels of h^2 noted by other authors for n(P+S) were much lower, ranging from 0.27 to 0.62 (Hancock et al, 1979; Jackson et al, 1975; Abouhief, 1980; Gregory, 1982a; Mortimer, 1987). The increased h^2 estimates could reflect the low number of dam/daughter pairs used and the presence of some animals outside the normal range for this trait.

Abouhief (1980) obtained h^2 estimates for nP of 0.36 to 0.39 depending on the method used. Those obtained by Hancock et al (1979) and Gregory (1982a) were much lower at 0.12 to 0.39 and 0.11 to 0.15 respectively. The differences between the estimates of Hancock et al (1979) and Gregory (1982b) and the estimates of Abouhief (1980) may reflect the breeds used, the former authors studied Australian Merinos while the latter examined Western crossbreds (U.S.A.). The present estimates do not exceed those just mentioned by more than one standard error.

For LWT, Gregory (1982a) obtained h^2 estimates of 0.37 to 0.68 (dam-offspring heritabilities were higher than paternal half-sib). These values are in line with the present results.

Gunawan et al (1985) studied Merino x Border Leicesters and obtained h^2 estimates of 0.06 (GFW), 0.11 (CFW) and 0.07 (SL). Mullaney et al (1970) using Corriedales, Polwarths and Merinos obtained h^2 estimates for of; GFW - 0.14 to 0.51, CFW - 0.28 to 0.50, and SL - 0.31 - 0.51. McGuirk et al (1985) and Gregory (1982a) published h^2 estimates of: 0.30, 0.27 to 0.56 (GFW), 0.25, 0.16 to 0.41 (CFW) and 0.25, 0.42 to 0.88 (MFD). The present estimates are higher than those of Gunawan et al (1985), but similar to the others.

Mullaney et al (1970) reported h^2 estimates for MFD at both 18 and 30 months of age, for three breeds: 0.49, 0.62 (Merinos); 0.44, 0.42 (Corriedales) and 0.53, 0.47 (Polwarths). These estimates were obtained using individual dam/daughter correlations. Other authors using Merinos, have obtained h^2 estimates of MFD of 0.25, (McGuirk et al, 1985), 0.42 to 0.45 (Gregory, 1982a) and 0.52 (Schinckel, 1958b). The present h^2 estimates are within the published range of h^2 estimates for MFD.

Gregory (1982a) compared the h^2 estimates obtained using data corrected and uncorrected for fixed effects. There was no increase in the accuracy of the h^2 estimates using corrected data. In the current study, the standard errors of h^2 estimates were slightly lower for the data corrected for fixed effects.

The results suggest that S/P, n(P+S), nP, GFW, CFW, LWT and MFD are all reasonably heritable. Due to the level of the standard errors of these estimates and the wide range, further conclusions should not be made from these estimates. Also, the h^2 estimates may be higher than expected due to the correction for fixed effects as noted by Turner and Young (1969).

4.5 STEPWISE MULTIPLE REGRESSION

4.5.1 Method of Analysis and Objective

Stepwise multiple regression techniques were used both within and across genotypes to evaluate whether the secondary to primary follicle ratio could be predicted reliably from other measured and/or appraised traits. Both the Minitab and REG computer packages were used for these analyses.

In this section, only animals having complete records for all traits were used. Thus the number of animals per data set was considerably reduced.

4.5.2 Results

4.5.2.1 Total Data Set (n = 464)

The most significant single factor in the prediction of S/P and ln S/P was mean fibre diameter.

$$S/P = 33.2 - 0.777 \text{ MFD} \quad (R^2 = 51.0\% \quad S.D. = 3.307)$$
$$\ln S/P = 4.11 - 0.0620 \text{ MFD} \quad (R^2 = 56.5\% \quad S.D. = 0.236)$$

This equation was extended to include other fleece factors which could be easily measured or assessed. The inclusion of liveweight increased the R^2 to 52.5% and 57.8% respectively for S/P and ln S/P. Table 4.8 shows the effect of including additional independent variables in the multiple regression model to predict S/P and ln S/P.

The regression equations including fixed effects were as follows:

$$S/P = 20.5 + 0.263 \text{ AGE} + 1.17 \text{ YRSAMP} - 0.626 \text{ BRR} - 0.136 \text{ LWT} + 2.06 \text{ GFW}$$
$$+ 0.142 \text{ QN}_m - 0.314 \text{ SL}_m - 0.594 \text{ MFD}$$

$$(R^2 = 60.5\% \quad S.D. = 2.99)$$

$$\ln S/P = 3.41 + 0.0074 \text{ AGE} + 0.0092 \text{ YRSAMP} - 0.0402 \text{ BRR} - 0.0086 \text{ LWT} + 0.162 \text{ GFW}$$
$$+ 0.0075 \text{ QN}_m - 0.0034 \text{ SL}_m - 0.050 \text{ MFD}$$

$$(R^2 = 65.9\% \quad S.D. = 0.211)$$

Equations without fixed effects were:

$$S/P = 22.0 - 0.113 \text{ LWT} + 2.07 \text{ GFW} + 1.36 \text{ QN}_m - 0.333 \text{ SL}_m - 0.607 \text{ MFD}$$

$$(R^2 = 58.5\% \quad S.D. = 3.06)$$

$$\ln S/P = 3.64 - 0.008 \text{ LWT} + 0.166 \text{ GFW} + 0.006 \text{ QN}_m - 0.035 \text{ SL}_m - 0.053 \text{ MFD}$$

$$(R^2 = 64.4\% \quad S.D. = 0.215)$$

Table 4.8: Effect of including additional independent variables
            in the multiple regression model to predict S/P and ln S/P

Independents	S/P		lnS/P	
	$R^2(\%)$	SD	$R^2(\%)$	SD
MFD	51.0	3.31	56.5	0.236
Above + LWT	52.5	3.26	57.8	0.233
Above + GFW	55.8	3.15	61.4	0.223
Above + QN_m	57.4	3.09	62.3	0.221
Above + SL_m	58.5	3.06	64.4	0.215
Above + Fixed Effects[*]	60.5	2.99	65.9	0.211

[*] Fixed effects were - Age, year sampled and birth/rearing rank.

Table 4.9: Effect of including additional independent variables
            in the equation to predict S/P or ln S/P

Independents	S/P		ln S/P	
	$R^2(\%)$	SD	$R^2(\%)$	SD
MFD	17.6	2.50	17.8	0.221
Above + LWT	20.8	2.45	21.3	0.217
Above + GFW	24.6	2.40	25.5	0.211
Above + QN_m	24.6	2.40	25.5	0.212
Above + SL_m	28.0	2.35	29.8	0.206
Above + Fixed Effects[*]	31.0	2.31	33.7	0.201

[*] Fixed effects were - Age, year sampled and birth/rearing rank.

In comparing the two sets of equations, the inclusion of fixed effects only improved R^2 for each equation respectively by 2.0% and 1.5%. This suggests that little would be lost by ignoring the fixed effects.

In comparing the equations created using S/P or ln S/P, the equations with ln S/P consistently gave higher R^2 and lower standard deviations.

The standard error of a predicted dependent value for an individual at the mean is the following:

$$SE_{\hat{y}} = s_{y.x} * SQRT(1 + 1/n)$$

For example, the 95% confidence interval for predicting an individual's S/P at the mean in the last two equations would be ± 5.89 and ± 2.40 for S/P and ln S/P respectively. From these results, it seems that in a flock of mixed genotypes, the accuracy of predicting S/P would be very low.

4.5.2.2 SFMR+LMR Data Set (n = 275)

Stepwise Multiple Regression techniques were also used with the combined halfbred (SFMR+LMR), data set to estimate both S/P and ln S/P. Table 4.9 contains the results of these analyses.

As with the Total data set, MFD was the most significant factor in predicting both S/P and ln S/P.

S/P = 3.36 - 0.036 MFD   (R^2 = 17.8% SD = 0.221)
ln S/P = 22.1 - 0.400 MFD   (R^2 = 17.6% SD = 2.495)

The R^2 was higher and the SD lower, in the equation using S/P instead of ln S/P.

The additions of LWT to the equations in Table 4.9 gave an increase in their respective R^2, of 3.2% and 3.5%. Including both LWT and GFW further lifted the R^2 to 24.6% for S/P and 25.5% for ln S/P. The addition of QN_m to these equations did not alter their R^2 values.

SL_m improved both predictive equations by 3.4% (S/P) and 4.4% (ln S/P).

The benefits of the inclusion of fixed effects in the latter equations were tested.

$$S/P = 26.8 - 0.188 \, AGE + 0.324 \, YRSAMP - 0.443 \, BRR - 0.056 \, LWT + 1.24 \, GFW$$
$$- 0.041 \, QN_m - 0.324 \, SL_m - 0.417 \, MFD$$

$$(R^2 = 31.0\% \quad SD = 2.31)$$

$$\ln S/P = 3.71 - 0.017 \, AGE + 0.059 \, YRSAMP - 0.044 \, BRR - 0.052 \, LWT + 0.117 \, GFW$$
$$- 0.003 \, QN_m - 0.032 \, SL_m - 0.037 \, MFD$$

$$(R^2 = 31.0\% \quad SD = 0.201)$$

The equations without fixed effects were only slightly improved.

$$S/P = 26.9 - 0.074 \, LWT + 1.32 \, GFW - 0.035 \, QN_m - 0.349 \, SL_m - 0.424 \, MFD$$

$$(R^2 = 28.0\% \quad SD = 2.349)$$

$$\ln S/P = 3.79 - 0.007 \, LWT + 0.126 \, GFW - 0.003 \, QN_m - 0.034 \, SL_m - 0.038 \, MFD$$

$$(R^2 = 31.0\% \quad SD = 0.206)$$

The R^2 calculated with the combined half-bred data set, for all equations and both S/P and ln S/P are lower R^2. The accuracy of predicting an individual at the mean using these last 2 equations and the formula explained above for S/P was ± 4.536 and for ln S/P ± 2.40.

4.5.3 Conclusion

Using the Total data set, an equation to predict S/P was determined which had a high R^2 and low SD. An equation containing similar variables but calculated with the pooled halfbred data was more accurate but neither gave very accurate estimation of an individual's S/P ratio. The improvement in accuracy of the predictive equation in the halfbred data set is expected for within genotype analysis.

The results suggest that S/P cannot be predicted with reasonable accuracy in either data set. The higher R^2 obtained with the total data set may reflect the higher variation in this data set and more random factors controlling S/P. The results suggest that if S/P is a desired selection criterion, its prediction rather than determination, although possible from other fleece characteristics would not be very accurate.

4.6 HETEROSIS

4.6.1 Method of Analysis

Hybrid vigour is often defined as the improved performance of the crossbred progeny over the mean of the parents for a given trait. Strictly, it is the difference between the mid-parent value and the F_1 or F_2 mean for a trait and may be negative or positive (Falconer, 1981). It is generally considered that most hybrid vigour arises from the combined action of a number of dominant genes for greater fitness, unfavourable genes tending to be recessive. Breed establishment tends to be associated with increased homozygosity while corssbreds, particulary first crosses, have a high level of heterozygosity and hence beneficial effects from more loci.

If heterosis is due to simple dominance at some or all the loci concerned, then heterosis is proportional to the proportion of heterozygote (heterozygosity) at individual loci. This is the basis of the method of estimating heterosis used. However, interactive effects among loci (epistasis) have been proposed as a cause of failure of the strict proportionality of heterosis and heterozygosis. Several models of epistasis as a component of heterosis have been proposed recently: Dickerson (1969), in terms of "recombination loss", Sheridan (1981), Kinghorn (1982) and Hill (1982). Present data did not permit the use of the epistatic model, due to the complicated nature of the analyses and the nature of the present data, i.e., the parental groups especially the Romneys were not the parents of the crossbreds.

In this project, heterosis was estimated in several ways using means of data uncorrected and corrected for fixed effects (age, year sampled, birth/rearing rank). The means of groups representing the parent breeds were compared with the mean of each generation of the crossbred genotypes. Unfortunately the original parents were dead at the time of starting the study and samples not available.

Methods used to calculate estimates of heterosis:

1. $H_{F1} = \overline{F}_1 - \dfrac{(\overline{R} + \overline{M})}{2}$

Where: H_{F1} = the estimate of heterosis as exhibited by either the first cross SFMxR or LMxR
    group

    $\overline{F}_1$ = the mean value of the F_1 (SFMxR or LMxR) group for a given trait

    $\overline{R}$ = the mean value of the Romneys for a given trait

    $\overline{M}$ = the mean value of either the Superfine Merino or Local Merino group
    for a given trait

2. $H_{F1\text{-}F2} = 2(\overline{F}_2 - \overline{F}_1)$

Where: $H_{F1}\text{-}H_{F2}$ = the heterosis as exhibited by either the F_2 SFMxR or LMxR group. This is
    based on the assumption that the dominance model applies so the heterosis in the
    F_2 is one-half that of the F_1. To equate with the F_1 estimate the value was
    doubled.

    $\overline{F}_1$ and $\overline{F}_2$ = the mean value of a trait for either the F_1 or F_2 groups in either the SFMxR or
    LMxR genotypes

3. $H_{F2\text{-}P} = 2(\overline{F}_2 - \dfrac{(\overline{R} + \overline{M})}{2})$

Where: $F_2\text{-}P$ = the heterosis estimate based on the difference in the mean values for a trait
    between the F_2 and parental groups. Note: each F_3 and F_4 group mean value
    was substituted into the above equation to estimate the heterosis based on the
    difference between the mid-parental group mean and the mean of either the F_3 or F_4
    group in either crossbred genotype. Dominance was assumed, so the estimate was
    doubled.

    $\overline{R}$ = the mean value of the Romney group for a given trait

    $\overline{M}$ = the mean value of either the SFM or LM group for a given trait

4.6.2 Results

The mean values, corrected and uncorrected for fixed effects, of several fleece and follicle traits are contained in Tables 4.10 - 4.13   The estimates of heterosis by different methods are shown in Tables 4.14 - 4.15.

The text will concentrate on those estimates of heterosis calculated using data corrected for fixed effects.

4.6.2.1 Parental vs. F_1; F_2; F_3; F_4

Most estimates of heterosis for follicle traits within and between genotypes were negative (see Tables 4.14 - 4.15).

Moderate levels of negative heterosis were noted for S/P in each generation and each genotype. When heterosis estimates were calculated using ln S/P, the level of heterosis dramatically decreased until it was not significantly different from zero.   This suggests the presence of a scale effect.

In the LMxR animals, estimates of the level of negative heterosis for S/P relative to the parental mean, increased from the F_1 to F_4 generations.

The greatest levels of negative heterosis were noted for n(P+S) in the F_2 to F_4 generations of the LMxR genotype. This pattern was reversed for n(P+S)corr, with both the SFMxR and LMxR genotypes showing positive estimates of heterosis. An effect of environmental noise and not heterosis may have been noted using the uncorrected density data.

The levels of heterosis for both nP and nP(corr) were variable ranging from -0.70 to 1.24 across generations and genotypes. In the SFMxR group, heterosis was consistently positive and in the LMxR group, it was negative.

For both genotypes, there was positive heterosis between the parental groups and each generation for LWT, GFW, TCN, CHR_m, TIP, COT, HND and SC_m.

TABLE 4.10: Means of fleece and follicle traits using data corrected for age, year sampled and birth/rearing rank

Trait	Genotype	(n)	$\frac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
S/P	R	5.55 (52)					
	SFM	19.73 (39)	12.64	10.27 (33)	10.81 (97)	11.28 (56)	10.26 (8)
	LM	19.89 (45)	12.72	10.35 (8)	10.47 (89)	10.59 (63)	9.05 (10)
ln S/P	R	1.74 (52)					
	SFM	2.94 (39)	2.34	2.32 (33)	2.37 (87)	2.42 (56)	2.35 (8)
	LM	2.96 (45)	2.35	2.33 (8)	2.33 (89)	2.35 (63)	2.23 (10)
n(P+S)	R	29.06 (52)					
	SFM	72.71 (39)	50.89	46.52 (33)	49.97 (97)	50.59 (56)	52.43 (8)
	LM	85.72 (45)	57.39	49.40 (8)	46.63 (89)	44.77 (63)	40.06 (10)
n(P+S)corr	R	12.35 (52)					
	SFM	43.81 (39)	28.08	28.51 (33)	29.78 (97)	29.04 (56)	31.72 (8)
	LM	51.79 (45)	32.07	34.74 (8)	32.43 (89)	31.36 (63)	29.26 (10)
nP	R	4.46 (52)					
	SFM	3.55 (39)	4.01	4.02 (33)	4.24 (97)	4.10 (56)	4.65 (8)
	LM	4.09 (45)	4.28	4.33 (8)	4.12 (89)	3.93 (63)	4.11 (10)
nP(corr)	R	2.01 (52)					
	SFM	2.20 (39)	2.11	2.21 (33)	2.25 (97)	2.13 (56)	2.48 (8)
	LM	2.46 (45)	2.24	2.34 (8)	2.20 (89)	2.09 (63)	2.16 (10)

Trait	Genotype	(n)	$\dfrac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
CF	R	0.46 (52)					
	SFM	0.65 (39)	0.56	0.55 (33)	0.54 (97)	0.54 (56)	0.56 (8)
	LM	0.62 (45)	0.54	0.55 (8)	0.54 (89)	0.54 (63)	0.55 (10)
LWT (kg)	R	50.53 (43)					
	SFM	38.67 (33)	44.60	51.44 (23)	49.49 (88)	48.78 (55)	43.32 (8)
	LM	43.36 (41)	46.95	52.94 (3)	53.72 (80)	52.97 (59)	53.96 (10)
GFW (kg)	R	3.64					
	SFM	3.11 (36)	3.38	3.56 (31)	3.60 (80)	3.68 (49)	3.69 (7)
	LM	3.77 (42)	3.71	4.18 (7)	4.19 (88)	4.06 (63)	4.42 (10)
CFW (kg)	R	2.98 (20)					
	SFM	2.17 (34)	2.58	2.53 (33)	2.63 (94)	2.60 (55)	2.58 (8)
	LM	2.67 (40)	2.83	3.01 (6)	2.08 (77)	2.94 (55)	3.15 (9)
YLD (%)	R	75.18 (21)					
	SFM	70.04 (37)	72.61	71.19 (31)	72.33 (83)	71.50 (50)	72.83 (7)
	LM	71.65 (43)	73.42	73.74 (6)	72.98 (77)	72.76 (55)	72.54 (9)
MFD (µm)	R	37.20 (21)					
	SFM	19.86 (37)	28.53	26.09 (31)	25.79 (83)	25.16 (52)	25.36 (8)
	LM	21.72 (43)	29.46	29.42 (7)	28.34 (78)	28.37 (58)	29.28 (9)

TABLE 4.10:   continued

Trait	Genotype	(n)	$\frac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
QN_r	R	46.54 (16)					
	SFM	72.68 (21)	59.61	56.16 (25)	56.46 (71)	56.50 (27)	
	LM	62.98 (20)	54.76	53.73 (3)	55.03 (69)	55.71 (34)	
QN_m	R	47.63 (21)					
	SFM	66.72 (38)	57.18	56.78 (31)	56.57 (86)	57.22 (51)	55.94 (8)
	LM	61.51 (44)	54.57	52.77 (7)	54.61 (80)	54.90 (57)	54.03 (9)
SL_r (cm)	R	13.72 (52)					
	SFM	7.45 (39)	10.59	8.89 (25)	9.44 (71)	9.33 (27)	
	LM	8.54 (20)	11.13	11.13 (3)	10.62 (69)	10.13 (34)	
SL_m (cm)	R	14.02 (21)					
	SFM	7.78 (38)	10.90	9.66 (31)	9.94 (86)	9.75 (51)	10.54 (8)
	LM	8.74 (44)	11.38	10.51 (7)	11.19 (80)	10.56 (57)	10.37 (9)
TCN	R	14.99 (21)					
	SFM	48.07 (38)	31.53	32.52 (31)	32.76 (86)	35.94 (51)	36.05 (8)
	LM	37.74 (44)	26.37	27.31 (7)	28.12 (80)	28.01 (57)	28.82 (9)
CPC	R	1.27 (21)					
	SFM	6.09 (38)	3.68	3.24 (31)	3.20 (86)	3.65 (51)	3.38 (8)
	LM	4.34 (44)	2.81	2.72 (7)	2.61 (80)	2.75 (57)	2.68 (9)

Trait	Genotype	(n)	$\dfrac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
CHR$_r$	R	3.55 (16)					
	SFM	5.38 (21)	4.47	3.74 (25)	3.94 (70)	2.73 (27)	
	LM	5.41 (20)	4.48	3.38 (3)	4.62 (69)	4.38 (34)	
CHR$_m$	R	3.95 (21)					
	SFM	5.71 (38)	4.83	5.08 (33)	5.18 (86)	5.17 (51)	5.36 (8)
	LM	5.53 (44)	4.74	5.27 (7)	5.26 (80)	5.36 (57)	5.50 (9)
LUS	R	6.60 (21)					
	SFM	2.90 (38)	4.75	4.59 (31)	4.55 (86)	4.50 (51)	4.64 (8)
	LM	3.80 (44)	5.20	5.02 (7)	4.90 (80)	4.80 (57)	4.99 (9)
TIP	R	3.90 (21)					
	SFM	5.49 (37)	4.70	5.48 (31)	5.51 (86)	5.45 (51)	5.54 (8)
	LM	5.08 (44)	4.49	5.38 (7)	5.39 (80)	5.62 (57)	5.04 (9)
COT	R	4.91 (21)					
	SFM	5.76 (37)	5.34	5.58 (31)	5.57 (86)	5.54 (51)	5.38 (8)
	LM	5.67 (44)	5.29	5.40 (7)	5.62 (80)	5.59 (57)	5.43 (9)
SOU	R	7.23 (21)					
	SFM	5.85 (38)	6.54	5.16 (31)	5.33 (86)	5.44 (51)	5.87 (8)
	LM	6.09 (44)	6.66	5.32 (7)	5.02 (80)	5.42 (57)	5.59 (9)

Trait	Genotype	$\dfrac{(\bar{R}+\bar{M})}{2}$ (n)	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
HND	R	4.48 (21)				
	SFM	5.89 (38)	5.19	5.11 (32)	5.30 (86)	5.42 (51)	5.23 (8)
	LM	5.50 (44)	4.99	5.26 (7)	5.41 (80)	5.32 (57)	4.77 (9)
GC_r	R	4.57 (15)				
	SFM	6.36 (21)	5.47	4.79 (25)	4.98 (71)	4.90 (27)	
	LM	5.72 (20)	5.15	4.46 (3)	5.13 (69)	5.23 (34)	
GC_m	R	4.22 (21)				
	SFM	6.13 (38)	5.18	4.84 (32)	5.02 (86)	5.07 (51)	5.19 (8)
	LM	5.56 (44)	4.89	4.99 (7)	5.17 (80)	5.03 (57)	4.68 (9)
SC_m	R	4.39 (21)				
	SFM	6.25 (37)	5.32	5.50 (32)	5.49 (85)	5.52 (48)	5.84 (8)
	LM	5.97 (44)	5.18	5.56 (6)	5.47 (76)	5.39 (55)	5.27 (9)

TABLE 4.11: Means of fleece and follicle traits using data uncorrected for age, year sampled and birth/rearing rank (Upper figure of each pair is SFMxR; lower LMxR)

Trait	Genotype	(n)	$\frac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
S/P	R	5.91 (52)					
	SFM	20.39 (39)	13.15	10.68 (33)	10.58 (97)	12.17 (56)	11.70 (8)
	LM	20.56 (45)	13.24	10.67 (8)	10.58 (89)	11.22 (63)	10.45 (10)
ln S/P	R	1.75 (52)					
	SFM	2.98 (39)	2.37	2.33 (33)	2.37 (87)	2.48 (56)	2.46 (8)
	LM	3.00 (45)	2.38	2.33 (8)	2.33 (89)	2.39 (63)	2.34 (10)
n(P+S)	R	31.06 (52)					
	SFM	76.79 (39)	53.93	41.70 (33)	50.75 (97)	57.79 (56)	66.54 (8)
	LM	89.87 (45)	60.47	44.55 (8)	45.93 (89)	50.50 (63)	54.08 (10)
n(P+S)corr	R	13.38 (52)					
	SFM	45.82 (39)	29.60	23.57 (33)	26.74 (97)	28.49 (56)	32.54 (8)
	LM	52.15 (45)	32.77	25.40 (8)	24.29 (89)	25.88 (63)	25.70 (10)
nP	R	4.52 (52)					
	SFM	3.66 (39)	4.09	3.61 (33)	4.27 (97)	4.36 (56)	5.23 (8)
	LM	4.20 (45)	4.36	3.93 (8)	4.05 (89)	4.17 (63)	4.70 (10)
nP(corr)	R	1.95 (52)					
	SFM	2.17 (39)	2.06	2.07 (33)	2.25 (97)	2.19 (56)	2.56 (8)
	LM	2.43 (45)	2.30	2.21 (8)	2.15 (89)	2.15 (63)	2.24 (10)

Trait	Genotype	(n)	$\dfrac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
CF	R	0.43 (52)					
	SFM	0.59 (39)	0.51	0.57 (33)	0.53 (97)	0.51 (56)	0.49 (8)
	LM	0.59 (45)	0.50	0.57 (8)	0.53 (89)	0.52 (63)	0.48 (10)
LWT (kg)	R	50.86 (43)					
	SFM	38.32 (33)	44.59	58.76 (23)	50.03 (88)	45.88 (55)	33.88 (8)
	LM	42.43 (41)	46.65	58.07 (3)	56.57 (80)	50.28 (59)	44.38 (10)
GFW (kg)	R	3.90					
	SFM	3.25 (36)	3.58	3.71 (31)	3.77 (80)	3.79 (49)	3.76 (7)
	LM	3.95 (42)	3.93	4.43 (7)	4.42 (88)	4.19 (63)	4.49 (10)
CFW (kg)	R	3.49 (20)					
	SFM	2.31 (34)	2.90	2.69 (33)	2.91 (94)	2.75 (55)	2.67 (8)
	LM	2.83 (40)	3.16	3.28 (6)	3.67 (77)	3.10 (55)	3.23 (9)
YLD (%)	R	78.33 (21)					
	SFM	70.72 (37)	74.53	71.80 (31)	74.48 (83)	72.78 (50)	72.47 (7)
	LM	72.34 (43)	75.34	74.95 (6)	74.86 (77)	74.43 (55)	72.14 (9)
MFD (μm)	R	37.86 (21)					
	SFM	19.69 (37)	28.78	27.63 (31)	26.73 (83)	25.66 (52)	25.28 (8)
	LM	21.61 (43)	29.74	30.34 (7)	28.62 (78)	28.26 (58)	28.48 (9)

Trait	Genotype	(n)	$\frac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
QN_r	R	46.63 (16)					
	SFM	73.48 (21)	60.06	56.56 (25)	56.97 (71)	56.93 (27)	
	LM	63.40 (20)	55.02	54.33 (3)	55.30 (69)	56.03 (34)	
QN_m	R	46.71 (21)					
	SFM	66.55 (38)	56.63	55.71 (31)	55.90 (86)	56.33 (51)	54.50 (8)
	LM	60.84 (44)	53.78	51.86 (7)	53.73 (80)	53.93 (57)	52.56 (9)
SL_r (cm)	R	14.67 (52)					
	SFM	7.74 (39)	11.21	8.94 (25)	9.71 (71)	9.59 (27)	
	LM	8.98 (20)	11.83	11.17 (3)	11.08 (69)	10.44 (34)	
SL_m (cm)	R	14.81 (21)					
	SFM	8.28 (38)	11.55	9.65 (31)	10.44 (86)	10.19 (51)	11.44 (8)
	LM	9.30 (44)	12.06	10.43 (7)	11.79 (80)	10.98 (57)	12.28 (9)
TCN	R	14.86 (21)					
	SFM	48.82 (38)	31.84	27.68 (31)	30.63 (86)	34.20 (51)	11.44 (8)
	LM	37.77 (44)	23.13	23.57 (7)	27.79 (80)	27.63 (57)	12.28 (9)
CPC	R	1.03 (21)					
	SFM	5.99 (38)	3.51	2.92 (31)	2.98 (86)	3.47 (51)	36.13 (8)
	LM	4.13 (44)	2.58	2.37 (7)	2.39 (80)	2.56 (57)	30.14 (9)

TABLE 4.11:   continued

Trait	Genotype	(n)	$\dfrac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
CHR$_r$	R	3.88 (16)					
	SFM	5.67 (21)	4.78	3.92 (25)	4.14 (70)	3.81 (27)	
	LM	5.65 (20)	4.77	3.67 (3)	4.83 (69)	4.50 (34)	
CHR$_m$	R	4.05 (21)					
	SFM	5.82 (38)	4.94	4.97 (33)	5.30 (86)	5.41 (51)	5.75 (8)
	LM	5.68 (44)	4.87	5.14 (7)	5.38 (80)	5.58 (57)	5.89 (9)
LUS	R	6.95 (21)					
	SFM	2.92 (38)	4.94	4.87 (31)	4.77 (86)	4.69 (51)	4.75 (8)
	LM	3.91 (44)	5.43	5.29 (7)	5.16 (80)	5.02 (57)	5.11 (9)
TIP	R	3.95 (21)					
	SFM	5.43 (37)	4.69	5.35 (31)	5.53 (86)	5.47 (51)	5.50 (8)
	LM	5.02 (44)	4.49	5.29 (7)	5.39 (80)	5.63 (57)	5.00 (9)
COT	R	4.90 (21)					
	SFM	5.84 (37)	5.37	5.58 (31)	5.58 (86)	5.65 (51)	5.63 (8)
	LM	5.77 (44)	5.34	5.43 (7)	5.64 (80)	5.67 (57)	5.67 (9)
SOU	R	6.57 (21)					
	SFM	5.50 (38)	6.04	5.32 (31)	4.71 (86)	4.37 (51)	4.38 (8)
	LM	5.48 (44)	6.03	5.57 (7)	4.48 (80)	4.47 (57)	4.11 (9)

Trait	Genotype	(n)	$\dfrac{(\bar{R}+\bar{M})}{2}$	$\bar{F}_1$ (n)	$\bar{F}_2$ (n)	$\bar{F}_3$ (n)	$\bar{F}_4$ (n)
HND	R	4.76 (21)					
	SFM	6.32 (38)	5.54	5.13 (32)	5.64 (86)	6.03 (51)	6.25 (8)
	LM	6.00 (44)	5.38	5.29 (7)	5.73 (80)	5.86 (57)	5.78 (9)
GC_r	R	3.87 (15)					
	SFM	5.52 (21)	4.82	4.04 (25)	4.23 (71)	4.07 (27)	
	LM	4.90 (20)	4.57	3.67 (3)	4.38 (69)	4.44 (34)	
GC_m	R	4.38 (21)					
	SFM	6.26 (38)	5.32	4.78 (32)	5.19 (86)	5.33 (51)	5.63 (8)
	LM	5.77 (44)	5.08	5.00 (7)	5.31 (80)	5.28 (57)	5.11 (9)
SC_m	R	4.95 (21)					
	SFM	6.41 (37)	5.68	5.69 (32)	5.89 (85)	6.00 (48)	6.13 (8)
	LM	6.23 (44)	5.59	5.83 (6)	5.87 (76)	5.91 (55)	5.56 (9)

TABLE 4.12: Means of fleece and follicle traits using data corrected for age,
year sampled and birth/rearing rank (Upper figure of each pair is
SFMxR; lower LMxR)

Trait	Genotype	(n)	$\dfrac{(\overline{\text{SFM}+\text{SFMxR}})}{2}$	$\bar{B}_1$ (n)	$\bar{B}_2$ (n)	$\bar{B}_3$ (n)
S/P	SFM	19.73 (39)	15.28	15.73 (69)	15.16 (63)	15.59 (5)
	SFMxR	10.83 (194)				
ln S/P	SFM	2.94 (39)	2.66	2.75 (69)	2.69 (63)	2.71 (5)
	SFMxR	2.39 (194)				
n(P+S)	SFM	72.71 (39)	61.19	68.57 (69)	66.86 (63)	76.23 (5)
	SFMxR	49.66 (194)				
n(P+S)corr	SFM	37.05 (39)	33.24	32.60 (69)	31.24 (63)	29.26 (5)
	SFMxR	29.43 (194)				
nP	SFM	3.55 (39)	3.87	4.12 (69)	4.07 (63)	4.50 (5)
	SFMxR	4.18 (194)				
nP(corr)	SFM	2.20 (39)	2.21	2.42 (69)	2.40 (63)	2.27 (5)
	SFMxR	2.22 (194)				
CF	SFM	0.65 (39)	0.60	0.61 (69)	0.61 (63)	0.51 (5)
	SFMxR	0.54 (194)				
LWT (kg)	SFM	38.67 (33)	43.96	43.91 (56)	43.63 (55)	42.82 (5)
	SFMxR	49.24 (174)				
GFW (kg)	SFM	3.11 (36)	3.37	3.28 (68)	3.29 (62)	3.16 (5)
	SFMxR	3.62 (190)				
CFW (kg)	SFM	2.17 (34)	2.39	2.30 (64)	2.32 (61)	2.18 (5)
	SFMxR	2.60 (167)				
YLD (%)	SFM	70.04 (37)	70.97	69.92 (64)	71.35 (62)	69.48 (5)
	SFMxR	71.90 (171)				
MFD (μm)	SFM	19.86 (37)	22.75	22.12 (64)	22.74 (62)	21.08 (5)
	SFMxR	25.64 (174)				
QN_r	SFM	72.68 (21)	64.55	61.46 (68)	61.43 (31)	58.80 (2)
	SFMxR	56.41 (123)				
QN_m	SFM	66.72 (38)	61.75	62.26 (67)	60.89 (63)	62.61 (5)
	SFMxR	56.77 (176)				
SL_r (cm)	SFM	7.45 (21)	8.38	8.29 (68)	8.54 (31)	8.42 (2)
	SFMxR	9.30 (123)				
SL_m (cm)	SFM	7.78 (38)	8.82	8.77 (68)	8.78 (63)	9.13 (5)
	SFMxR	9.86 (176)				

TABLE 4.12: continued

Trait	Genotype	(n)	$\dfrac{\overline{(\overline{SFM}+\overline{SFM\times R})}}{2}$	$\bar{B}_1$ (n)	$\bar{B}_2$ (n)	$\bar{B}_3$ (n)
TCN	SFM	48.07 (38)	40.93	43.54 (68)	41.33 (62)	44.44 (5)
	SFMxR	33.79 (176)				
CPC	SFM	6.09 (38)	4.72	4.90 (68)	4.78 (62)	4.90 (5)
	SFMxR	3.34 (176)				
CHR_r	SFM	5.38 (21)	4.62	4.53 (68)	4.15 (31)	3.06 (2)
	SFMxR	3.86 (122)				
CHR_m	SFM	5.71 (38)	5.44	5.44 (68)	5.36 (63)	4.90 (5)
	SFMxR	5.17 (178)				
LUS	SFM	2.90 (38)	3.73	3.79 (68)	4.02 (63)	4.07 (5)
	SFMxR	4.55 (176)				
TIP	SFM	5.49 (37)	5.49	5.47 (68)	5.46 (63)	5.41 (5)
	SFMxR	5.49 (176)				
COT	SFM	5.76 (37)	5.66	5.67 (68)	5.67 (63)	5.63 (5)
	SFMxR	5.56 (176)				
SOU	SFM	5.85 (38)	5.61	5.85 (68)	5.54 (63)	5.38 (5)
	SFMxR	5.36 (176)				
HND	SFM	5.89 (38)	5.60	5.74 (68)	5.56 (63)	5.67 (5)
	SFMxR	5.30 (177)				
GC_r	SFM	6.36 (21)	4.14	5.46 (68)	5.43 (31)	4.85 (2)
	SFMxR	4.92 (123)				
GC_m	SFM	6.13 (38)	5.57	5.50 (68)	5.32 (63)	5.07 (5)
	SFMxR	5.01 (177)				
SC_m	SFM	6.25 (37)	5.89	6.10 (64)	6.10 (63)	5.64 (5)
	SFMxR	5.52 (173)				

TABLE 4.13: Means of fleece and follicle traits using data uncorrected for fixed effects

Trait	Genotype	(n)	$\dfrac{(\overline{SFM}+\overline{SFM \times R})}{2}$	$\bar{B}_1$ (n)	$\bar{B}_2$ (n)	$\bar{B}_3$ (n)
S/P	SFM	20.39 (39)	15.84	15.64 (69)	15.90 (63)	16.70 (5)
	SFMxR	11.28 (194)				
ln S/P	SFM	2.98 (39)	2.69	2.73 (69)	2.74 (63)	2.79 (5)
	SFMxR	2.40 (194)				
n(P+S)	SFM	76.79 (39)	64.35	65.81 (69)	73.32 (63)	86.30 (5)
	SFMxR	51.90 (194)				
n(P+S)corr	SFM	45.82 (39)	36.38	39.45 (69)	40.89 (63)	41.10 (5)
	SFMxR	26.94 (194)				
nP	SFM	3.66 (39)	3.95	3.98 (69)	4.33 (63)	4.88 (5)
	SFMxR	4.23 (194)				
nP(corr)	SFM	2.17 (39)	2.19	2.37 (69)	2.43 (63)	2.38 (5)
	SFMxR	2.21 (194)				
CF	SFM	0.59 (39)	0.56	0.60 (69)	0.57 (63)	0.49 (5)
	SFMxR	0.53 (194)				
LWT (kg)	SFM	38.32 (33)	43.73	49.51 (56)	40.47 (55)	38.28 (5)
	SFMxR	49.13 (174)				
GFW (kg)	SFM	3.25 (36)	3.51	3.56 (68)	3.43 (62)	3.14 (5)
	SFMxR	3.76 (190)				
CFW (kg)	SFM	2.31 (34)	2.56	2.62 (64)	2.49 (61)	2.22 (5)
	SFMxR	2.81 (167)				
YLD (%)	SFM	70.72 (37)	72.10	72.90 (64)	72.72 (62)	70.44 (5)
	SFMxR	73.42 (171)				
MFD (μm)	SFM	19.69 (37)	23.10	22.59 (64)	22.47 (62)	20.68 (5)
	SFMxR	26.50 (174)				
QN_r	SFM	73.48 (21)	65.18	61.79 (68)	61.74 (31)	59.50 (2)
	SFMxR	56.88 (123)				
QN_m	SFM	66.55 (38)	61.24	61.78 (67)	59.94 (63)	61.60 (5)
	SFMxR	55.93 (176)				
SL_r (cm)	SFM	7.74 (21)	8.64	8.68 (68)	8.77 (31)	8.00 (2)
	SFMxR	9.53 (123)				
SL_m (cm)	SFM	8.28 (38)	9.28	9.09 (68)	9.32 (63)	9.40 (5)
	SFMxR	10.27 (176)				

TABLE 4.13: continued

Trait	Genotype	(n)	$\overline{(\text{SFM}+\overline{\text{SFM}\times\text{R}})}$ / 2	$\overline{B}_1$ (n)	$\overline{B}_2$ (n)	$\overline{B}_3$ (n)
TCN	SFM	48.82 (38)	40.11	41.96 (68)	41.44 (62)	44.40 (5)
	SFMxR	31.39 (176)				
CPC	SFM	5.99 (38)	4.56	4.66 (68)	4.60 (62)	4.78 (5)
	SFMxR	3.12 (176)				
CHR_r	SFM	5.67 (21)	4.85	4.75 (68)	4.32 (31)	3.00 (2)
	SFMxR	4.02 (122)				
CHR_m	SFM	5.82 (38)	5.56	5.49 (68)	5.57 (63)	5.20 (5)
	SFMxR	5.29 (178)				
LUS	SFM	2.92 (38)	3.42	4.01 (68)	4.17 (63)	4.20 (5)
	SFMxR	3.91 (176)				
TIP	SFM	5.43 (37)	5.46	5.49 (68)	5.44 (63)	5.40 (5)
	SFMxR	5.48 (176)				
COT	SFM	5.84 (37)	5.72	5.62 (68)	5.76 (63)	5.80 (5)
	SFMxR	5.60 (176)				
SOU	SFM	5.50 (38)	5.10	5.50 (68)	4.63 (63)	4.20 (5)
	SFMxR	4.70 (176)				
HND	SFM	6.32 (38)	6.01	5.93 (68)	6.16 (63)	6.40 (5)
	SFMxR	5.69 (177)				
GC_r	SFM	5.52 (21)	4.84	4.74 (68)	4.68 (31)	4.00 (2)
	SFMxR	4.15 (123)				
GC_m	SFM	6.26 (38)	5.72	5.62 (68)	5.60 (63)	5.40 (5)
	SFMxR	5.18 (177)				
SC_m	SFM	6.41 (37)	6.16	6.56 (64)	6.49 (63)	6.00 (5)
	SFMxR	5.90 (173)				

TABLE 4.14: Estimates of heterosis by various methods using data corrected for age, year sampled and birth/rearing rank (Upper figure of each pair is SFMxR; lower LMxR)

Trait	Genotype	$\bar{F}_1 - \frac{(\bar{R}+\bar{M})}{2}$	$2[\bar{F}_2 - \frac{(\bar{R}+\bar{M})}{2}]$	$2(\bar{F}_1 - \bar{F}_2)$	$2[\bar{F}_3 - \frac{(\bar{R}+\bar{M})}{2}]$	$2[\bar{F}_4 - \frac{(\bar{R}+\bar{M})}{2}]$
S/P	SFMxR	-2.37	-3.66	-1.08	-2.72	-4.76
	LMxR	-2.37	-4.50	-0.24	-4.26	-7.34
ln S/P	SFMxR	-0.02	-0.06	-0.10	-0.16	-0.02
	LMxR	-0.02	-0.04	0.00	0.00	-0.24
n(P+S)	SFMxR	-4.37	-1.84	-1.24	-0.60	-0.38
	LMxR	-7.99	-21.52	-5.54	-25.24	-34.66
n(P+S)corr	SFMxR	0.43	3.40	-2.54	1.92	7.28
	LMxR	2.67	0.72	4.62	-1.42	-5.62
nP	SFMxR	0.01	0.46	-0.44	0.18	1.28
	LMxR	0.05	-0.32	0.42	-0.70	-0.34
nP(corr)	SFMxR	0.10	0.28	-0.08	0.04	0.74
	LMxR	0.10	-0.08	0.28	-0.30	-0.16
CF	SFMxR	-0.01	-0.04	0.02	-0.04	0.00
	LMxR	0.01	0.00	0.02	0.00	0.02
LWT (kg)	SFMxR	6.84	9.78	3.90	8.36	2.56
	LMxR	5.99	13.54	-1.56	12.04	14.02
GFW (kg)	SFMxR	0.18	0.44	-0.08	0.60	0.62
	LMxR	0.47	0.96	-0.02	0.70	1.42
CFW (kg)	SFMxR	-0.05	0.10	-0.20	0.04	0.00
	LMxR	0.18	0.50	-0.14	0.22	0.64
YLD (%)	SFMxR	-1.42	-0.56	1.52	0.30	-0.14
	LMxR	0.32	-0.88	15.2	-1.32	-1.76
MFD (µm)	SFMxR	-2.44	-5.48	0.60	-6.74	-6.34
	LMxR	-0.04	-2.24	2.16	-2.18	-0.36
QN_r	SFMxR	-3.45	-6.30	-0.60	-6.22	
	LMxR	-1.03	0.54	-2.60	1.90	
QN_m	SFMxR	-0.40	-1.22	0.42	0.08	-2.48
	LMxR	-1.80	0.08	-3.68	0.66	-1.08
SL_r (cm)	SFMxR	-1.70	-2.30	-1.10	-2.52	
	LMxR	0.00	-1.02	1.02	-2.00	

TABLE 4.14:   continued

Trait	Genotype	$\bar{F}_1 - \dfrac{(\bar{R}+\bar{M})}{2}$	$2[\bar{F}_2 - \dfrac{(\bar{R}+\bar{M})}{2}]$	$2(\bar{F}_1 - \bar{F}_2)$	$2[\bar{F}_3 - \dfrac{(\bar{R}+\bar{M})}{2}]$	$2[\bar{F}_4 - \dfrac{(\bar{R}+\bar{M})}{2}]$
SL_m (cm)	SFMxR	-1.24	-1.92	-0.56	-2.30	-0.72
	LMxR	-0.87	-0.38	-1.38	-1.64	-2.02
TCN	SFMxR	0.99	2.46	-0.48	8.82	9.04
	LMxR	0.94	3.50	-1.62	3.28	4.90
CPC	SFMxR	-0.44	-0.96	0.08	-0.06	-0.60
	LMxR	-0.09	-0.40	0.22	-0.12	-0.26
CHR_r	SFMxR	-0.73	-1.06	-0.40	-1.48	
	LMxR	-1.10	0.28	-2.48	-0.20	
CHR_m	SFMxR	0.25	0.70	-0.20	0.68	1.06
	LMxR	0.53	1.04	0.02	1.24	1.52
LUS	SFMxR	-0.16	-0.40	0.08	-0.50	-0.22
	LMxR	-0.18	-.060	0.24	-0.80	-0.42
TIP	SFMxR	0.78	1.62	-0.06	1.50	1.68
	LMxR	0.89	1.80	-0.02	2.26	1.10
COT	SFMxR	0.24	0.46	0.02	0.40	0.08
	LMxR	0.11	0.66	-0.44	0.60	0.28
SOU	SFMxR	-1.38	-2.42	-0.34	-2.20	-1.34
	LMxR	-1.34	-3.28	0.60	-2.48	-2.14
HND	SFMxR	-0.08	0.22	-0.38	0.46	0.08
	LMxR	0.27	0.84	-0.30	0.66	-0.44
GC_r	SFMxR	-0.68	-0.98	-0.38	-1.14	
	LMxR	-0.69	-0.04	-1.34	0.16	
GC_m	SFMxR	-0.34	-0.32	-0.36	-0.22	0.02
	LMxR	0.10	0.56	-0.36	0.28	-0.42
SC_m	SFMxR	0.18	0.34	0.02	0.40	1.04
	LMxR	0.38	0.58	0.18	0.42	0.18

TABLE 4.15: Estimates of heterosis by various methods using data uncorrected for age, year sampled and birth/rearing rank

Trait	Genotype	$\bar{F}_1-(\bar{R}+\bar{M})$	$\dfrac{2[\bar{F}_2-(\bar{R}+\bar{M})]}{2}$	$2(\bar{F}_1-\bar{F}_2)$	$\dfrac{2[\bar{F}_3-(\bar{R}+\bar{M})]}{2}$	$\dfrac{2[\bar{F}_4-(\bar{R}+\bar{M})]}{2}$
S/P	SFMxR	-2.47	-5.14	0.20	-1.96	-2.90
	LMxR	-2.57	-5.32	0.18	-4.04	-5.58
ln S/P	SFMxR	-0.04	0.00	-0.08	0.22	0.18
	LMxR	-0.05	-0.10	0.00	0.02	-0.08
n(P+S)	SFMxR	-12.23	-6.36	-18.10	7.72	25.22
	LMxR	-15.92	-29.08	-2.70	-19.94	-12.78
n(P+S)corr	SFMxR	-6.03	-5.72	-6.34	-2.22	5.88
	LMxR	-7.37	-16.96	-2.22	-13.78	-14.14
nP	SFMxR	-0.48	0.36	1.32	0.54	2.28
	LMxR	-0.43	-0.62	0.24	-0.38	0.68
nP(corr)	SFMxR	0.01	0.38	-0.36	0.26	1.00
	LMxR	-0.09	-0.30	0.12	-0.30	-0.12
CF	SFMxR	0.06	0.04	0.08	0.00	-0.04
	LMxR	0.07	0.06	0.08	0.04	-0.04
LWT (kg)	SFMxR	14.17	10.88	17.46	2.58	-21.42
	LMxR	11.42	19.84	3.00	7.26	-4.54
GFW (kg)	SFMxR	0.13	0.38	-0.12	0.42	0.36
	LMxR	0.50	0.98	0.02	0.52	1.12
CFW (kg)	SFMxR	-0.21	0.02	-0.44	-0.30	-0.46
	LMxR	0.12	1.02	-0.78	-0.12	0.14
YLD (%)	SFMxR	-2.73	-0.10	-5.36	-3.50	-4.12
	LMxR	-0.39	-0.96	0.18	-1.82	-6.40
MFD (μm)	SFMxR	-1.15	-4.10	1.80	-6.24	-7.00
	LMxR	0.60	-2.24	3.44	-2.96	-2.52
QN_r	SFMxR	-3.50	-6.18	-0.82	-6.26	
	LMxR	-0.69	0.56	-0.94	2.02	
QN_m	SFMxR	-0.92	-1.46	-0.38	-0.60	-4.26
	LMxR	-1.92	-0.10	-3.74	0.30	-2.44
SL_r (cm)	SFMxR	-2.27	-3.00	-1.54	-3.24	
	LMxR	-0.66	-1.50	0.18	-2.78	

TABLE 4.15:   continued

Trait	Genotype	$\bar{F}_1-(\bar{R}+\bar{M})$	$\dfrac{2[\bar{F}_2-(\bar{R}+\bar{M})]}{2}$	$2(\bar{F}_1-\bar{F}_2)$	$\dfrac{2[\bar{F}_3-(\bar{R}+\bar{M})]}{2}$	$\dfrac{2[\bar{F}_4-(\bar{R}+\bar{M})]}{2}$
SL_m (cm)	SFMxR	-1.90	-2.22	-1.58	-2.72	-0.22
	LMxR	-1.63	-0.54	-2.72	-2.16	0.44
TCN	SFMxR	-4.16	-2.42	-5.90	4.72	8.58
	LMxR	0.44	9.32	-8.44	9.00	14.02
CPC	SFMxR	-0.59	-1.06	-0.12	-0.08	-0.66
	LMxR	-0.21	-0.39	-0.04	-0.04	-0.20
CHR_r	SFMxR	-0.86	-1.28	-0.44	-1.94	
	LMxR	-1.10	0.12	-2.32	-0.54	
CHR_m	SFMxR	0.03	0.72	-0.66	0.94	1.62
	LMxR	0.27	1.02	-0.48	1.42	2.04
LUS	SFMxR	-0.07	-0.34	0.20	-0.50	-0.38
	LMxR	-0.14	-0.54	0.26	-0.82	-0.64
TIP	SFMxR	0.66	1.68	-0.36	1.56	1.62
	LMxR	0.80	1.80	-0.20	2.28	1.02
COT	SFMxR	0.21	0.42	0.00	0.56	0.52
	LMxR	0.09	0.60	-0.42	0.66	0.66
SOU	SFMxR	-0.72	-2.66	1.22	-3.34	-3.32
	LMxR	-0.46	-3.10	2.18	-3.12	-3.84
HND	SFMxR	-0.41	0.20	-1.02	1.00	1.42
	LMxR	-0.09	0.70	-0.88	0.96	0.80
GC_r	SFMxR	-0.78	-1.18	-0.38	-1.50	
	LMxR	-0.90	-0.38	-1.42	-0.26	
GC_m	SFMxR	-0.54	-0.26	-0.82	0.02	0.62
	LMxR	-0.08	0.46	-0.62	0.40	0.06
SC_m	SFMxR	0.01	0.42	-0.40	0.32	0.90
	LMxR	0.24	0.56	-0.08	0.64	-0.06

Liveweight had the highest level of heterosis. The estimates increased in the LMxR crossbreds from the F_1 to the F_4 generations (5.99 to 14.02 kg). In the SFMxR animals, heterosis for LWT increased from the F_1 to F_2 generations and then decreased.

For both crossbred genotypes, heterosis for GFW increased in subsequent generations. In the SFMxR group, the largest between generation increase occurred between the F_1 and F_2 groups (0.26 kg), while in the LMxR this happened between the F_3 and F_4 generations (0.72 kg). There was no concomitant heterosis for CFW.

The heterosis estimates for TCN for both genotypes increased between subsequent generations, the highest level occuring in the SFMxR F_4 group (9.04).

A similar pattern of increasing heterosis between generations was seen for CHR_m, with heterosis increasing from 0.25 to 1.06 (SFMxR; F_1 to F_4) and 0.53 to 1.52 (LMxR; F_1 to F_4).

That the character of the fleece was improved in subsequent generations was reflected in the levels of heterosis for both TIP and COT (see Tables 4.14 - 4.15). Although both GC_r and GC_m showed negative heterosis, for SC_m the opposite occurred. This indicates the improved scoured colour of the crossbreds compared with the parental groups.

4.6.2.2 F_1 vs. F_2

In comparing the 2 genotypes no consistent pattern emerged. In both genotypes, the F_1 animals had lower mean S/P ratios than the F_2. The negative heterosis estimates were far smaller when the data were log transformed.

In the LMxR animals there was a low negative estimate of heterosis for n(P+S) (-1.24), which increased to (-2.54) using data corrected for skin shrinkage. A similar pattern was noted for the SFMxR group where the heterosis estimate for n(P+S) was -2.54 and for n(P+S)corr 4.62.

The heterosis estimates for nP and nP(corr) varied between genotypes; negative in the SFMxR (-0.44, -0.08) and positive in the LMxR (0.42, 0.28).

In the LMxR group both LWT and MFD showed moderate levels of positive heterosis at 3.90 kg and 2.16 μm. There were also high levels of negative heterosis for: QN_r, Qn_m and CHR_r.

In both genotypes, for several traits, the F_2 animals often had higher mean values than did the F_1. The variation in heterosis estimates between genotypes is probably due to the small size of sample in some generations.

4.6.3 Discussion

The low number of F_1 animals in the LMxR crossbreds (8), gives little credence to heterosis estimates between the parental groups and this generation.

4.6.3.1 Follicle Characteristics

Generally workers have found negative heterosis for follicle characteristics. The level of decline in S/P and n(P+S) between the F_1 and parental groups in the present data is in line with the studies using Merino x Border Leicester crossbreds (Schinckel and Hayman, 1960; Pattie and Smith, 1964; McGuirk et al, 1978).

In the present data, the F_2 animals generally had higher S/P and n(P+S) than the F_1. These results agree with those obtained by Schinckel and Hayman (1960) using Merino x Border Leicesters but are not in accord with those of Pattie and Smith (1964). The latter reported little difference between F_1 and F_2 Merino x Border Leicester animals for either the means of S/P and n(P+S) although in the F_2, there was a slight increase in the variance of S/P.

Recently, Charyulu and Acharya (1984), looked at the heterosis for fleece and follicle characteristics using Rambouillet x Malpura (RM) and Rambouillet x Chokla (RC) animals.

The F_1 RM animals were inferior to the parental breed averages for follicle density, S/P ratio and primary follicle diameter. In contrast the F_2 animals had higher S/P ratios and follicle density than the F_1's. Charyulu and Acharya (1984) suggested that the greater S/P and n(P+S) in the second generation could have been due to maternal effects of the crossbred dams.

4.6.3.2 Fleece Traits and Liveweight

Charyulu and Acharya (1984) using six monthly measurements of fleece traits showed positive heterosis in the F_1 for fleece weight and staple length of 22.79% and 18.60%. McGuirk et al (1978) obtained 7.8% and 12.1% heterosis for GFW and CFW and -0.4% of SL.

The present levels of heterosis for the F_1 SFMxR and LMxR animals respectively were: 6.84 kg, 5.99 kg (LWT); 0.18 kg, 0.47 kg (GFW); -0.05 kg, 0.18 kg (CFW). Dobbie and Smart (1984) reported similar improvements in the peformance of Merino x Romney flocks from which the study animals were obtained.

The F_2 animals produced slightly heavier finer, longer, more crimped fleeces with better greasy colour than did the F_1 crossbreds. The F_2 sheep in the study by Pattie and Smith (1964) had lower GFW[**], CFW[**], similar SL, but higher CPC, CHR and GC than the F_1 animals. The results for CHR and GC agree with those of Pattie and Smith (1964). The small increase in MFD between generations noted by these authors was not seen in the present study.

The increased heterosis noted between the F_1 and F_2 generations, especially for LWT and GFW may have been partly due to maternal effects. The F_1 dams of the F_2 animals may have provided a better maternal environment than that of the purebred dams.

It appears that in the LMxR flocks LWT and GFW increased in each generation, the maximum heterosis occurring in the F_4 generation. In contrast, in the SFMxR group LWT peaked in the F_1 while GFW reached a maximum in the F_4 animals. These results suggest a combination of heterosis, maternal effects and selection acting on these traits. Improved performance through adaptation to the grazing conditions at Tokanui must also be considered. In contrast, for both genotypes, MFD remained lower than the parental mean [(R+M)/2], in both genotypes and all generations.

The slight increase in CHR in subsequent generations was in line with the increases in QN, TCN, HND and GC.

The levels of heterosis in the present study will have been affected by the small size of the parental groups. That these groups are not the true parents of the F_1 crossbreds must also be considered.

The increased negative heterosis noted from the F_1 to F_4 generations may not reflect standard heterosis but natural selection and adaptation. Bigham (1984) noted that N.Z. Feral Merinos had very low S/P ratios and coloured fleeces. In these sheep reduced S/P ratios appear to have provided increased survivability under harsh conditions. The between-generation decrease in S/P ratios and other follicle characteristics, noted in the present study may have been a partial adaptation to the conditions at Tokanui.

The improved between-generation positive heterosis for LWT and GFW also indicates adaptation and better utilization of the Tokanui grazing conditions. The present results indicate that the interbred crossbreds weigh more and produce heavier better quality fleeces than expected from the mid-parental group averages but without a concomitant increase in MFD. It appears that the Merino x Romney crossbreds have successfully adapted to the Tokanui grazing conditions.

CHAPTER 5

METHODS OF GENE DETECTION

The flocks from which wool and skin sample data were obtained were not established for the purpose of main gene detection. These flocks were used in the absence of an experimental flock especially established for main gene studies.

5.1 FREQUENCY DISTRIBUTIONS

5.1.1 S/P

The frequency distributions of S/P follicle ratio both within and between genotypes were examined initially. Figures 5.1 - 5.28 were created using the Minitab computer package.

Figure 5.1 shows the variation in S/P within 6 genotypes from the Romneys, through the crossbreds, to the two Merino types. In each of the Romney, BX and SFM genotypes there were 1 or 2 animals with S/P ratios outside the expected genotype range. This suggests that the animals may have been tagged incorrectly for genotype. As expected S/P increased from the Romneys to the crossbreds to the Merinos. A similar pattern was noted for ln S/P (see figure 5.8).

In figures 5.2 - 5.3 the graphs were broken down to compare parental groups with their respective crossbred progeny groups (i.e. R and SFM vs. SFMxR). There was some overlap in the range of S/P between the parental and progeny groups. The mean S/P values of the crossbreds were between those of the parental genotypes (see Tables 4.10 - 4.13).

Figures 5.8 - 5.14 illustrate the frequency distribution of ln S/P for various genotypic combinations. The graphs are more platykurtic than those for S/P. The distribution of S/P in the crossbreds was closer to the Romneys than to the Merinos.

When the mean S/P ratios (uncorrected for fixed effects) of the parental groups (R (5.91), SFM (20.39), LM (20.56)) were compared with the actual and expected mean S/P ratios of the progeny groups (SFMxR (11.28 Obs.; 13.15 Exp.); LMxR (10.82 Obs.; 13.24 Exp.); and BX (15.80 Obs.; 15.84 Exp.)) only the latter progeny group had a mean S/P ratio close to that expected from the parental means. This is illustrated in figures 5.2 - 5.3.
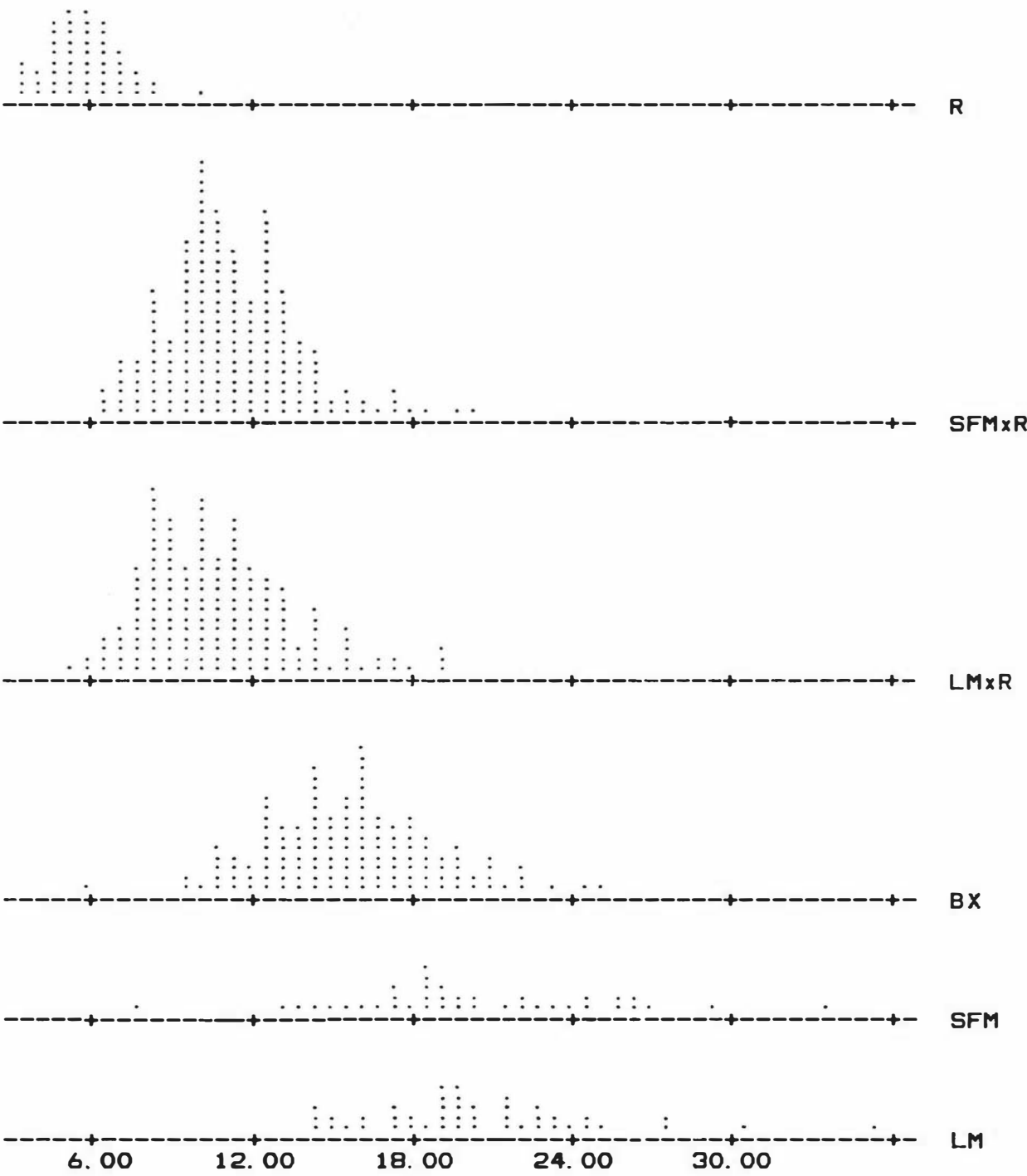
Figure 5.1: Frequency distributions of S/P for all genotypes
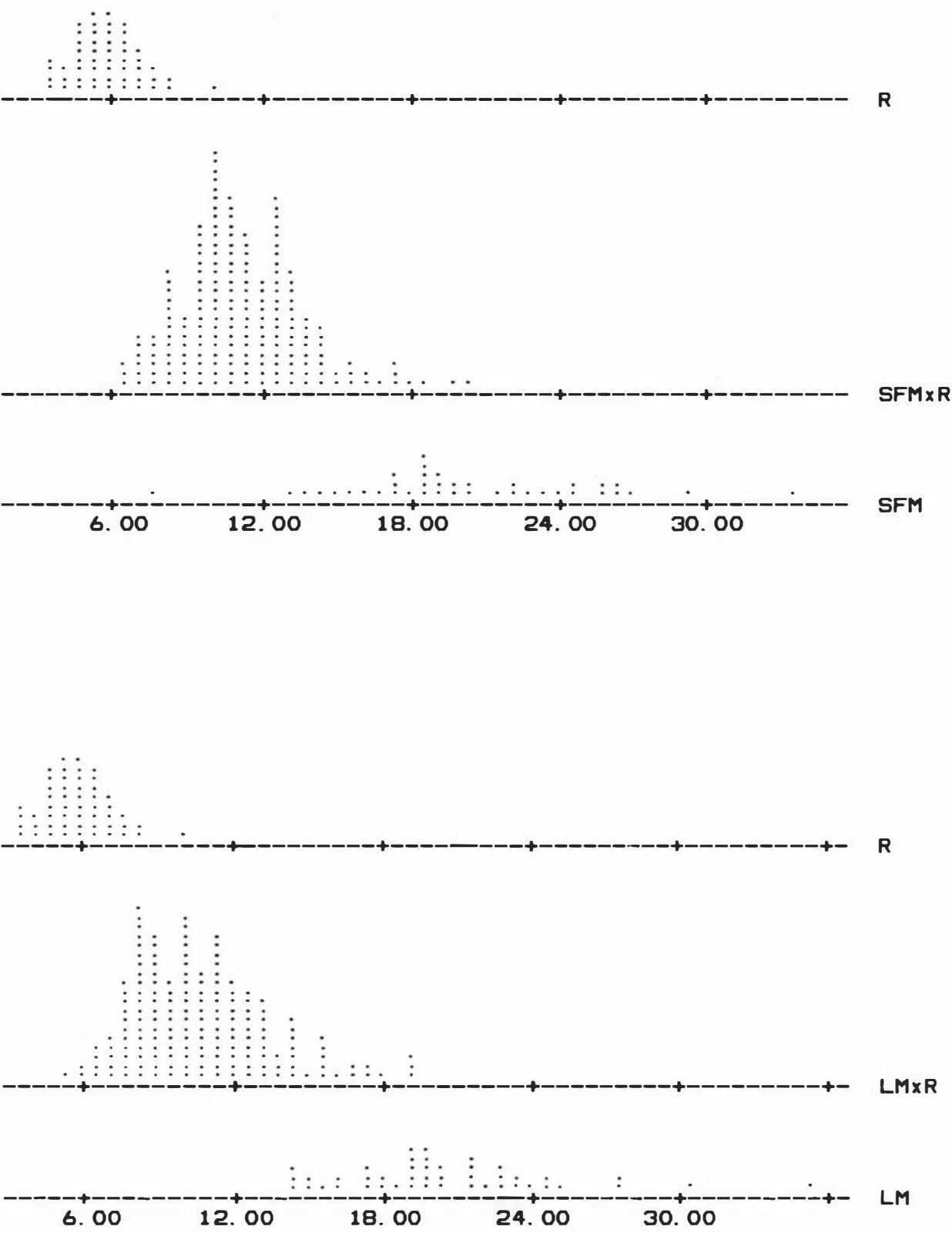
Figure 5.2: Frequency distributions of S/P for parental groups and their respective crossbreds
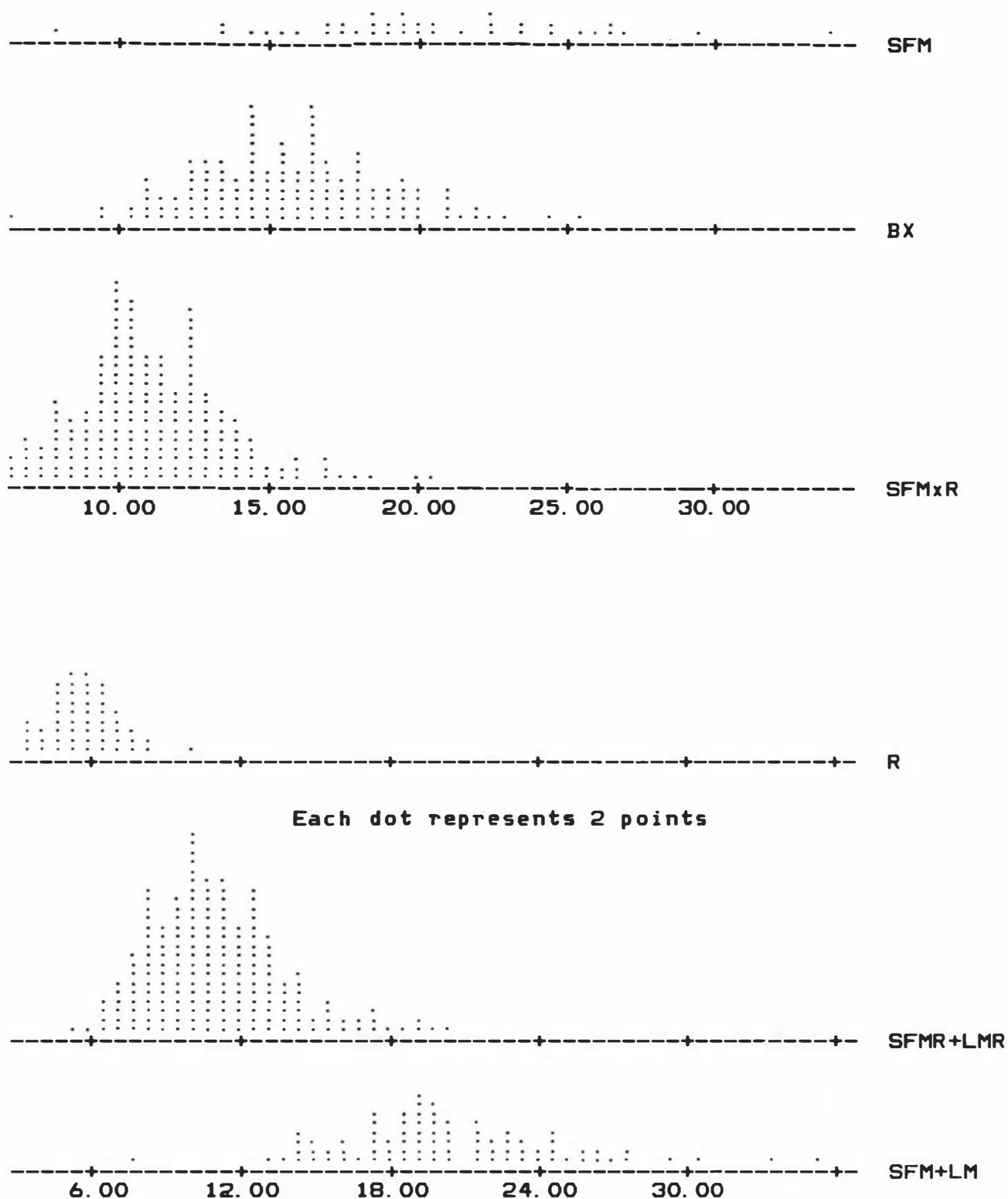
Figure 5.3: Frequency distributions of S/P for parental groups and their respective crossbreds
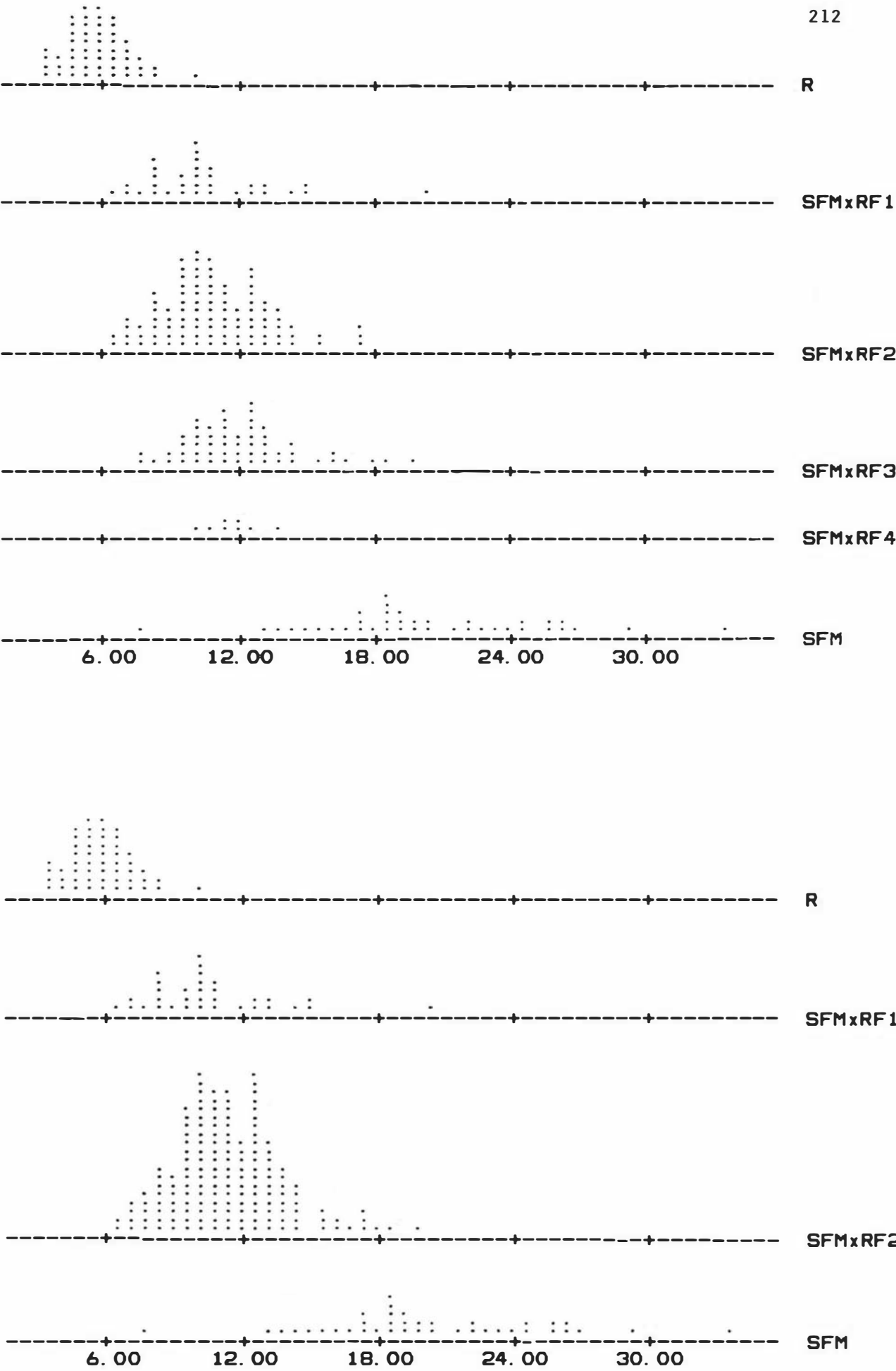
Figure 5.4: Frequency distributions of S/P
within crossbred genotypes
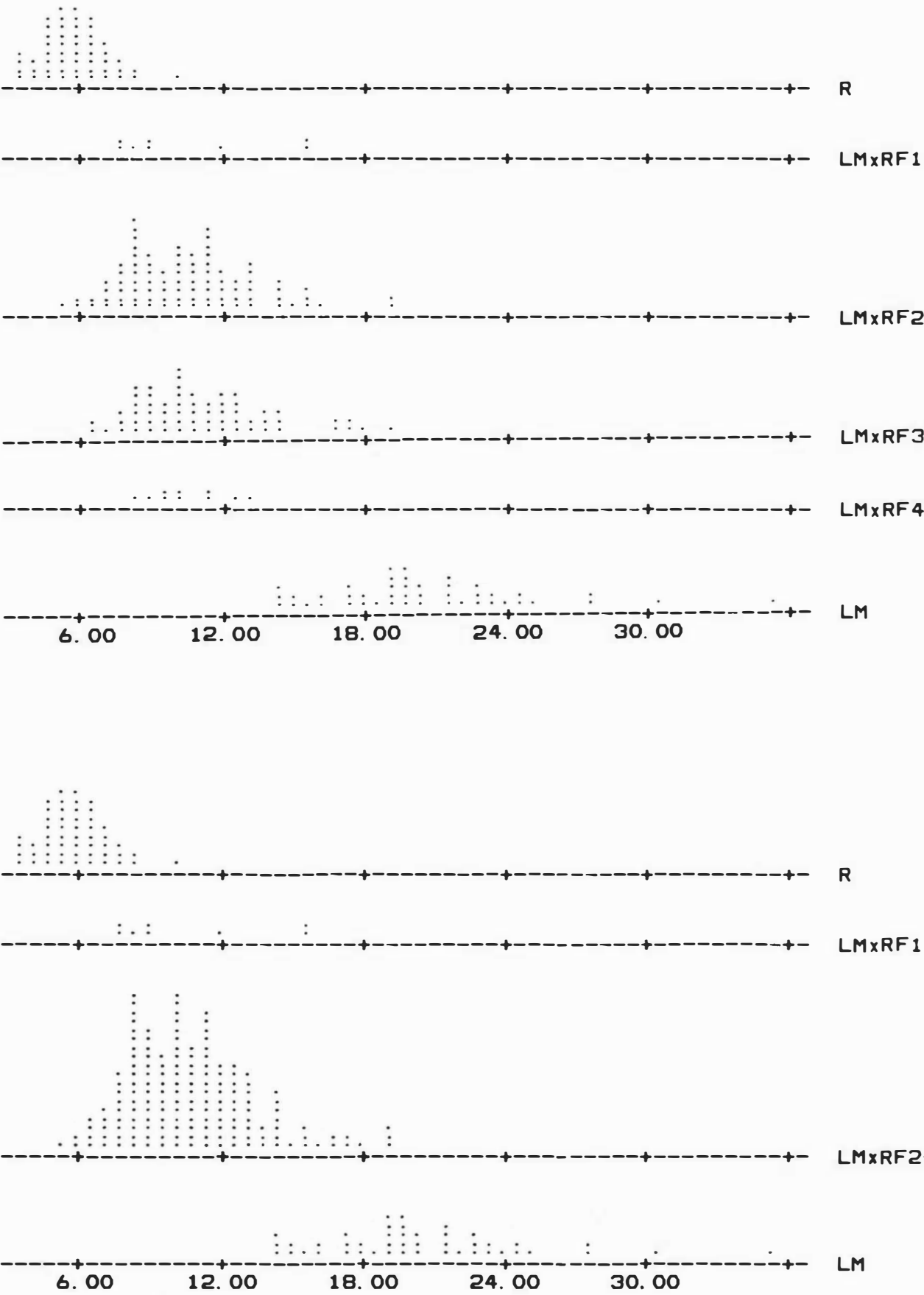
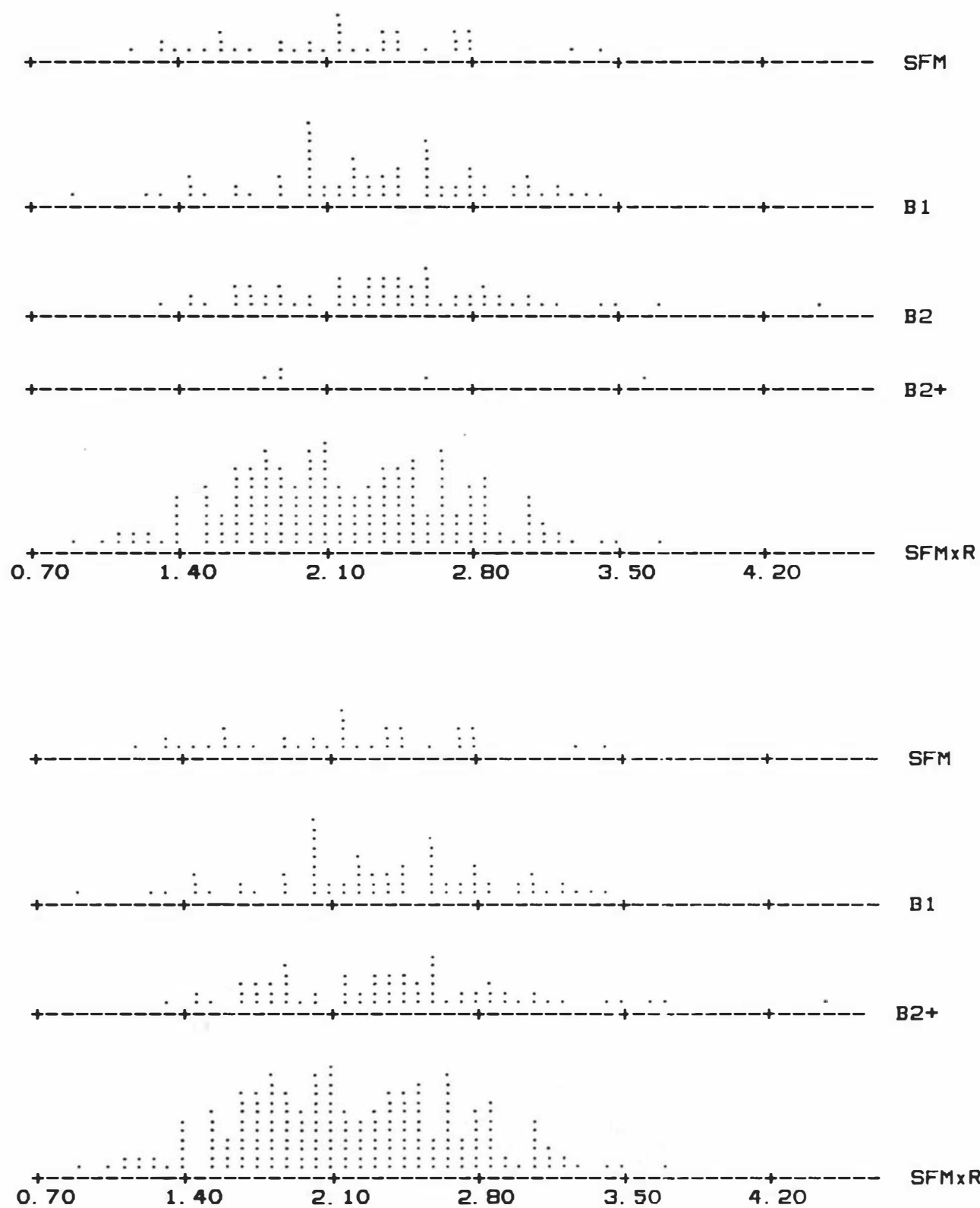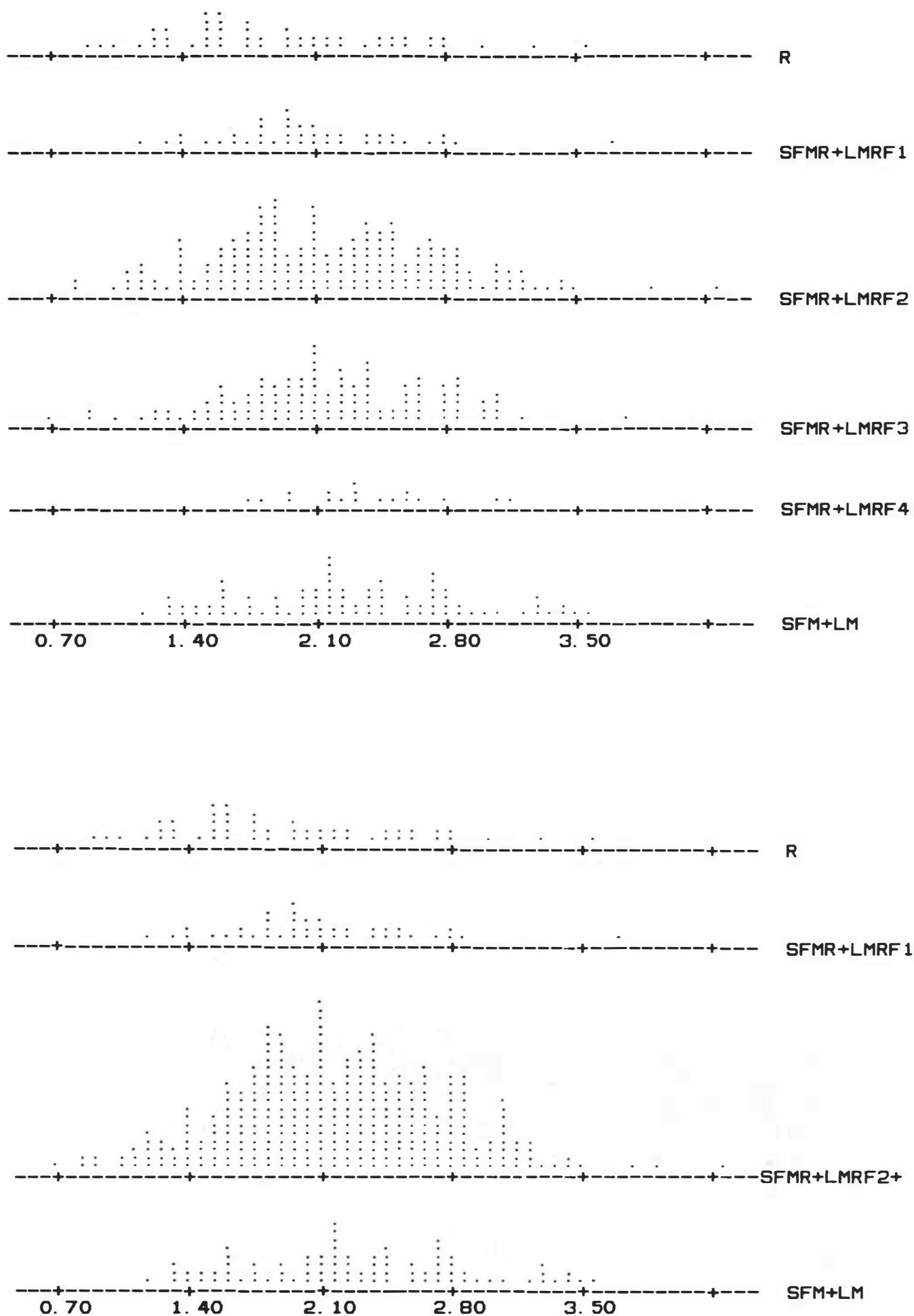Figure 5.5: Frequency distributions of S/P
within crossbred genotypes
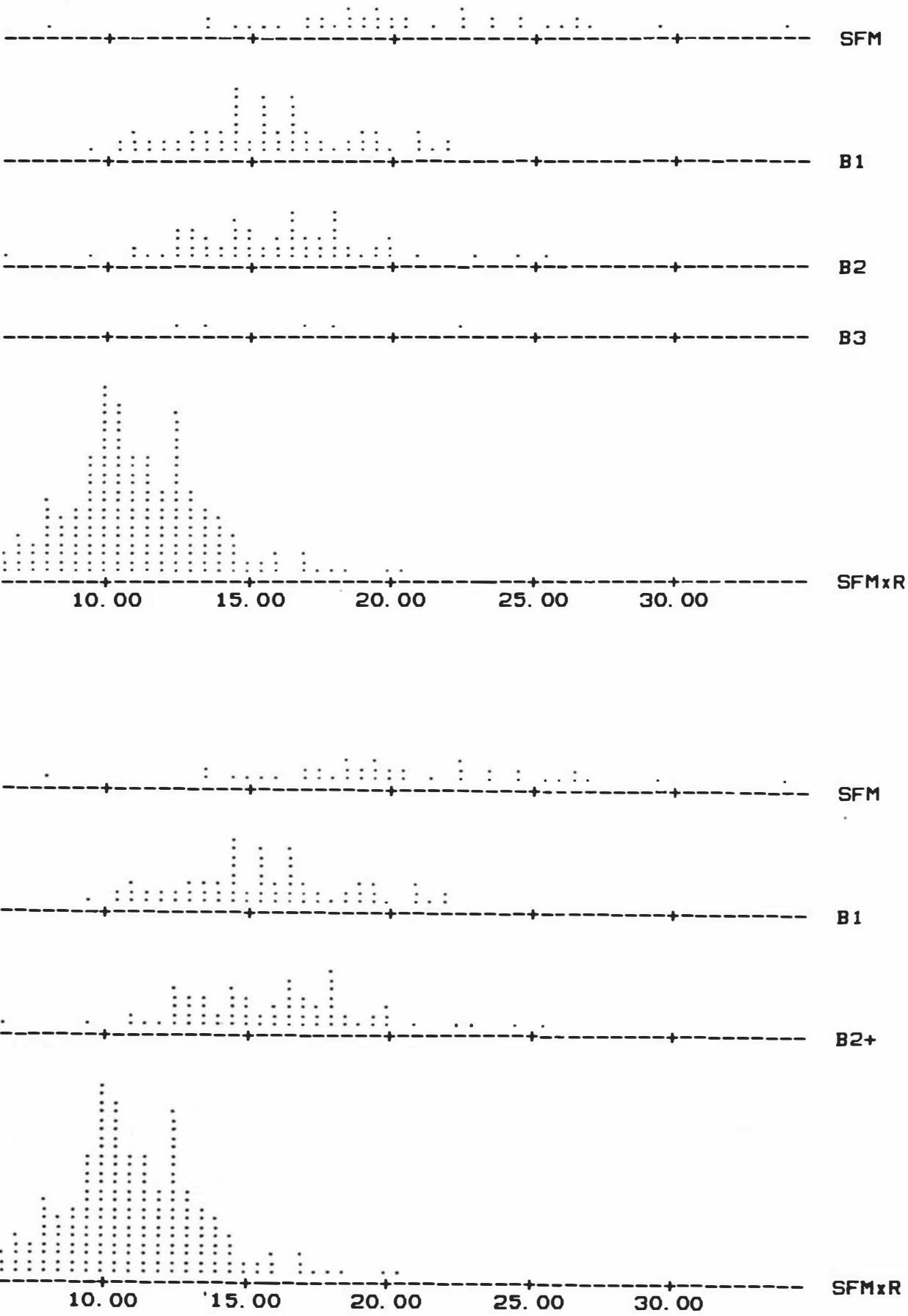
Figure 5.6:   Frequency distributions of S/P
within crossbred genotypes
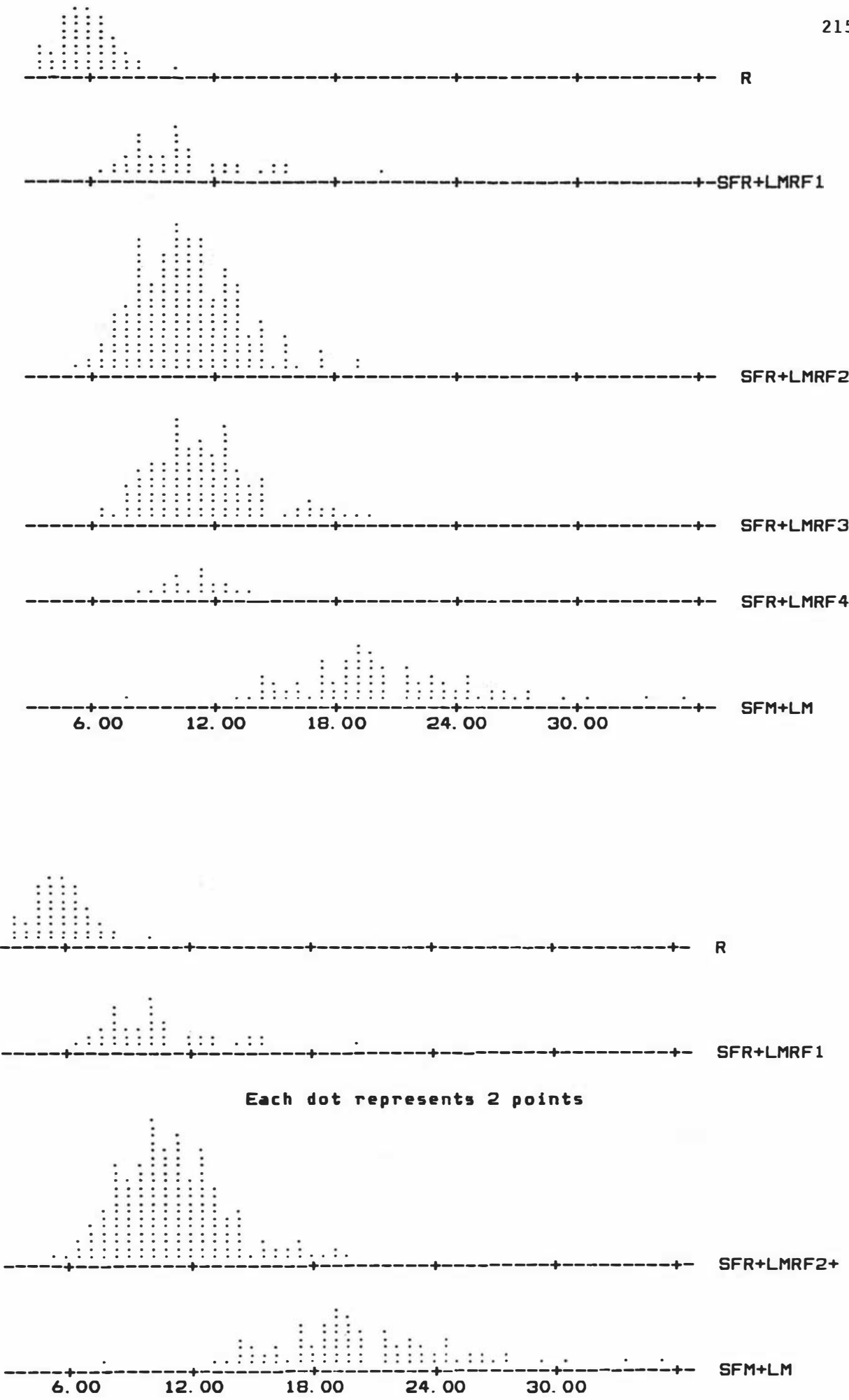
Figure 5.7:   Frequency distributions of S/P
within crossbred genotypes
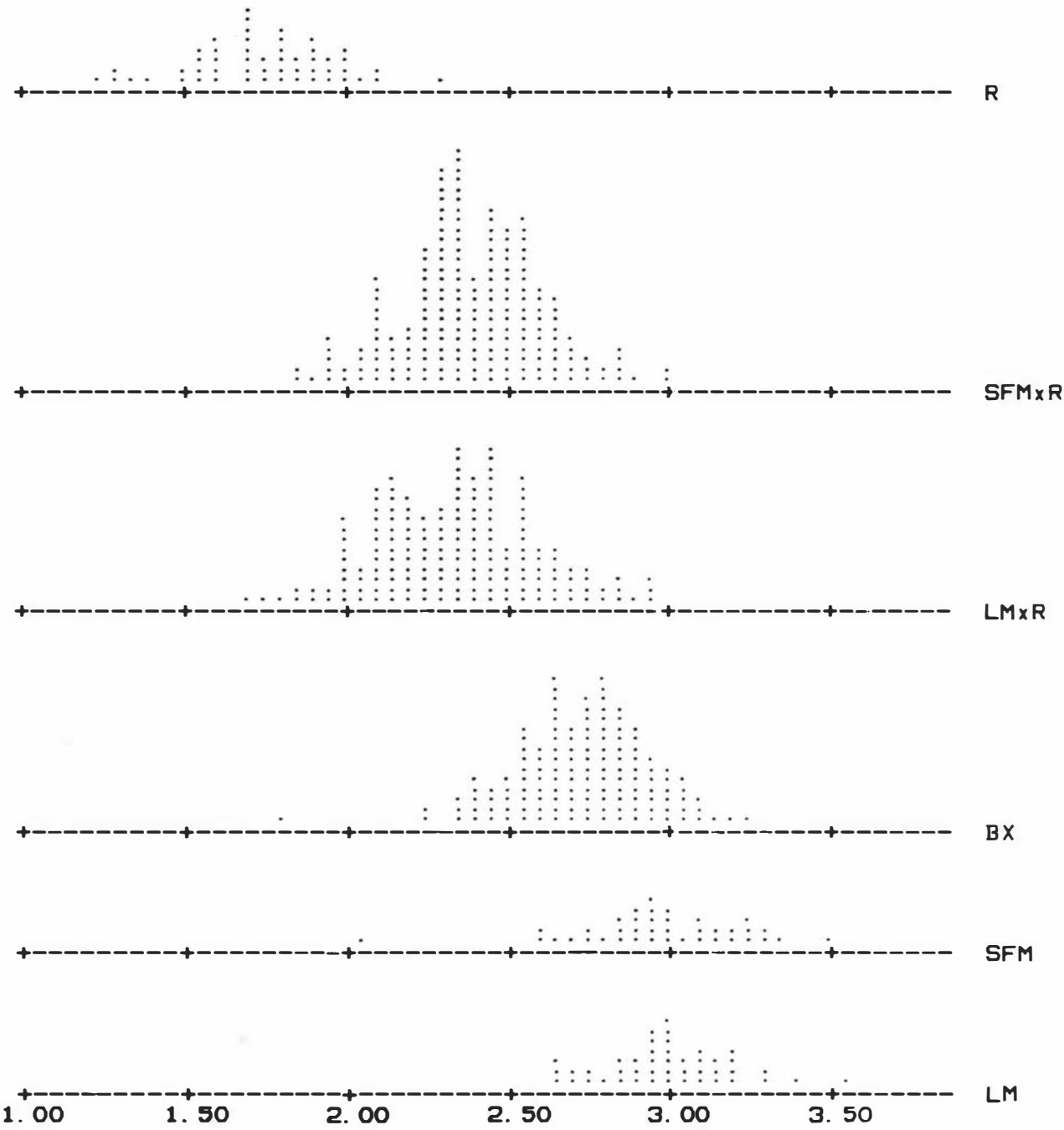
Figure 5.8: Frequency distributions of ln S/P for all genotypes

Figure 5.9: Frequency distributions of ln S/P for parental groups and their respective crossbreds
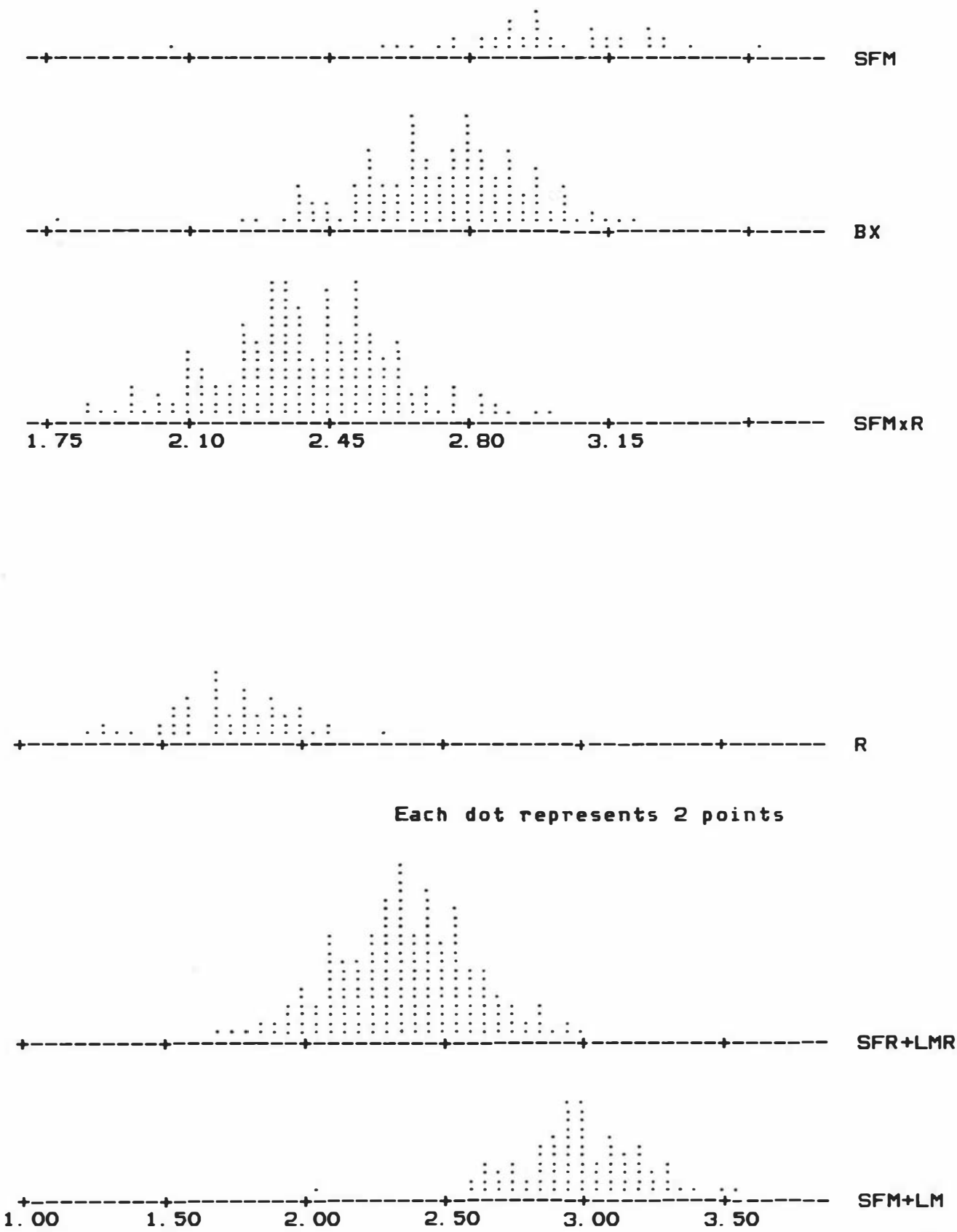
Figure 5.10: Frequency distributions of ln S/P for
parental groups and their respective crossbreds
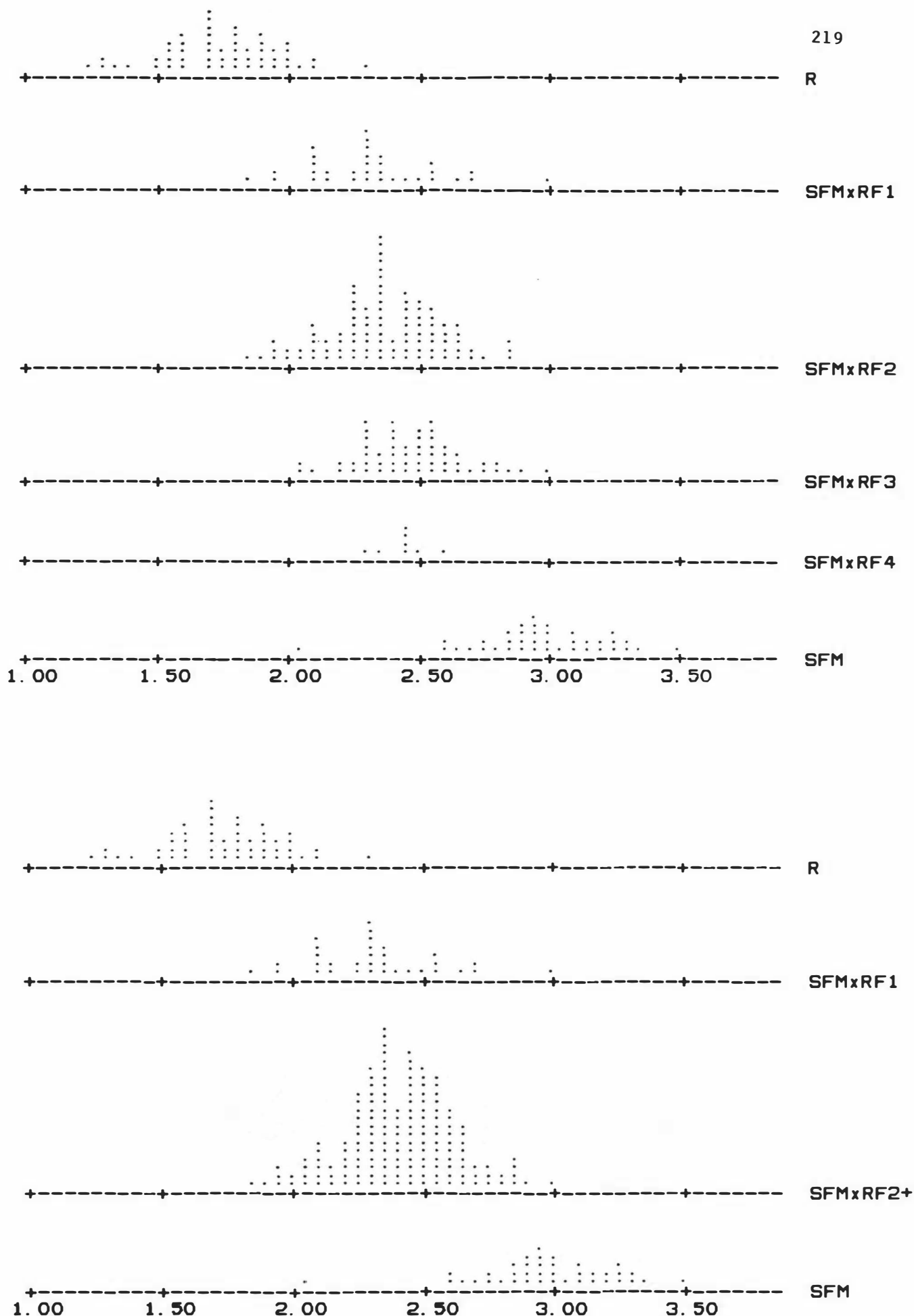
Figure 5.11:   Frequency distributions of ln S/P
within crossbred genotypes
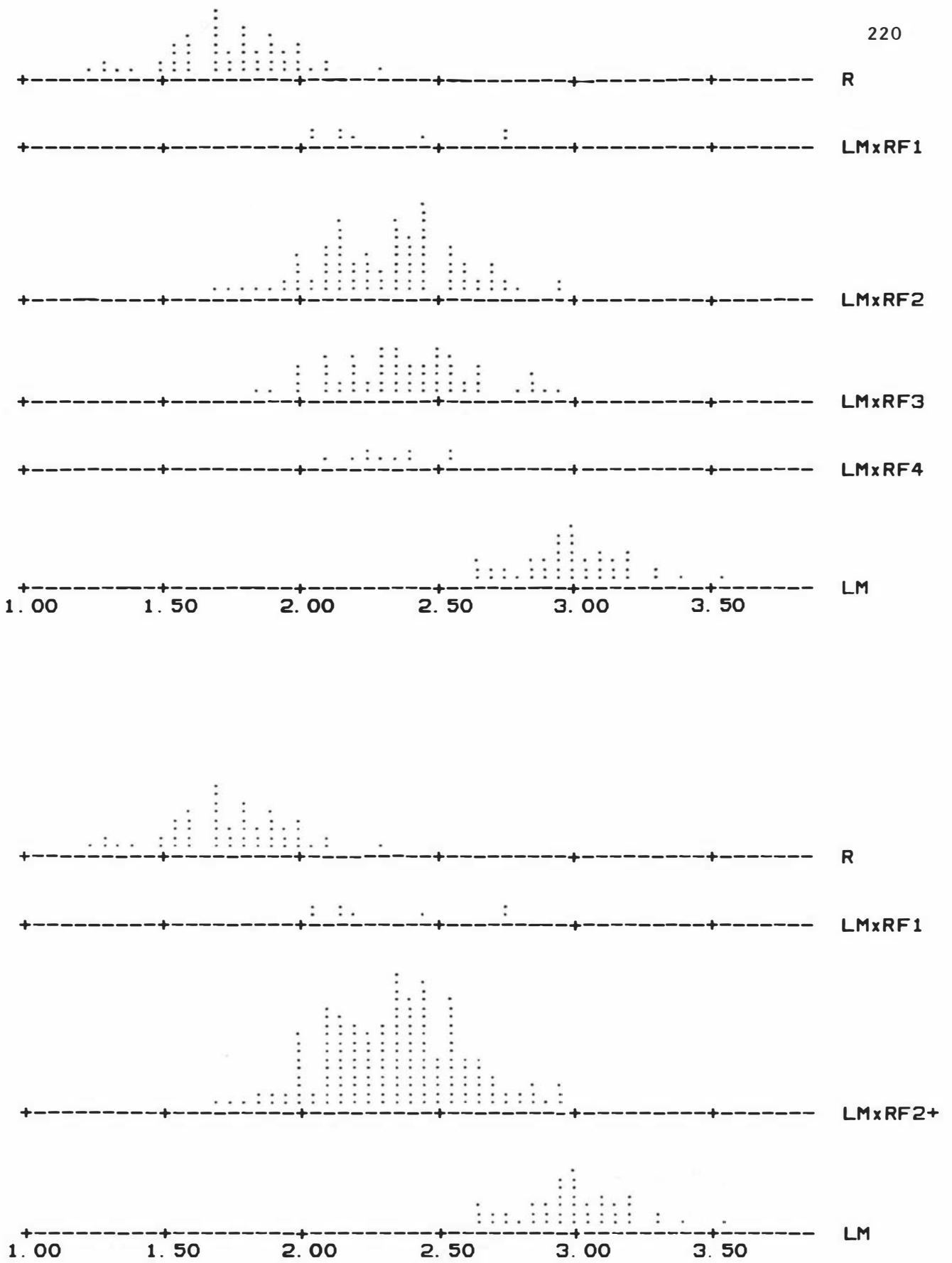
Figure 5.12: Frequency distributions of ln S/P within crossbred genotypes
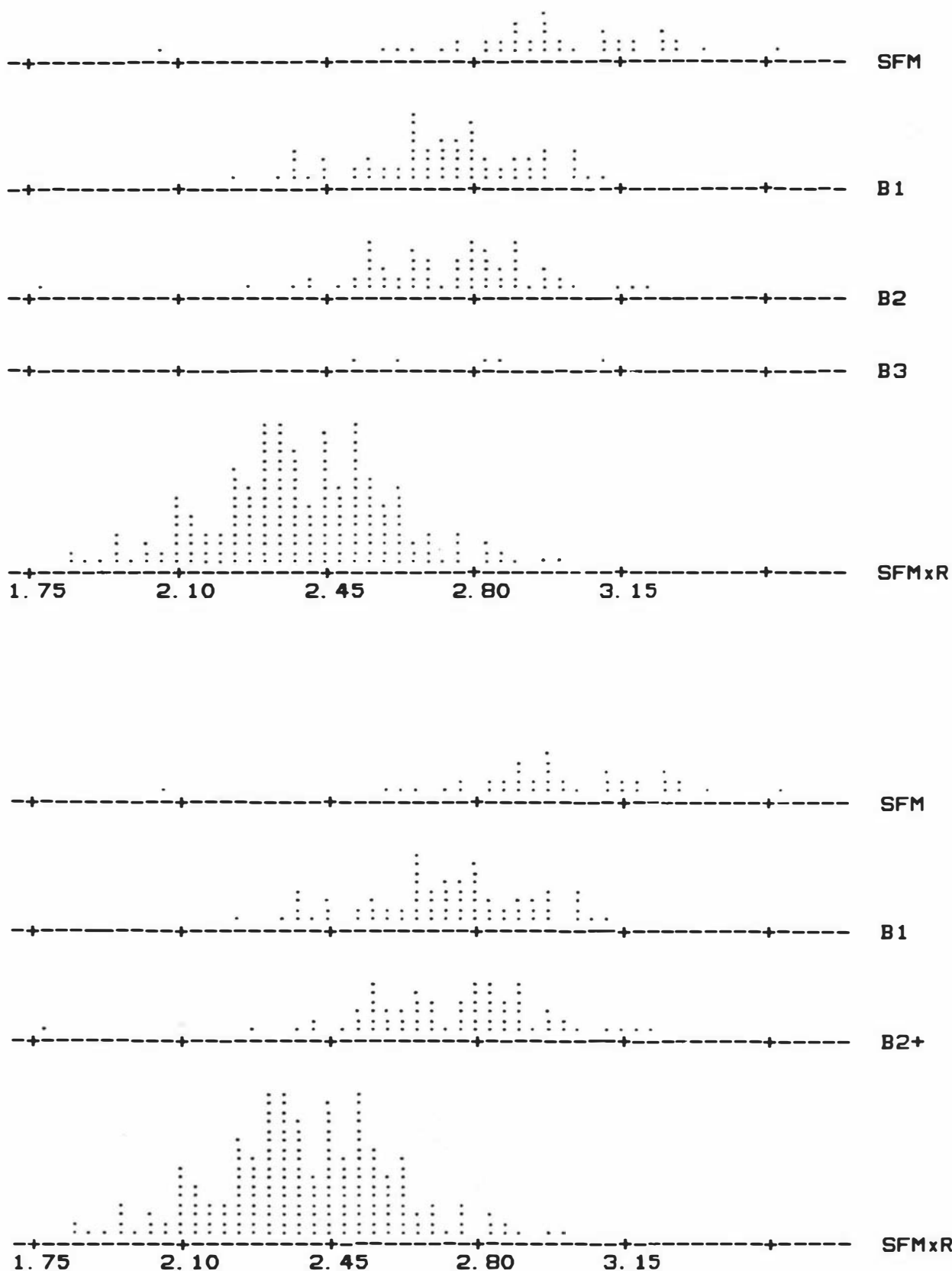
Figure 5.13:   Frequency distributions of ln S/P
within crossbred genotypes
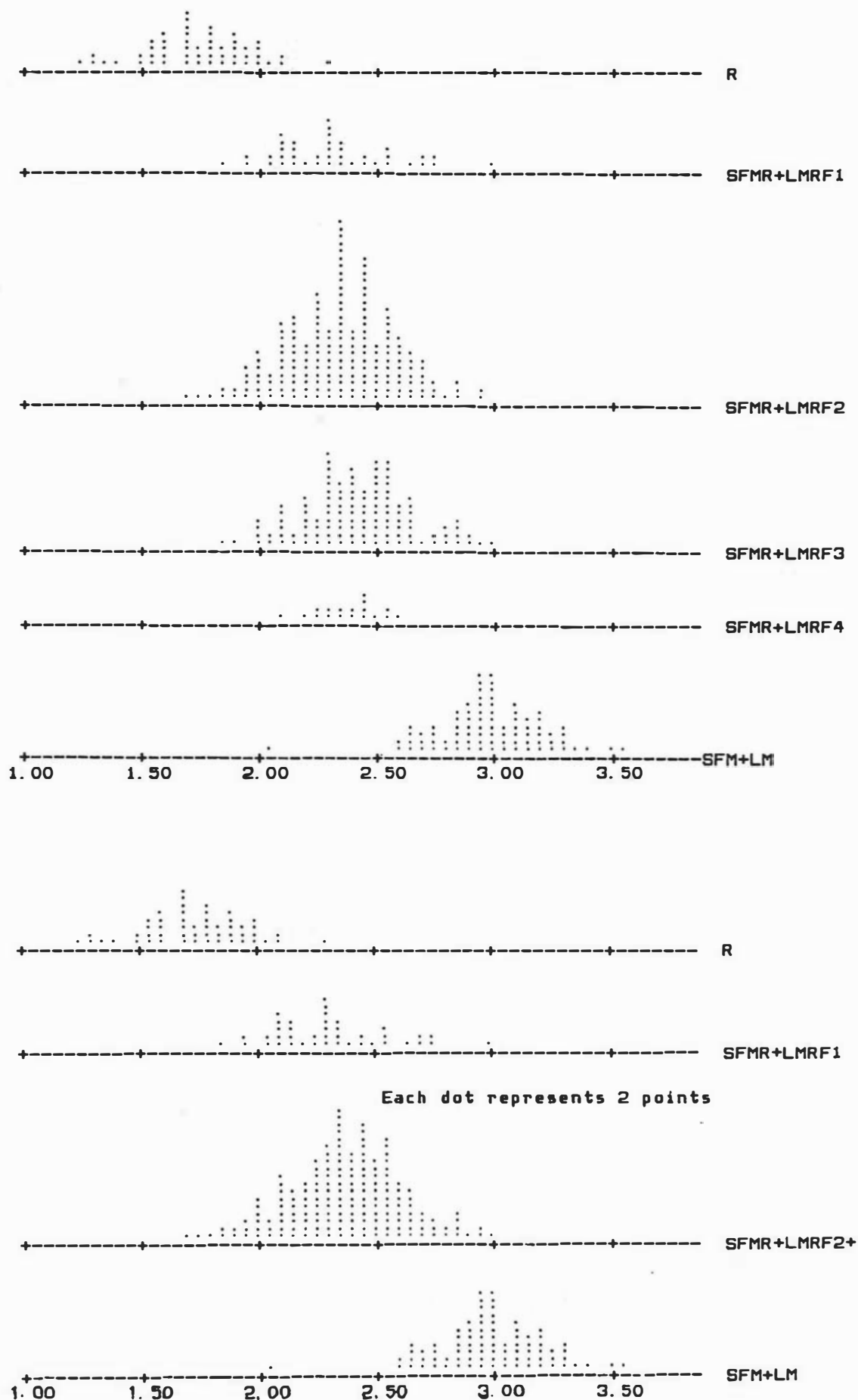
Figure 5.14:   Frequency distributions of ln S/P
within crossbred genotypes
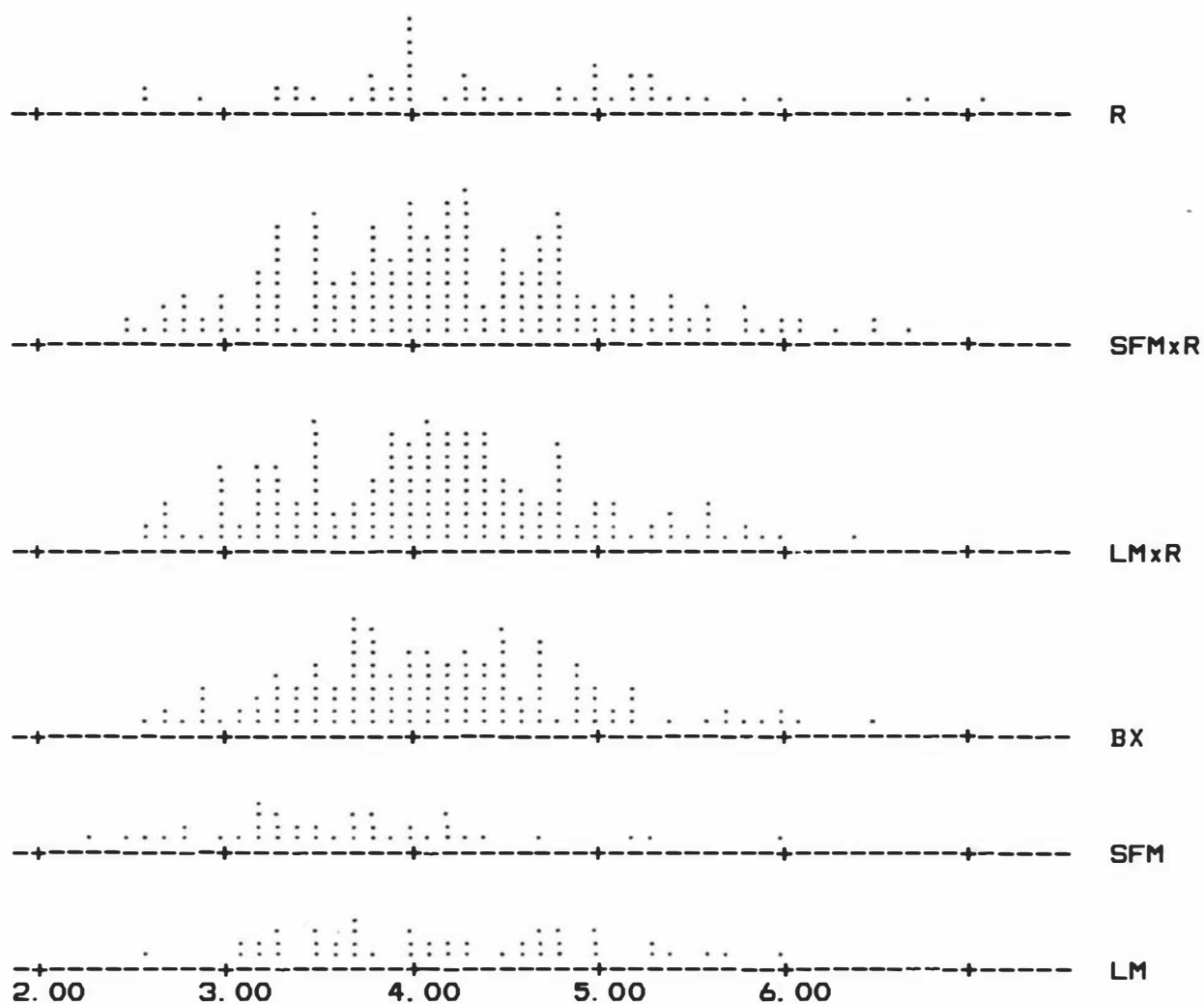
Figure 5.15:   Frequency distributions of nP
                for all genotypes
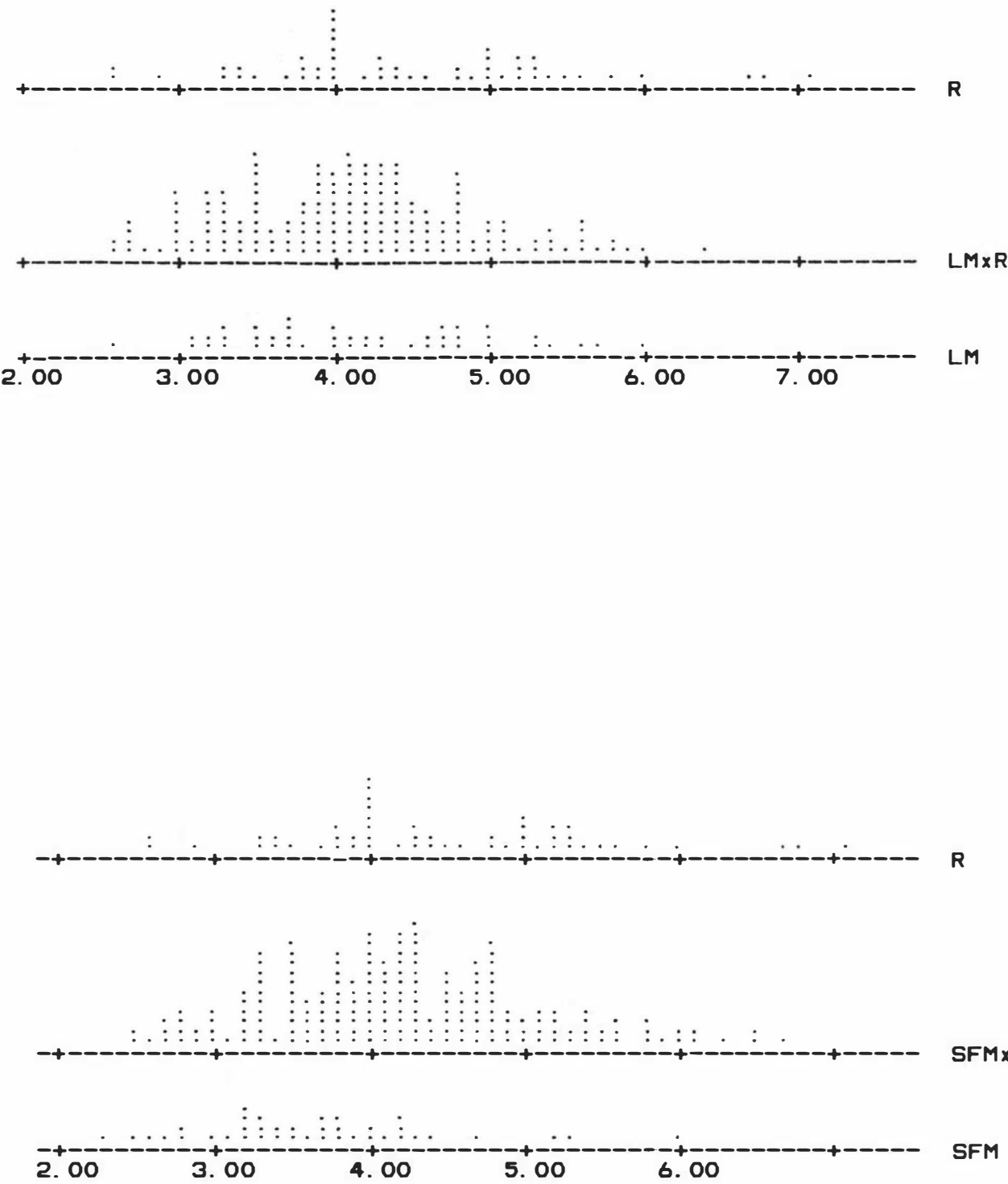
Figure 5.16: Frequency distributions of nP for parental groups and their respective crossbreds
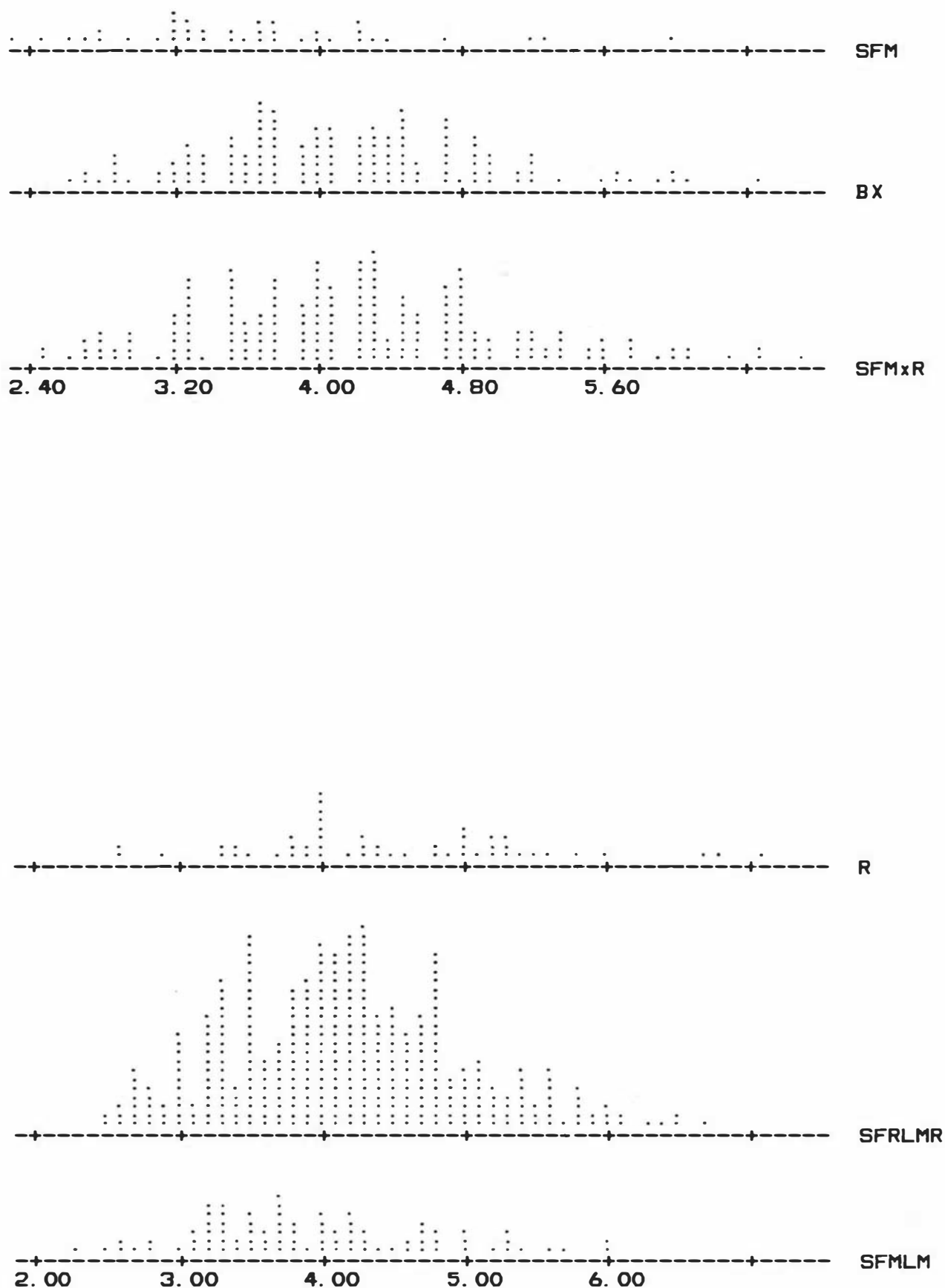
Figure 5.17:   Frequency distributions of nP for parental
groups and their respective crossbreds
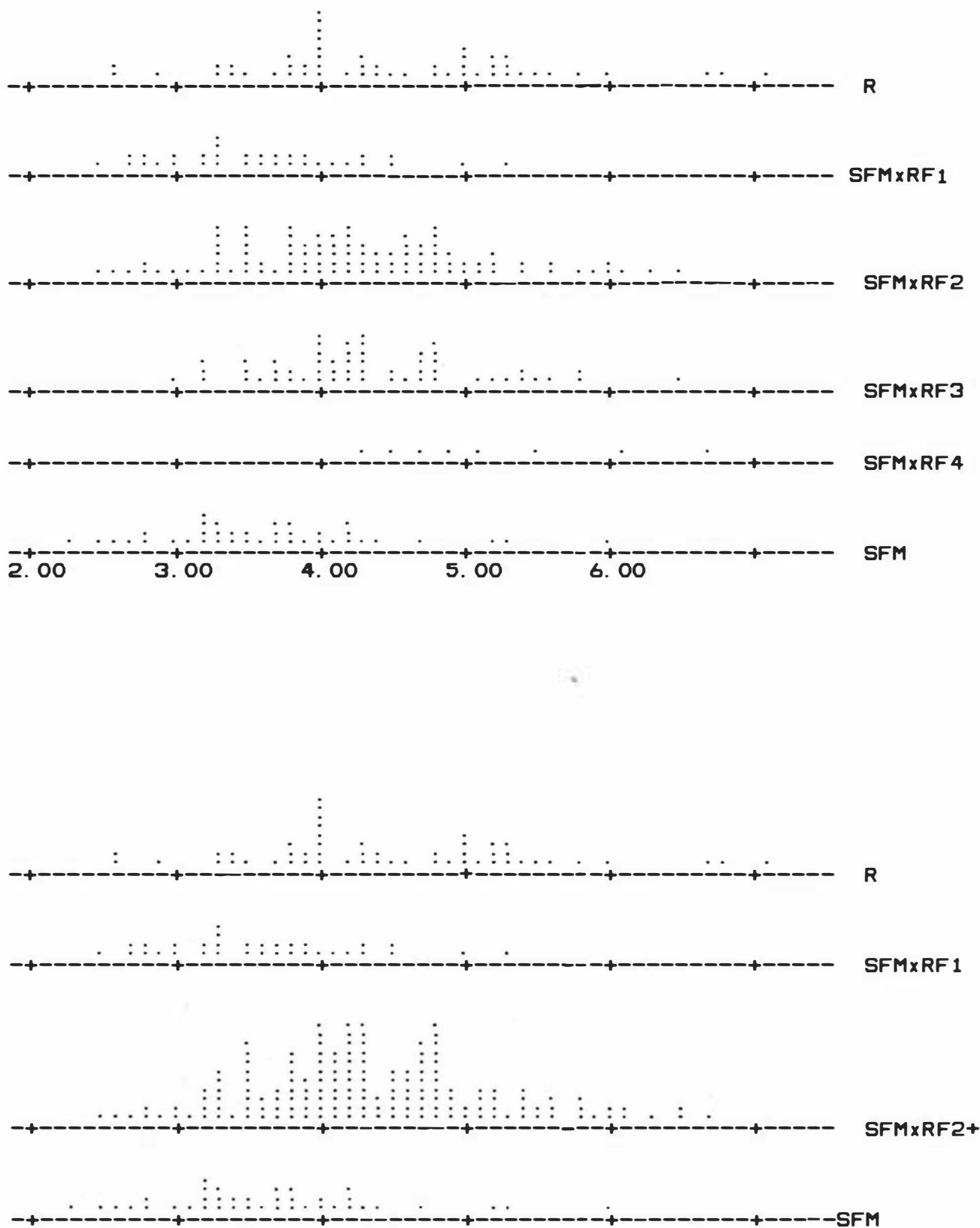
Figure 5.18:   Frequency distributions of nP
                within crossbred genotypes
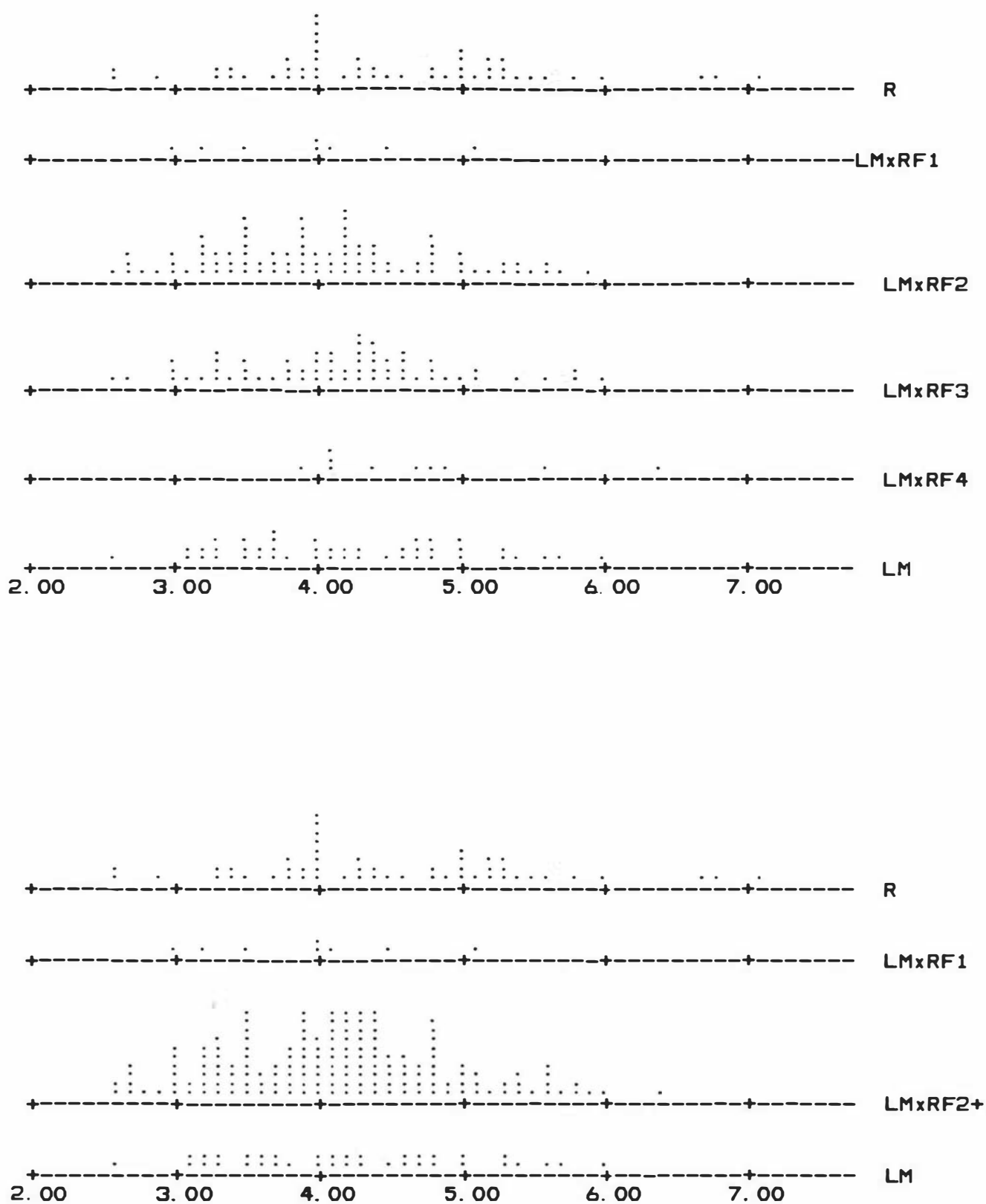
Figure 5.19: Frequency distributions of nP
within crossbred genotypes
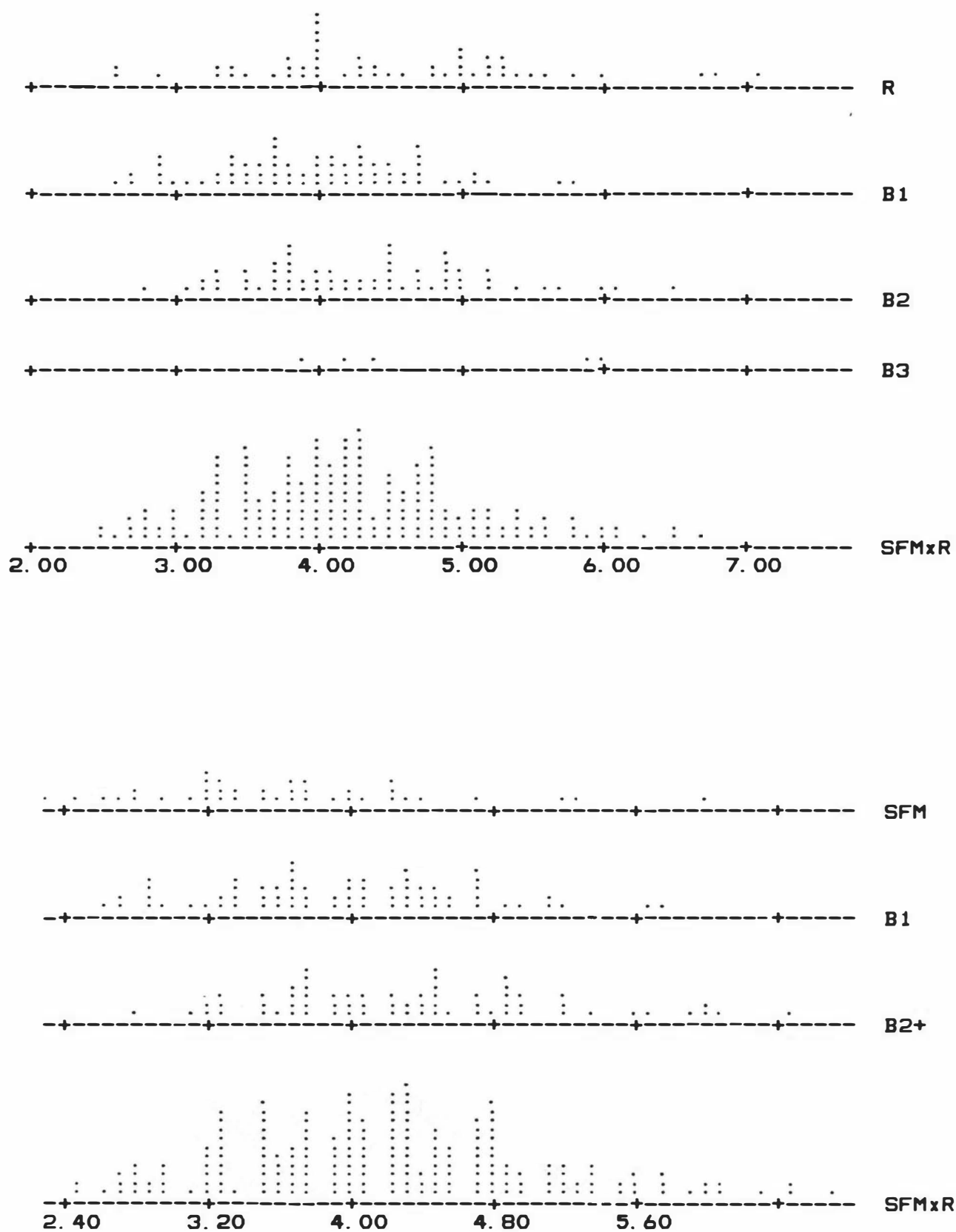
Figure 5.20:   Frequency distributions of nP
                within crossbred genotypes
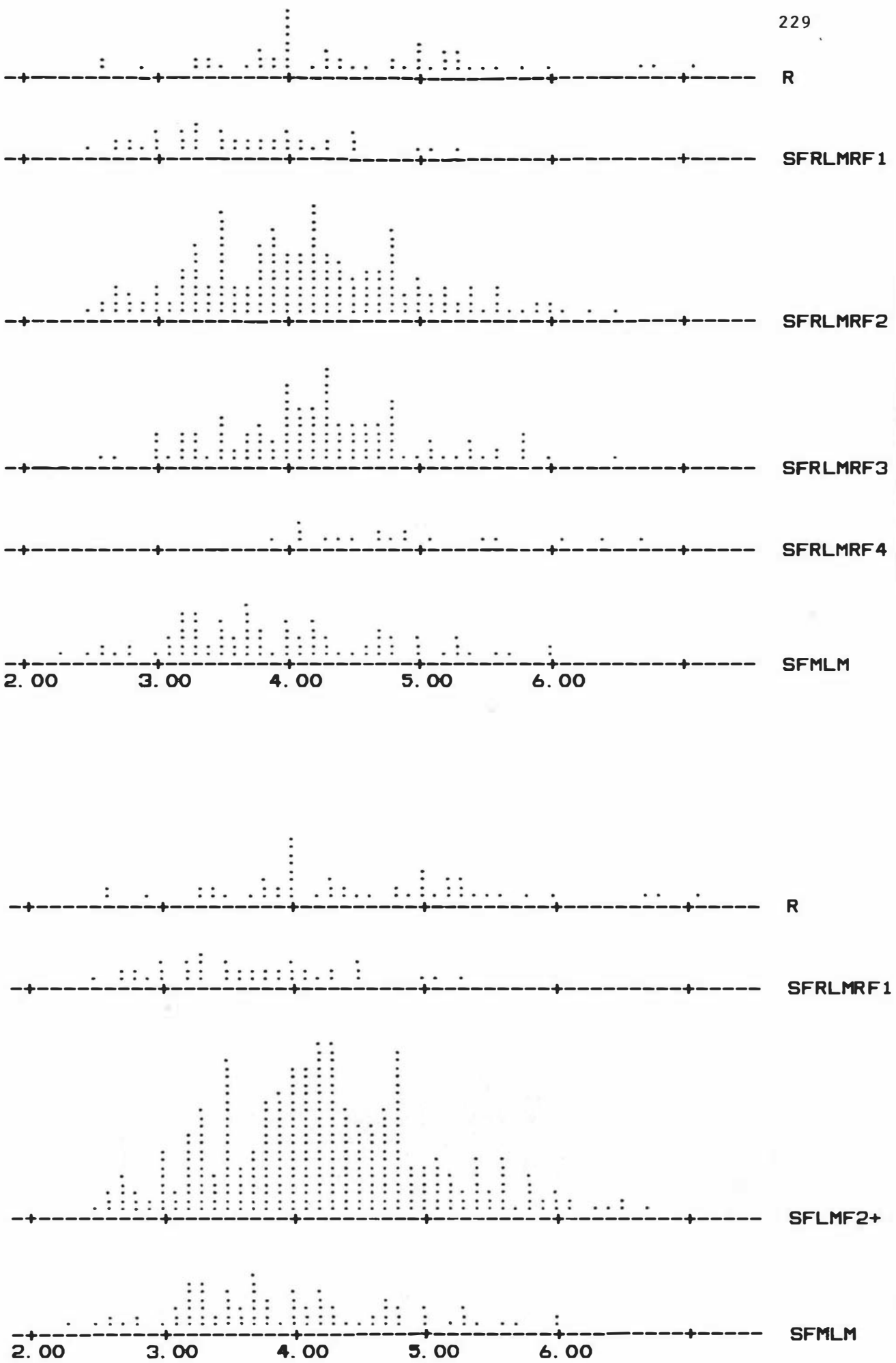
Figure 5.21:   Frequency distributions of nP
within crossbred genotypes
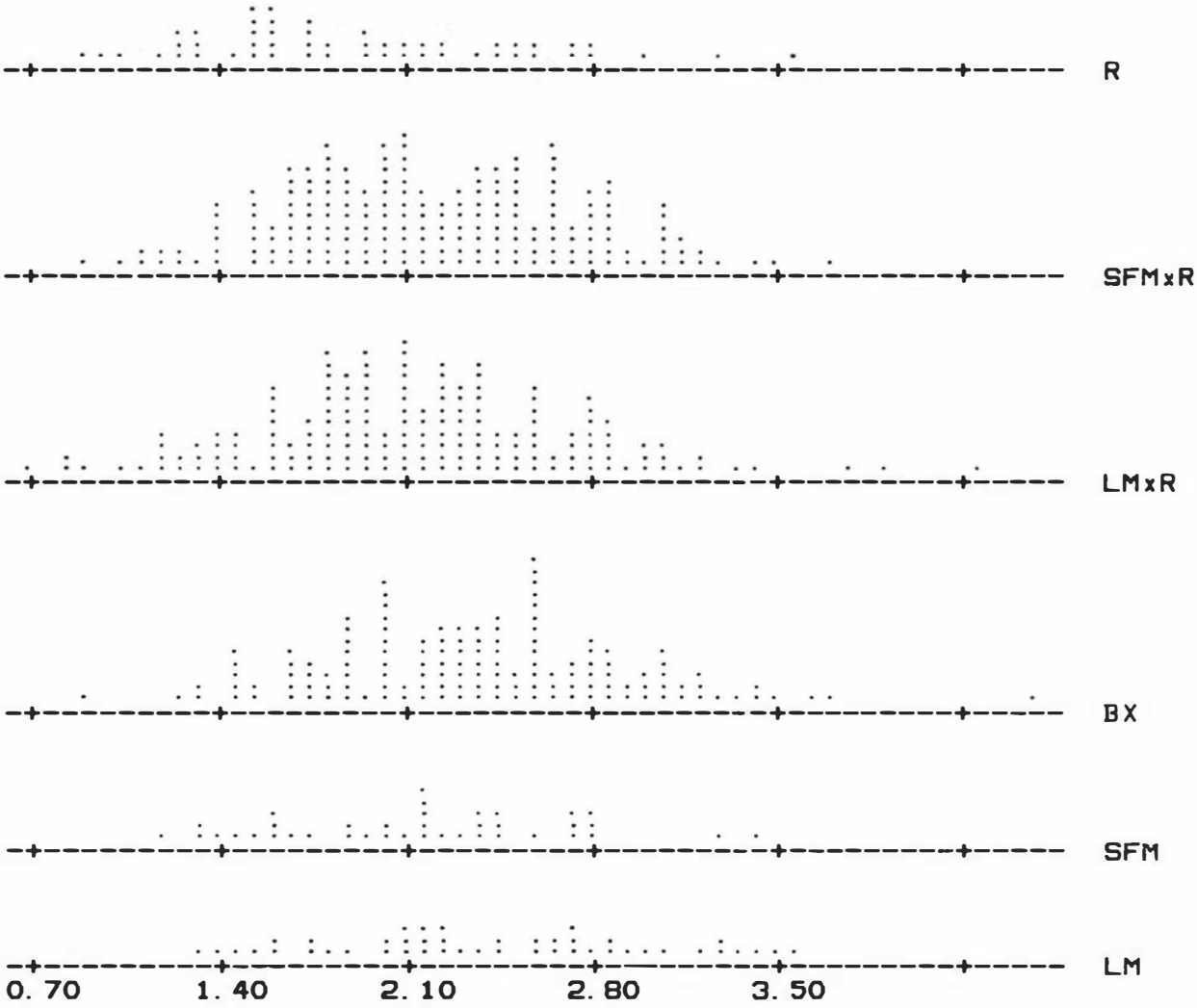
Figure 5.22 : Frequency distributions of nP(corr)
for all genotypes
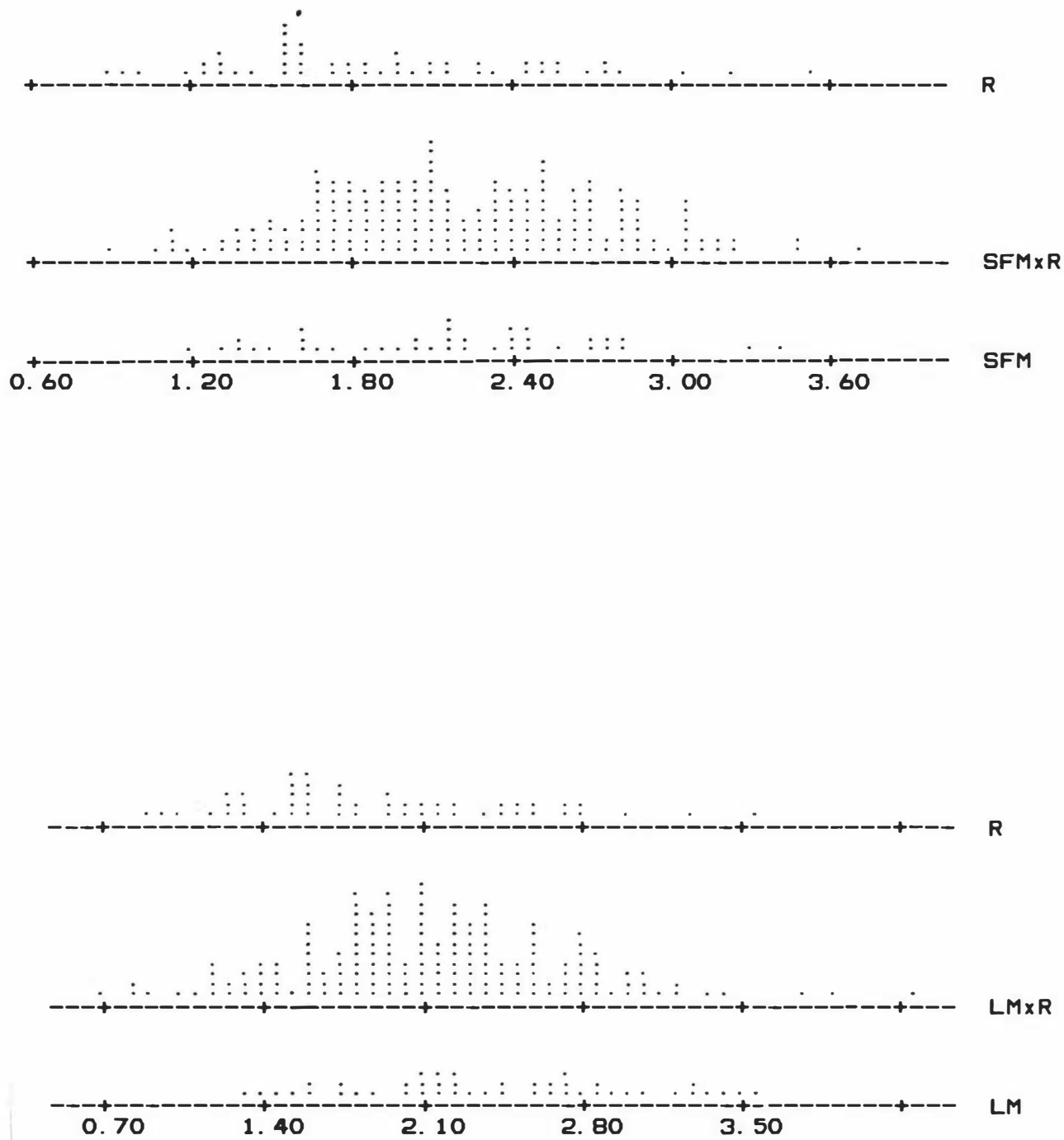
Figure 5.23:   Frequency distributions of nP(corr) for
              parental groups and their respective crossbreds
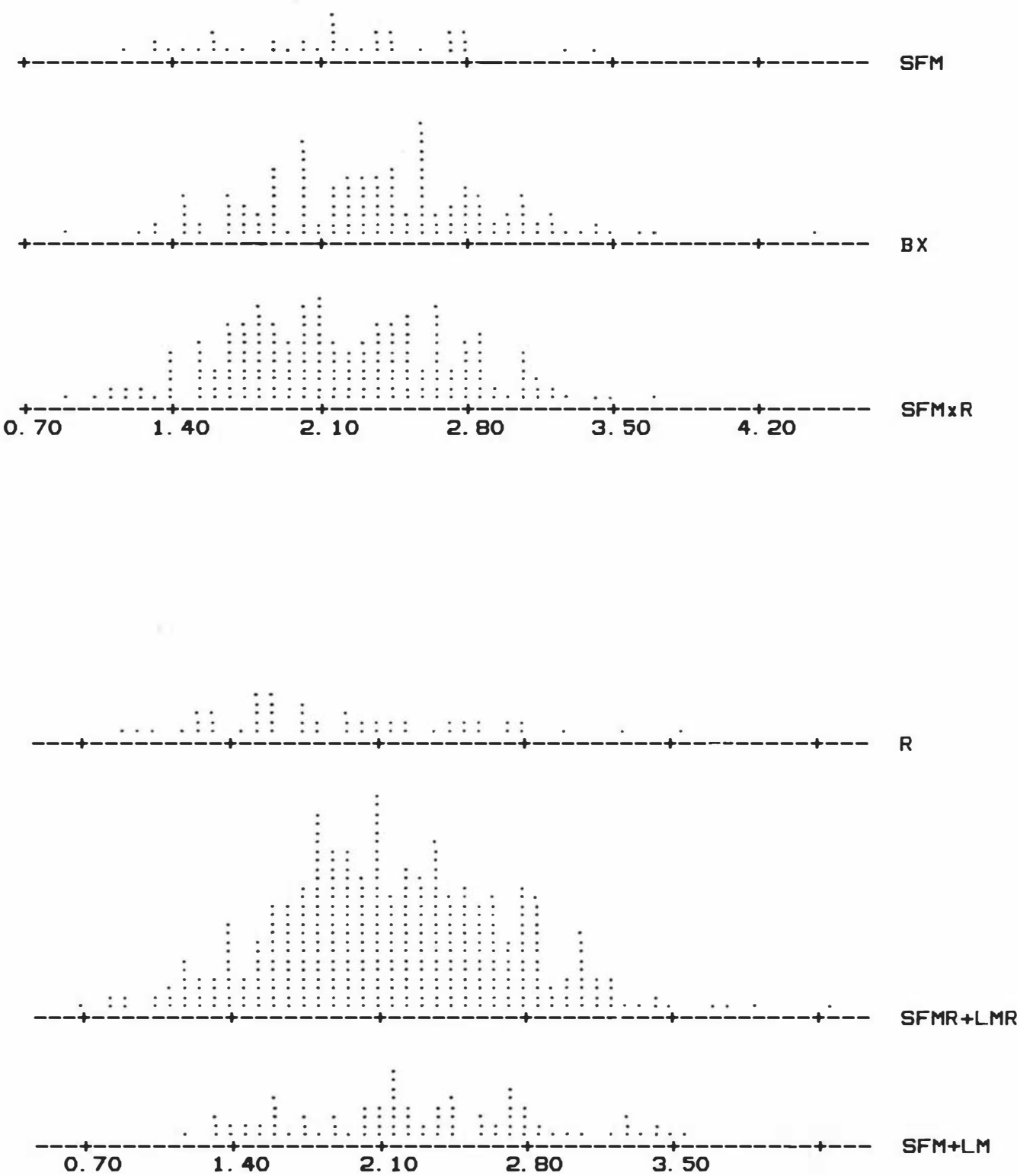
Figure 5.24:   Frequency distributions of nP(corr) for
parental groups and their respective crossbreds
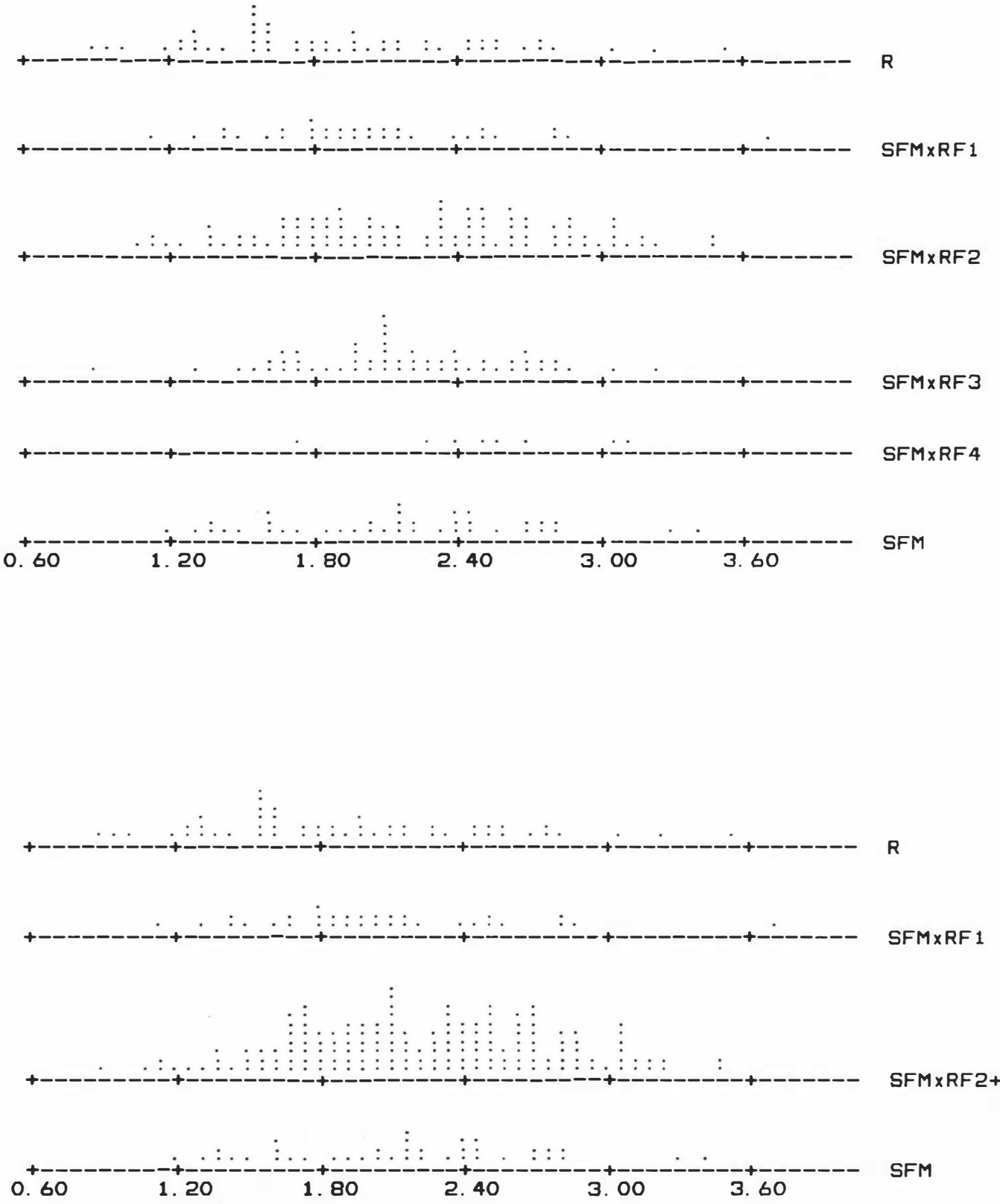
Figure 5.25:   Frequency distributions of nP(corr)
within crossbred genotypes
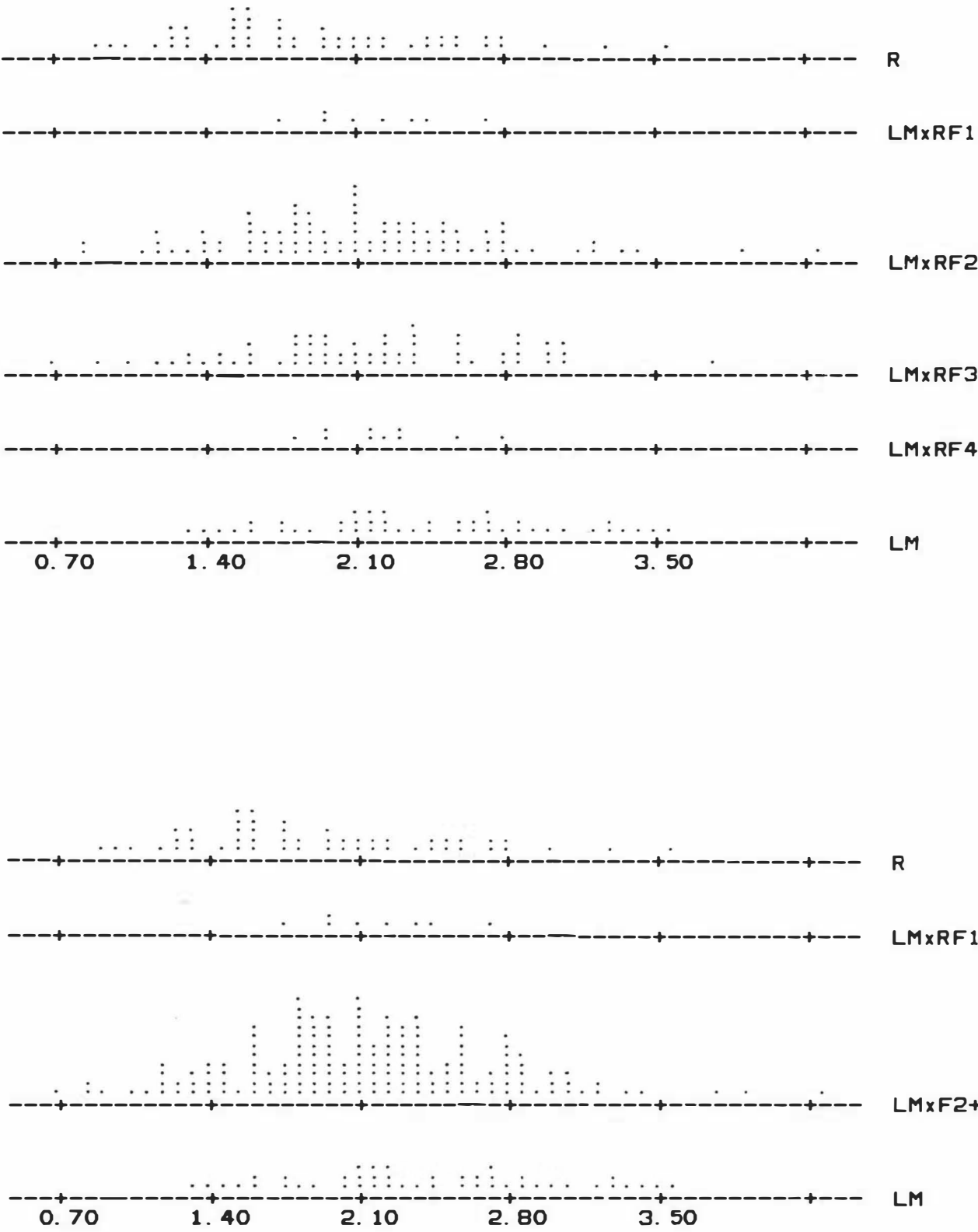
Figure 5.26: Frequency distributions of nP(corr) within crossbred genotypes

Figure 5.27:   Frequency distributions of nP(corr)
                within crossbred genotypes

Figure 5.28: Frequency distributions of nP(Corr) within crossbred genotypes

Figures 5.4 - 5.7, 5.11 - 5.14 demonstrate the S/P and ln S/P frequency distributions between generations within the SFMxR, LMxR, BX and SFMR+LMR classes. The presence of a major gene might have shown up as a bi-modal distribution in the F_2 generation. However, a major gene was suggested by only the F_2 SFMxR group distribution.

There was a small increase in the variance of ln S/P between the F_1 and F_2 generations in the LMxR group (see figure 5.12). This may reflect an increase in the number of animals between generations (i.e., 8 vs. 89) rather than the presence of a major gene.

In contrast, in the SFMxR genotype, the variation in ln S/P decreased between the F_1 and F_2 generations. The removal of one animal from the SFMxR F_1 data altered these results, as this animal was outside the data range. Then, there was no difference in variance between the F_1 and F_2 generations. The variance of ln S/P decreased further between the F_3 and F_4 generations. Mean S/P per generation increased (see Tables 4.10 - 4.11). This suggests that within this genotype there may have been some indirect selection for S/P.

The frequency distributions of ln S/P for the combined crossbreds (SFMR+LMR) - F_1 vs. F_2 and F_{2+} generations are shown in figure 5.14. There is a suggestion of bimodality in the F_2 generation but this did not persist in the F_{2+} group.

The accuracy of comparisons of frequency distributions of S/P and ln S/P between generations was hampered by the limited number of F_1 animals sampled. Due to the starting date of the present study, no additional F_1 animals were available for sampling. Increased data from F_1 animals would have added to the understanding of the genetic mechanisms controlling S/P in these flocks.

In general, the variance of a trait is expected to increase between the F_1 and F_2 generations (Wright, 1952; Pattie and Smith, 1964; Henderson, 1968). This did not occur in some genotypes in the present study.

From the frequency distributions of S/P, the genetic factors controlling S/P appear to act in a recessive manner with the crossbred animals having mean S/P ratios closer to the Romneys than the Merinos. The BX animals had S/P ratios as expected midway between the SFM and SFMxR groups. This pattern is consistent with a recessive mode of inheritance for S/P. It is clear from figure 5.1 that S/P increases as the proportion of Merino in the genotype increases.

5.1.2 nP

The frequency distributions of nP across genotypes are shown in Figure 5.15. Unlike S/P, there was a similar range of nP for each breed. The frequency distributions are platykurtic. Figures 5.16 - 5.17 show the distributions of nP for the parental groups and their respective crossbreds. With the exception of the Romneys the variance of nP within each crossbred genotype was slightly greater than that in the parental groups.

Figures 5.18 - 5.21 contain comparisons of the frequency distributions of nP in the parental groups with the appropriate F_1 to F_4 generations of crossbreds (i.e., R, SFM vs SFMxR F_1 - F_4). In the SFMxR the F_2 group had a higher variance for nP than the F_1. In the SFMxR F_2 and F_{2+} groups there was a slight suggestion of bimodality. Similar patterns were noted for these generations in the LMxR crossbreds.

The SFMxR F_1 to F_4 and BX B_1 to B_3 generations had higher than expected nP means. The values (nP mean), for the same generations in the LMxR crossbreds were variable and lower than the expected parental group mean (see Tables 4.10 - 4.13).

The nP frequency distribtuions, in both the SFMxR and LMxR show only vague suggestions of the presence of a main gene for nP. The presence/absence of a main gene will be further discussed in section 5.4. The present frequency distributions suggest that in each genotype nP is controlled by several genetic factors.

The frequency distributions for nP(corr) are shown in figures 5.21 - 5.28. They resembled the nP distributions.

5.2 BARTLETT'S TEST OF HOMOGENEITY OF VARIANCE

Bartlett's Test of Homogeneity of Variance is used frequently to assess distributional properties of data. In one form it reflects non-normality of the data, in another inequality of variance among samples (Sokal and Rohlf, 1981; Steel and Torrie, 1981).

If a major gene, or a few major genes, were involved in the control of follicle inheritance then its/their presence may be detected by changes in variance between genotypes and between generations of hybrids (crossbreds) (Fain, 1978).

Using Bartlett's Test of Homogeneity of Variance, and data corrected and uncorrected for fixed effects the following comparisons were made:

1. Rom vs. SFM vs. LM vs. SFMxR vs. LMxR vs. BX
2. SFM vs. LM
3. SFMxR vs. LMxR
4. Within the SFMxR group: F_1 vs. F_2 vs. F_3 vs. F_4
5. Within the LMxR group: F_1 vs. F_2 vs. F_3 vs. F_4
6. Within the BX group: B_1 vs. B_2 vs. B_3

The text will cover those results obtained using data corrected for age, year sampled and birth/rearing rank. The results are given in Tables 5.1 - 5.4.

5.2.1 R vs. SFM vs. LM vs. SFMxR vs LMxR vs. BX

For both data sets, there were significant differences (p<0.01) in variance between the six genotypes for: S/P, n(P+S), n(P+S)corr, QN_r, QN_m, SL_r, SL_m, TCN, MFD and CF.

For the data set uncorrected for fixed effects, the differences between the genotypes were also significant (p<0.01) for: LWT, FWT and SL_m.

Given the range of genotypes and wide contrast in values of the fleece and follicle traits, as well as the differences in numbers of animals per genotype, these results were not unexpected.

5.2.2 SFMxR: F_1 vs. F_2 vs. F_3 vs. F_4

For follicle traits the only significant difference in the variances between generations for both data sets was for nP in the data corrected for fixed effects.

With the exception of n(P+S)corr and nP the variance of the F_2's was greater than for the F_1's. If the parent breeds differed substantially in the presence of main genes, it is expected that genetic segregation would lead to greater variance in the later generation than in F_1.

TABLE 5.1: Variances of fleece and follicle traits, and significances of differences between generations by Bartlett's test of homogeneity of variances using data corrected for age, year sampled and and birth/rearing rank (Upper figure of each pair is SFMxR; lower LMxR)

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)	χ^2
S/P	R	2.68 (52)					
	SFM	23.75 (39)	7.18 (33)	4.92 (97)	5.47 (56)	1.48 (8)	5.673 NS
	LM	16.96 (45)	9.15 (8)	6.94 (89)	7.23 (63)	2.17 (10)	4.471 NS
ln S/P	R	0.06 (52)					
	SFM	0.07 (39)	0.06 (33)	0.04 (97)	0.03 (56)	0.01 (8)	7.286 NS
	LM	0.04 (45)	0.07 (8)	0.06 (89)	0.05 (63)	0.02 (10)	4.218 NS
n(P+S)	R	102.38 (52)					
	SFM	285.49 (39)	150.09 (33)	103.39 (97)	148.55 (56)	175.64 (8)	3.420 NS
	LM	322.97 (45)	76.41 (8)	93.68 (89)	130.81 (63)	196.61 (10)	4.169 NS
n(P+S)corr	R	22.44 (52)					
	SFM	160.59 (39)	43.00 (33)	47.44 (97)	33.06 (56)	42.17 (8)	2.155 NS
	LM	237.48 (45)	46.45 (8)	54.84 (89)	63.88 (63)	29.49 (10)	2.136 NS
nP	R	0.83 (52)					
	SFM	0.51 (39)	0.41 (33)	0.60 (97)	0.31 (56)	0.66 (8)	7.907 *
	LM	0.32 (45)	0.47 (8)	0.43 (89)	0.55 (63)	0.61 (10)	1.347 NS
nP(corr)	R	0.34 (52)					
	SFM	0.24 (39)	0.28 (33)	0.28 (97)	0.19 (56)	0.19 (8)	3.186 NS
	LM	0.32 (45)	0.11 (8)	0.35 (89)	0.32 (63)	0.10 (10)	7.621 NS

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)	χ^2
CF	R	0.02 (52)					
	SFM	0.03 (39)	0.01 (33)	0.01 (97)	0.01 (56)	0.01 (8)	0.313 NS
	LM	0.02 (45)	0.01 (8)	0.01 (89)	0.02 (63)	0.02 (10)	4.464 NS
LWT	R	37.57 (43)					
	SFM	29.64 (33)	26.93 (23)	25.96 (88)	23.85 (55)	7.82 (8)	3.412 NS
	LM	14.90 (41)	29.46 (3)	26.50 (80)	27.83 (59)	21.14 (10)	0.271 NS
GFW	R	0.41 (51)					
	SFM	0.35 (36)	0.16 (33)	0.32 (94)	0.15 (55)	0.32 (8)	11.604 **
	LM	0.28 (42)	0.34 (7)	0.35 (88)	0.21 (63)	0.42 (10)	4.810 NS
CFW	R	0.26 (20)					
	SFM	0.17 (34)	0.11 (31)	0.25 (80)	0.12 (49)	0.16 (7)	10.801 *
	LM	0.14 (40)	0.18 (6)	0.24 (77)	0.18 (55)	0.30 (9)	1.584 NS
YLD	R	19.01 (21)					
	SFM	23.14 (37)	14.18 (31)	22.23 (83)	33.21 (50)	15.63 (7)	6.930 NS
	LM	25.96 (43)	26.57 (6)	18.28 (77)	21.63 (55)	10.62 (9)	1.865 NS
MFD	R	4.33 (21)					
	SFM	3.36 (37)	6.78 (31)	5.58 (83)	7.18 (52)	12.90 (8)	3.207 NS
	LM	2.06 (43)	6.71 (7)	5.48 (78)	8.20 (57)	9.38 (9)	3.057 NS

TABLE 5.1: continued

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)	χ^2
QN_r	R	2.68 (16)					
	SFM	20.04 (21)	4.86 (25)	7.28 (71)	4.04 (27)		3.632 NS
	LM	6.70 (20)	22.14 (3)	4.93 (69)	5.60 (34)		3.359 NS
QN_m	R	20.56 (21)					
	SFM	12.46 (38)	13.08 (31)	8.74 (80)	9.38 (51)	3.76 (8)	4.172 NS
	LM	11.32 (44)	23.63 (7)	10.45 (80)	5.36 (57)	6.31 (9)	11.279 *
SL_r	R	2.15 (15)					
	SFM	1.26 (21)	0.90 (25)	2.12 (71)	1.61 (27)		5.607 NS
	LM	1.24 (20)	2.14 (69)	2.64 (69)	2.58 (34)		0.041 NS
SL_m	R	2.77 (21)					
	SFM	0.69 (38)	2.21 (31)	1.97 (86)	1.90 (51)	0.86 (8)	2.044 NS
	LM	1.09 (44)	3.63 (7)	1.95 (80)	2.22 (57)	0.94 (9)	3.257 NS
TCN	R	21.01 (21)					
	SFM	75.30 (38)	59.92 (31)	57.67 (86)	98.08 (51)	65.84 (8)	4.935 NS
	LM	61.28 (44)	33.22 (7)	31.63 (80)	32.02 (57)	47.72 (9)	0.683 NS
CPC	R	0.18 (21)					
	SFM	1.41 (38)	0.76 (31)	0.68 (86)	1.69 (51)	0.56 (8)	15.317 **
	LM	0.99 (44)	0.61 (7)	0.29 (80)	0.39 (57)	0.32 (9)	2.756 NS

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)		χ^2
CHR_r	R	0.73 (16)						
	SFM	1.11 (21)	1.17 (25)	1.17 (70)	1.00 (27)			0.238 NS
	LM	0.60 (20)	2.00 (3)	1.41 (69)	1.27 (34)			0.258 NS
CHR_m	R	0.56 (21)						
	SFM	0.33 (38)	0.70 (33)	0.53 (86)	0.47 (51)	0.21	(8)	3.824 NS
	LM	0.71 (44)	0.26 (7)	0.46 (80)	0.31 (57)	0.11	(9)	7.109 NS
LUS	R	0.42 (21)						
	SFM	0.47 (38)	0.89 (33)	0.59 (86)	0.35 (51)	0.20	(8)	10.875 *
	LM	0.47 (44)	1.57 (7)	0.72 (80)	0.39 (47)	0.10	(9)	17.485 **
TIP	R	0.46 (21)						
	SFM	0.31 (37)	0.44 (31)	0.38 (86)	0.32 (51)	0.58	(8)	1.671 NS
	LM	0.41 (44)	0.23 (7)	0.36 (80)	0.36 (57)	0.50	(9)	0.945 NS
COT	R	1.06 (21)						
	SFM	0.17 (37)	0.24 (31)	0.41 (86)	0.25 (51)	0.53	(8)	6.481 NS
	LM	0.16 (44)	0.32 (7)	0.39 (80)	0.29 (57)	0.27	(9)	1.473 NS
SOU	R	2.18 (21)						
	SFM	1.87 (38)	3.55 (31)	2.15 (86)	1.89 (51)	0.32	(8)	11.913 **
	LM	2.11 (44)	4.39 (7)	1.61 (80)	1.66 (57)	1.29	(9)	4.048 NS

TABLE 5.1:   continued

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)	χ^2
HND	R	0.44 (21)					
	SFM	0.39 (38)	0.75 (31)	0.46 (86)	0.43 (51)	0.24 (8)	5.329 NS
	LM	0.50 (44)	0.48 (7)	0.40 (80)	0.38 (57)	0.47 (9)	0.277 NS
GC_r	R	1.01 (15)					
	SFM	1.60 (21)	0.23 (25)	0.63 (71)	0.74 (27)		8.655 *
	LM	0.81 (20)	0.37 (3)	0.71 (69)	1.52 (34)		6.912 *
GC_m	R	0.39 (21)					
	SFM	0.38 (38)	0.49 (32)	0.53 (86)	0.50 (51)	0.28 (8)	1.049 NS
	LM	0.42 (44)	0.48 (7)	0.51 (80)	0.54 (57)	0.37 (9)	0.427 NS
SC_m	R	0.41 (21)					
	SFM	0.32 (37)	0.45 (32)	0.81 (85)	0.65 (48)	0.41 (55)	4.273 NS
	LM	0.37 (44)	0.64 (6)	0.88 (76)	0.76 (55)	0.53 (9)	1.044 NS

* $P < 0.05$
** $P < 0.01$
NS   non-significant

TABLE 5.2: Variances of fleece and follicle traits, and significances of differences between generations by Bartlett's Test of homogeneity of variances using data uncorrected for fixed effects (Upper figure of each pair is SFMxR; lower LMxR)

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)	χ^2
S/P	R	1.74 (52)					
	SFM	24.42 (39)	7.95 (33)	5.48 (97)	6.49 (56)	1.18 (8)	7.560 NS
	LM	18.67 (45)	10.86 (8)	7.63 (89)	8.36 (63)	2.52 (10)	4.549 NS
ln S/P	R	0.05 (52)					
	SFM	0.07 (39)	0.06 (33)	0.05 (97)	0.04 (56)	0.01 (8)	7.699 NS
	LM	0.04 (45)	0.08 (8)	0.07 (89)	0.06 (63)	0.02 (10)	3.793 NS
n(P+S)	R	67.22 (52)					
	SFM	309.27 (39)	165.95 (33)	177.51 (97)	274.98 (56)	169.19 (8)	4.261 NS
	LM	472.76 (45)	81.55 (8)	145.75 (89)	179.26 (63)	199.79 (10)	2.237 NS
n(P+S)corr	R	19.00 (52)					
	SFM	185.36 (39)	46.04 (33)	63.34 (97)	42.60 (56)	41.71 (8)	3.245 NS
	LM	251.44 (45)	44.72 (8)	64.29 (89)	72.81 (63)	30.71 (10)	2.770 NS
nP	R	0.98 (52)					
	SFM	0.60 (39)	0.45 (33)	0.74 (97)	0.53 (56)	0.69 (8)	3.576 NS
	LM	0.65 (45)	0.10 (8)	0.40 (89)	0.37 (63)	0.08 (10)	10.270 *
nP(corr)	R	0.36 (52)					
	SFM	0.29 (39)	0.28 (33)	0.33 (97)	0.21 (56)	0.19 (8)	3.741 NS
	LM	0.37 (45)	0.47 (8)	0.62 (89)	0.57 (63)	0.62 (10)	0.328 NS

TABLE 5.2:   continued

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)	χ^2
CF	R	0.01 (52)					
	SFM	0.01 (39)	0.01 (33)	0.02 (97)	0.01 (56)	0.01 (8)	1.862 NS
	LM	0.02 (45)	0.01 (8)	0.01 (89)	0.02 (63)	0.01 (10)	4.850 NS
LWT	R	141.50 (43)					
	SFM	46.65 (33)	37.76 (23)	84.58 (88)	30.65 (55)	6.63 (8)	15.206 **
	LM	59.17 (41)	35.37 (3)	93.66 (80)	79.15 (59)	21.78 (10)	6.189 NS
GFW	R	0.58 (51)					
	SFM	0.37 (36)	0.21 (33)	0.45 (94)	0.25 (55)	0.32 (8)	9.383 *
	LM	0.33 (42)	0.23 (7)	0.61 (88)	0.35 (63)	0.41 (10)	6.888 NS
CFW	R	0.28 (20)					
	SFM	0.18 (34)	0.14 (31)	0.28 (80)	0.19 (49)	0.17 (7)	6.819 NS
	LM	0.17 (40)	0.17 (6)	0.40 (77)	0.27 (55)	0.29 (9)	3.140 NS
YLD	R	22.21 (21)					
	SFM	25.26 (37)	12.72 (31)	27.24 (83)	34.46 (50)	15.62 (7)	8.776 *
	LM	27.17 (43)	27.63 (6)	22.37 (77)	23.39 (55)	10.44 (9)	1.929 NS
MFD	R	4.01 (21)					
	SFM	3.16 (37)	7.13 (31)	5.90 (83)	8.05 (52)	12.98 (8)	3.243 NS
	LM	2.41 (43)	7.11 (7)	6.59 (78)	8.42 (57)	9.39 (9)	1.188 NS

TABLE 5.2: continued

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)	χ^2
QN_r	R	2.38 (16)					
	SFM	25.06 (21)	3.34 (25)	8.40 (71)	3.92 (27)		9.511 **
	LM	6.36 (20)	30.33 (3)	4.66 (69)	5.18 (34)		5.978 NS
QN_m	R	19.71 (21)					
	SFM	18.09 (38)	16.75 (31)	11.81 (80)	8.95 (51)	3.71 (8)	6.911 NS
	LM	18.83 (44)	19.14 (7)	8.15 (80)	5.78 (57)	7.03 (9)	5.514 NS
SL_r	R	1.95 (15)					
	SFM	1.12 (21)	0.84 (25)	2.88 (71)	3.19 (27)		11.626 **
	LM	1.14 (20)	2.58 (3)	3.75 (69)	3.92 (34)		0.140 NS
SL_m	R	3.36 (21)					
	SFM	1.06 (38)	1.94 (31)	2.45 (86)	2.86 (51)	0.89 (8)	3.932 NS
	LM	1.17 (44)	3.12 (7)	2.52 (80)	2.77 (57)	1.01 (9)	2.820 NS
TCN	R	17.23 (21)					
	SFM	73.99 (38)	65.69 (31)	63.44 (86)	112.48 (51)	66.13 (8)	5.872 NS
	LM	67.39 (44)	32.95 (7)	35.92 (80)	36.27 (57)	47.53 (9)	0.335 NS
CPC	R	0.14 (21)					
	SFM	1.52 (38)	0.80 (31)	0.69 (86)	1.76 (51)	0.56 (8)	16.058 **
	LM	0.98 (44)	0.72 (7)	0.29 (80)	0.40 (57)	0.32 (9)	3.497 NS

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)		χ^2
CHR_r	R	0.78 (16)						
	SFM	1.13 (21)	1.16 (25)	1.20 (70)	1.00 (27)			0.285 NS
	LM	0.56 (20)	2.33 (3)	1.38 (69)	1.41 (34)			0.291 NS
CHR_m	R	0.55 (21)						
	SFM	0.32 (38)	0.72 (33)	0.59 (86)	0.53 (51)	0.21	(8)	3.949 NS
	LM	0.78 (44)	0.14 (7)	0.47 (80)	0.32 (57)	0.11	(9)	8.527 *
LUS	R	0.35 (21)						
	SFM	0.83 (38)	1.12 (33)	0.72 (86)	0.38 (51)	0.21	(8)	14.535 **
	LM	0.74 (44)	1.24 (7)	0.67 (80)	0.41 (47)	0.11	(9)	12.374 **
TIP	R	0.45 (21)						
	SFM	0.31 (37)	0.44 (31)	0.37 (86)	0.33 (51)	0.57	(8)	1.373 NS
	LM	0.39 (44)	0.24 (7)	0.39 (80)	0.38 (57)	0.50	(9)	0.879 NS
COT	R	1.19 (21)						
	SFM	0.20 (37)	0.25 (31)	0.41 (86)	0.27 (51)	0.55	(8)	4.803 NS
	LM	0.18 (44)	0.29 (7)	0.41 (80)	0.33 (57)	0.25	(9)	1.426 NS
SOU	R	2.56 (21)						
	SFM	3.66 (38)	3.16 (31)	2.61 (86)	2.08 (51)	0.27	(8)	10.883 *
	LM	4.30 (44)	3.62 (7)	2.25 (80)	1.72 (57)	1.36	(9)	2.855 NS

Trait	Genotype	(n)	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)	χ^2
HND	R	0.39 (21)					
	SFM	0.55 (38)	0.82 (32)	0.66 (86)	0.60 (51)	0.21 (8)	4.085 NS
	LM	0.84 (44)	0.57 (7)	0.43 (80)	0.59 (57)	0.44 (9)	1.668 NS
GC_r	R	0.98 (15)					
	SFM	1.76 (21)	0.21 (25)	0.63 (71)	0.69 (27)		9.785 **
	LM	0.73 (20)	0.33 (3)	0.74 (69)	1.59 (34)		7.193 *
GC_m	R	0.45 (21)					
	SFM	0.52 (38)	0.50 (32)	0.58 (86)	0.59 (51)	0.27 (8)	1.749 NS
	LM	0.51 (44)	0.33 (7)	0.50 (80)	0.53 (57)	0.36 (9)	0.854 NS
SC_m	R	0.85 (21)					
	SFM	0.75 (37)	0.74 (32)	0.81 (85)	0.77 (48)	0.41 (55)	1.243 NS
	LM	0.51 (44)	0.97 (6)	1.02 (76)	0.79 (55)	0.53 (9)	1.990 NS

* $P < 0.05$
** $P < 0.01$
NS non-significant

TABLE 5.3: Variances of fleece and follicle traits, and significances of differences between generations by Bartletts test of homogeneity of variances using data corrected for age, year sampled and birth/rearing rank

Trait	Genotype	(n)	B_1 (n)	B_2 (n)	B_3 (n)	χ^2
S/P	SFM	23.75 (39)	9.16 (69)	10.76 (63)	13.88 (5)	0.632 NS
	SFMxR	5.38 (194)				
ln S/P	SFM	0.07 (39)	0.04 (69)	0.05 (63)	0.05 (5)	0.775 NS
	SFMxR	0.04 (194)				
n(P+S)	SFM	285.49 (39)	206.10 (69)	276.85 (63)	499.90 (5)	2.625 NS
	SFMxR	127.32 (194)				
n(P+S)corr	SFM	160.59 (39)	125.31 (69)	136.09 (63)	126.43 (5)	0.108 NS
	SFMxR	42.15 (194)				
nP	SFM	0.51 (39)	0.52 (69)	0.41 (63)	1.05 (5)	2.426 NS
	SFMxR	0.49 (194)				
nP(corr)	SFM	0.24 (39)	0.30 (69)	0.33 (63)	0.47 (5)	0.570 NS
	SFMxR	0.25 (194)				
CF	SFM	0.03 (39)	0.01 (69)	0.02 (63)	0.01 (5)	2.414 NS
	SFMxR	0.01 (194)				
LWT	SFM	26.94 (33)	28.36 (56)	30.19 (55)	7.93 (5)	2.219 NS
	SFMxR	26.60 (174)				
GFW	SFM	0.35 (36)	0.36 (68)	0.21 (62)	0.25 (5)	4.282 NS
	SFMxR	0.24 (190)				
CFW	SFM	0.17 (34)	0.28 (64)	0.13 (61)	0.18 (5)	8.754 *
	SFMxR	0.18 (167)				
YLD	SFM	23.14 (37)	29.40 (64)	20.22 (62)	16.69 (2)	2.321 NS
	SFMxR	23.61 (171)				
MFD	SFM	3.36 (37)	3.79 (64)	4.68 (62)	1.70 (2)	1.837 NS
	SFMxR	6.58 (174)				
QN_r	SFM	20.04 (21)	13.49 (68)	21.14 (31)	0.42 (2)	4.126 NS
	SFMxR	6.01 (123)				
QN_m	SFM	12.46 (38)	16.07 (67)	13.49 (63)	1.60 (5)	5.531 NS
	SFMxR	9.43 (176)				
SL_r	SFM	1.26 (21)	2.26 (68)	1.77 (31)	1.76 (2)	0.526 NS
	SFMxR	1.78 (123)				
SL_m	SFM	0.69 (38)	1.79 (68)	2.21 (63)	0.57 (5)	2.700 NS
	SFMxR	1.95 (176)				

TABLE 5.3:   continued

Trait	Genotype	(n)	B_1 (n)	B_2 (n)	B_3 (n)	χ^2
TCN	SFM	75.30 (38)	130.93 (68)	73.40 (63)	19.36 (6)	8.265 *
	SFM>R	71.33 (176)				
CPC	SFM	1.41 (38)	1.60 (68)	1.59 (62)	0.41 (5)	2.334 NS
	SFMxR	1.01 (176)				
CHR$_r$	SFM	1.11 (21)	1.11 (68)	0.91 (31)	0.00 (2)	6.274 *
	SFMxR	1.12 (122)				
CHR$_m$	SFM	0.33 (38)	0.43 (68)	0.31 (63)	0.46 (5)	1.882 NS
	SFMxR	0.52 (178)				
LUS	SFM	0.47 (38)	0.79 (68)	0.45 (63)	0.16 (5)	7.061*
	SFMxR	0.55 (176)				
TIP	SFM	0.31 (37)	0.42 (68)	0.33 (63)	0.35 (5)	0.889 NS
	SFMxR	0.37 (176)				
COT	SFM	0.17 (37)	0.26 (68)	0.16 (63)	0.18 (5)	3.443 NS
	SFMxR	0.34 (176)				
SOU	SFM	1.87 (38)	2.95 (68)	1.70 (63)	2.07 (5)	4.610 NS
	SFMxR	2.23 (176)				
HND	SFM	0.39 (38)	0.86 (68)	0.47 (63)	0.25 (5)	6.609 *
	SFMxR	0.49 (177)				
GC$_r$	SFM	1.60 (21)	1.18 (68)	1.35 (31)	0.01 (2)	3.892 NS
	SFMxR	0.57 (123)				
GC$_m$	SFM	0.38 (38)	0.91 (68)	0.54 (63)	0.56 (5)	4.349 NS
	SFMxR	0.50 (177)				
SC$_m$	SFM	0.32 (37)	0.42 (64)	0.46 (63)	0.09 (5)	3.165 NS
	SFMxR	0.68 (173)				

* $P < 0.05$
** $P < 0.01$
NS   non-significant

TABLE 5.4: Variances of fleece and follicle traits, and significances of differences between generations by Bartletts test of homogeneity of variances using data uncorrected for age, year sampled and birth/rearing rank

Trait	Genotype	(n)	B_1 (n)	B_2 (n)	B_3 (n)	χ^2
S/P	SFM	24.52 (39)	9.46 (69)	11.63 (63)	15.34 (5)	0.985 NS
	SFMxR	18.67 (194)				
ln S/P	SFM	0.07 (39)	0.04 (69)	0.05 (63)	0.05 (5)	1.235 NS
	SFMxR	0.05 (194)				
n(P+S)	SFM	309.27 (39)	224.48 (69)	380.81 (63)	553.18 (5)	5.175 NS
	SFMxR	237.71 (194)				
n(P+S)corr	SFM	185.36 (39)	141.67 (69)	146.35 (63)	120.80 (5)	0.070 NS
	SFMxR	56.76 (194)				
nP	SFM	0.60 (39)	0.50 (69)	0.61 (63)	0.99 (5)	1.419 NS
	SFMxR	0.73 (194)				
nP(corr)	SFM	0.29 (39)	0.30 (69)	0.34 (63)	0.61 (5)	1.183 NS
	SFMxR	0.29 (194)				
CF	SFM	0.01 (39)	0.01 (69)	0.02 (63)	0.02 (5)	1.631 NS
	SFMxR	0.01 (194)				
LWT	SFM	46.65 (33)	39.78 (56)	67.91 (55)	40.72 (5)	3.815 NS
	SFMxR	99.62 (174)				
GFW	SFM	0.37 (36)	0.43 (68)	0.17 (62)	0.19 (5)	12.613 **
	SFMxR	0.34 (190)				
CFW	SFM	0.18 (34)	0.33 (64)	0.11 (61)	0.17 (5)	16.230 **
	SFMxR	0.22 (167)				
YLD	SFM	25.26 (37)	30.05 (64)	25.11 (62)	22.07 (2)	0.564 NS
	SFMxR	27.05 (171)				
MFD	SFM	3.16 (37)	4.00 (64)	4.56 (62)	2.49 (2)	0.719 NS
	SFMxR	7.46 (174)				
QN_r	SFM	25.06 (21)	14.11 (68)	22.66 (31)	0.50 (2)	4.256 NS
	SFMxR	6.34 (123)				
QN_m	SFM	18.09 (38)	20.69 (67)	16.71 (63)	2.80 (5)	4.677 NS
	SFMxR	11.46 (176)				
SL_r	SFM	1.12 (21)	2.81 (68)	2.28 (31)	2.00 (2)	0.407 NS
	SFMxR	2.59 (123)				
SL_m	SFM	1.06 (38)	2.56 (68)	2.56 (63)	2.43 (5)	0.005 NS
	SFMxR	2.52 (176)				

TABLE 5.4 continued

Trait	Genotype	(n)	B_1 (n)	B_2 (n)	B_3 (n)	χ^2
TCN	SFM	73.99 (38)	152.82 (68)	83.50 (63)	33.50 (6)	7.550 *
	SFM×R	82.90 (176)				
CPC	SFM	1.52 (38)	1.65 (68)	1.59 (62)	0.37 (5)	2.715 NS
	SFM×R	1.05 (176)				
CHR$_r$	SFM	1.13 (21)	1.18 (68)	1.03 (31)		0.186 NS
	SFM×R	1.15 (122)				
CHR$_m$	SFM	0.32 (38)	0.43 (68)	0.38 (63)	0.70 (5)	0.936 NS
	SFM×R	0.60 (178)				
LUS	SFM	0.83 (38)	0.91 (68)	0.47 (63)	0.20 (5)	8.617 *
	SFM×R	0.66 (176)				
TIP	SFM	0.31 (37)	0.43 (68)	0.35 (63)	0.30 (5)	0.854 NS
	SFM×R	0.38 (176)				
COT	SFM	0.20 (37)	0.27 (68)	0.22 (63)	0.20 (5)	0.802 NS
	SFM×R	0.34 (176)				
SOU	SFM	3.66 (38)	3.42 (68)	2.65 (63)	1.70 (5)	1.509 NS
	SFM×R	2.52 (176)				
HND	SFM	0.55 (38)	0.85 (68)	0.78 (63)	0.80 (5)	0.097 NS
	SFM×R	0.75 (177)				
GC$_r$	SFM	1.76 (21)	1.43 (68)	1.43 (31)		0.366 NS
	SFM×R	0.56 (123)				
GC$_m$	SFM	0.52 (38)	0.93 (68)	0.60 (63)	0.80 (5)	2.911 NS
	SFM×R	0.59 (177)				
SC$_m$	SFM	0.75 (37)	0.60 (64)	0.58 (63)	0.20 (5)	1.597 NS
	SFM×R	0.77 (173)				

* $P < 0.05$
** $P < 0.01$
NS non-significant

In the data corrected for fixed effects, the F_2's were significantly more variable than the F_1's for GFW, CPC, SOU ($p<0.01$) and CFW, LUS, GC_r ($p<0.05$). LWT, YLD, QN_r and SL_r were also significant in the uncorrected data.

For several fleece characteristics, including TCN and CPC, the variance increased between the F_2 and F_3 generations and not between the F_1 and F_2 groups.

5.2.3 LMxR: F_1 vs. F_2 vs. F_3 vs. F_4

There were no significant differences in the variance between generations for most follicle characteristics. The exceptions were n(P+S) and n(P+S)corr, where the F_1's were more variable than the F_2's. Large differences in number of animals per generation (8, 89), may have led to this unexpected result.

In the data set corrected for fixed effects the following traits showed significant differences: LUS**, QN_m* and GC_r*. In the uncorrected data, LUS** and GC_r* were also significant.

5.2.4 BX: B_1 vs. B_2 vs. B_3

With data corrected for fixed effects, only CFW, TCN, CHR_r, LUS and HND showed significant ($p,0.05$) between generation differences, in variance. Interestingly, for most follicle and fleece traits there was an increase in the variance between the B_1 and B_2 generations. These results contrast with those noted for the SFMxR and LMxR groups.

For all genotypes, the lack of significant differences between generations, for most traits confirms the validity of subsequent statistical tests. The results with reference to major gene detection will be considered in the discussion.

5.3 SKEWNESS AND KURTOSIS

Both skewness and kurtosis are used to check the symmetry or normality of distributions. In the presence of a major gene the frequency distribution would be changed (Merat, 1968). In the studies of Merat (1968) and Hammond and James (1970) the analyses were done within families. Due to the nature of the present data sets, the creation of families of sibships resulted in very small numbers of animals. Thus the present analyses were carried out within genotypes not families.

5.3.1 Method of Analysis

Skewness and kurtosis coefficients were calculated using REG. The computations used the equations of Snedecor (1946):

Skewness Coefficient

$$g_1 = k_3/\sqrt{k_2{}^3}$$

Where: $k_2 = S_2/(n-1)$

$$k_3 = nS_3/(n-1)(n-2)$$

$$S_2 = \Sigma(x - \bar{x})^2$$

$$S_3 = \Sigma(x - \bar{x})^3$$

n = the number of observations

Kurtosis Coefficient

$$g_2 = k_4/k_2{}^2$$

Where: $k_4 = \dfrac{n[(n+1)S_4 - 3(n-1)S_2{}^2/n]}{(n-1)(n-2)(n-3)}$

$$S_4 = \Sigma(x - \bar{x})^4$$

Tables 5.5 - 5.10 contain skewness and kurtosis coefficients plus their significance using uncorrected data and data corrected for age, year sampled and birth/rearing rank.

The text will concentrate on the results obtained using data corrected for fixed effects.

TABLE 5.5: Skewness coefficients and their significance for various fleece and follicle traits calculated using data corrected for age, year sampled and birth/rearing rank (Upper figure of each pair is SFMxR; lower LMxR)

Trait	Genotype	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)
S/P	SFM	1.45^{**} (33)	0.59^{*} (97)	0.95^{**} (56)	
	LMxR		0.73^{**} (89)	1.13^{**} (63)	0.46^{NS} (10)
ln S/P	SFMxR	0.41^{NS} (33)	0.25^{NS} (97)	0.32^{NS} (56)	
	LMxR		0.01^{NS} (89)	0.47^{NS} (63)	0.33^{NS} (10)
n(P+S)	SFMxR	1.83^{**} (33)	0.86^{**} (97)	1.78^{**} (56)	
	LMxR		0.58^{*} (89)	0.72^{*} (63)	1.54^{*} (10)
n(P+S)corr	SFMxR	0.99^{*} (33)	0.06^{NS} (97)	-0.04^{NS} (56)	
	LMxR		1.08^{**} (89)	0.52^{NS} (63)	0.73^{NS} (10)
nP	SFMxR	0.40^{NS} (33)	0.41^{NS} (97)	0.81^{*} (56)	
	LMxR		0.30^{NS} (89)	0.07^{NS} (63)	1.25^{NS} (10)
nP(corr)	SFMxR	0.41^{*} (33)	0.25^{NS} (97)	0.32^{NS} (56)	
	LMxR		0.76^{**} (89)	-0.10^{NS} (63)	0.27^{NS} (10)
CF	SFMxR	0.39^{NS} (33)	-0.30^{NS} (97)	0.02^{NS} (56)	
	LMxR		0.16^{NS} (89)	0.06^{NS} (63)	1.31^{NS} (10)
LWT	SFMxR	0.04^{NS} (23)	0.18^{NS} (88)	0.55^{NS} (55)	
	LMxR		0.19^{NS} (80)	-0.18^{NS} (59)	-0.79^{NS} (10)
GFW	SFMxR	0.24^{NS} (33)	0.39^{NS} (94)	0.35^{NS} (55)	
	LMxR		0.63^{NS} (88)	0.24^{NS} (63)	0.09^{NS} (10)
CFW	SFMxR	0.32^{NS} (31)	0.57^{*} (80)	0.01^{NS} (49)	
	LMxR		0.39^{NS} (77)	0.08^{NS} (55)	0.51^{NS} (9)
YLD	SFMxR	-0.23^{NS} (31)	0.04^{NS} (83)	0.60^{NS} (50)	
	LMxR		0.19^{NS} (77)	-0.30^{NS} (55)	-0.18^{NS} (9)
MFD	SFMxR	0.45^{NS} (31)	0.68^{*} (83)	-0.11^{NS} (52)	
	LMxR		0.03^{NS} (78)	0.47^{NS} (57)	0.61^{NS} (9)
QN_r	SFMxR	-1.82^{**} (25)	2.74^{*} (71)	-0.56^{NS} (27)	
	LMxR		-0.57^{*} (69)	-0.82^{*} (34)	
QN_m	SFMxR	-0.43^{NS} (31)	-0.29^{NS} (86)	0.41^{NS} (51)	
	LMxR		-1.12^{**} (80)	-0.28^{NS} (57)	-0.36^{NS} (9)
SL_r	SFMxR	-0.05^{NS} (25)	-0.16^{NS} (71)	0.41^{NS} (27)	
	LMxR		-0.30^{NS} (69)	-0.02^{NS} (34)	

TABLE 5.5: continued

Trait	Genotype	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)
SL_m	SFMxR	-0.04^{NS} (31)	-0.11^{NS} (86)	-0.55^{NS} (51)	
	LMxR		0.12^{NS} (80)	0.33^{NS} (57)	0.69^{NS} (9)
TCN	SFMxR	0.56^{NS} (31)	-0.17** (86)	0.66* (51)	
	LMxR		0.36^{NS} (80)	0.21^{NS} (57)	0.54^{NS} (9)
CPC	SFMxR	0.06^{NS} (31)	0.55* (86)	0.84* (51)	
	LMxR		0.07^{NS} (80)	0.46^{NS} (57)	-0.09^{NS} (9)
CHR_r	SFMxR	-0.22^{NS} (25)	0.14^{NS} (70)	0.30^{NS} (27)	
	LMxR		-0.57* (69)	-0.17^{NS} (34)	
CHR_m	SFMxR	-0.14^{NS} (33)	-0.45^{NS} (86)	-1.19** (51)	
	LMxR		-0.86** (80)	-0.64^{NS} (57)	-2.47** (9)
LUS	SFMxR	0.26^{NS} (31)	0.04^{NS} (86)	-0.80* (51)	
	LMxR		0.23^{NS} (80)	0.58^{NS} (57)	0.36** (9)
TIP	SFMxR	-0.50^{NS} (31)	-0.51* (86)	-0.47^{NS} (51)	
	LMxR		0.17^{NS} (80)	-0.98** (57)	0.00^{NS} (9)
COT	SFMxR	-0.32^{NS} (31)	-1.67** (86)	-0.88** (51)	
	LMxR		-2.40** (80)	-1.44** (57)	-0.70^{NS} (9)
SOU	SFMxR	0.33^{NS} (31)	0.13^{NS} (86)	0.28^{NS} (51)	
	LMxR		0.48^{NS} (80)	0.11^{NS} (57)	0.85^{NS} (9)
HND	SFMxR	-0.08^{NS} (32)	-0.44^{NS} (86)	-0.14^{NS} (51)	
	LMxR		-0.60* (80)	-0.73* (57)	0.01^{NS} (9)
GC_r	SFMxR	0.22^{NS} (25)	0.06^{NS} (71)	-0.55^{NS} (27)	
	LMxR		-0.46^{NS} (69)	0.51^{NS} (34)	
GC_m	SFMxR	0.62^{NS} (32)	-0.20^{NS} (86)	-0.17^{NS} (51)	
	LMxR		-0.45^{NS} (80)	0.05^{NS} (57)	0.00^{NS} (9)
SC_m	SFMxR	0.08^{NS} (32)	-0.54* (85)	-0.96** (48)	
	LMxR		-0.82** (76)	-0.32^{NS} (55)	-1.25^{NS} (9)

* $P < 0.05$
** $P < 0.01$
NS non-significant

TABLE 5.6: Skewness coefficients and their significance for various fleece and follicle traits calculated using data uncorrected for age, year sampled and birth/rearing rank (Upper figure of each pair is SFMxR; lower LMxR)

Trait	Genotype	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)
S/P	SFM	1.42^{**} (33)	0.47^{NS} (97)	0.90^{**} (56)	
	LMxR		0.73^{**} (89)	0.83^{**} (63)	0.37^{NS} (10)
ln S/P	SFMxR	0.53^{NS} (33)	-0.11^{NS} (97)	0.32^{NS} (56)	
	LMxR		0.02^{NS} (89)	0.21^{NS} (63)	0.21^{NS} (10)
n(P+S)	SFMxR	1.96^{**} (33)	1.13^{**} (97)	1.27^{**} (56)	
	LMxR		1.03^{**} (89)	0.49^{NS} (63)	1.58^{*} (10)
n(P+S)corr	SFMxR	1.10^{**} (33)	0.22^{NS} (97)	0.14^{NS} (56)	
	LMxR		0.93^{**} (89)	0.47^{NS} (63)	0.70^{NS} (10)
nP	SFMxR	0.51^{NS} (33)	0.31^{NS} (97)	0.58^{NS} (56)	
	LMxR		0.31^{NS} (89)	0.21^{NS} (63)	1.08^{NS} (10)
nP(corr)	SFMxR	0.88^{*} (33)	0.02^{NS} (97)	-0.16^{NS} (56)	
	LMxR		0.60^{*} (89)	0.06^{NS} (63)	0.44^{NS} (10)
CF	SFMxR	0.09^{NS} (33)	-0.20^{NS} (97)	-0.30^{NS} (56)	
	LMxR		0.06^{NS} (89)	0.20^{NS} (63)	1.21 (10)
LWT	SFMxR	0.08^{NS} (23)	0.00^{NS} (88)	0.57^{NS} (55)	
	LMxR		-0.48^{NS} (80)	0.52^{NS} (59)	-0.36^{NS} (10)
GFW	SFMxR	0.10^{NS} (33)	0.57^{*} (94)	0.21^{NS} (55)	
	LMxR		0.35^{NS} (88)	0.24^{NS} (63)	-0.04^{NS} (10)
CFW	SFMxR	0.36^{NS} (31)	1.01^{**} (80)	0.12^{NS} (49)	
	LMxR		0.41^{NS} (77)	0.56^{NS} (55)	0.44^{NS} (9)
YLD	SFMxR	-0.12^{NS} (31)	-0.08^{NS} (83)	0.43^{NS} (50)	
	LMxR		0.17^{NS} (77)	-0.37^{NS} (55)	-0.13^{NS} (9)
MFD	SFMxR	0.62^{NS} (31)	0.67^{**} (83)	-0.24^{NS} (52)	
	LMxR		0.11^{NS} (78)	0.41^{NS} (57)	0.61^{NS} (9)
QN_r	SFMxR	-2.21^{**} (25)	3.14^{**} (71)	-0.38^{NS} (27)	
	LMxR		-0.54^{NS} (69)	-1.04^{**} (34)	
QN_m	SFMxR	0.52^{NS} (31)	0.83^{NS} (86)	0.64^{NS} (51)	
	LMxR		0.06^{NS} (80)	-0.29^{NS} (57)	-0.30^{NS} (9)
SL_r	SFMxR	-0.19^{NS} (25)	-0.04^{NS} (71)	-0.02^{NS} (27)	
	LMxR		-0.01^{NS} (69)	-0.30^{NS} (34)	

TABLE 5.6: continued

Trait	Genotype	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)
SL_m	SFMxR	0.07^{NS} (31)	0.11^{NS} (86)	-0.28^{NS} (51)	
	LMxR		0.12^{NS} (80)	-0.13^{NS} (57)	0.65^{NS} (9)
TCN	SFMxR	0.63^{NS} (31)	-0.03^{NS} (86)	0.45^{NS} (51)	
	LMxR		0.63^{*} (80)	0.13^{NS} (57)	0.54^{NS} (9)
CPC	SFMxR	0.30^{NS} (31)	0.65^{*} (86)	0.91^{**} (51)	
	LMxR		0.20^{NS} (80)	0.37^{NS} (57)	-0.10^{NS} (9)
CHR_r	SFMxR	-0.25^{NS} (25)	0.12^{NS} (70)	0.14^{NS} (27)	
	LMxR		-0.59^{*} (69)	0.06^{NS} (34)	
CHR_m	SFMxR	-0.26^{NS} (33)	-0.41^{NS} (86)	-1.12^{**} (51)	
	LMxR		-0.87^{**} (80)	-0.91^{**} (57)	-2.48^{**} (9)
LUS	SFMxR	0.09^{NS} (31)	-0.35^{NS} (86)	-0.74^{*} (51)	
	LMxR		0.11^{NS} (80)	0.81^{*} (57)	2.48^{**} (9)
TIP	SFMxR	-0.51^{NS} (31)	-0.61^{*} (86)	-0.51^{NS} (51)	
	LMxR		0.12^{NS} (80)	-0.97^{**} (57)	0.00^{NS} (9)
COT	SFMxR	-0.33^{NS} (31)	-1.79^{**} (86)	-1.04^{**} (51)	
	LMxR		-2.41^{**} (80)	-1.52^{**} (57)	-0.71^{NS} (9)
SOU	SFMxR	0.23^{NS} (31)	0.43^{NS} (86)	0.74^{*} (51)	
	LMxR		0.69^{**} (80)	0.13^{NS} (57)	0.78^{NS} (9)
HND	SFMxR	0.02^{NS} (32)	-0.46^{NS} (86)	-0.33^{NS} (51)	
	LMxR		-0.47^{NS} (80)	-0.48^{NS} (57)	0.21^{NS} (9)
GC_r	SFMxR	0.18^{NS} (25)	-0.08^{NS} (71)	-0.55^{NS} (27)	
	LMxR		-0.38^{NS} (69)	0.60^{NS} (34)	
GC_m	SFMxR	0.88^{*} (32)	-0.16^{NS} (86)	-0.10^{NS} (51)	
	LMxR		-0.30^{NS} (80)	0.09^{NS} (57)	0.02^{NS} (9)
SC_m	SFMxR	-0.29^{NS} (32)	-0.58^{*} (85)	-0.77^{*} (48)	
	LMxR		-0.36^{NS} (76)	-0.14^{NS} (55)	-1.24^{NS} (9)

* $P < 0.05$

** $P < 0.01$

NS non-significant

TABLE 5.7:   Kurtosis coefficients and their significance calculated using data corrected for age, year sampled and birth/rearing rank   (Upper figure of each pair is SFMxR; lower LMxR)

Trait	Genotype	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)
S/P	SFM	2.64^{**} (33)	0.34^{NS} (97)	1.22 (56)	
	LMxR		1.08^{*} (89)	1.13^{NS} (63)	-1.37^{NS} (10)
ln S/P	SFMxR	0.52^{NS} (33)	-0.08^{NS} (97)	0.20^{NS} (56)	
	LMxR		0.11^{NS} (89)	0.17^{NS} (63)	-1.41^{NS} (10)
n(P+S)	SFMxR	4.88^{**} (33)	2.13^{**} (97)	4.12^{**} (56)	
	LMxR		1.22^{*} (89)	1.07^{NS} (63)	1.52^{NS} (10)
n(P+S)corr	SFMxR	0.43^{NS} (33)	-0.75^{NS} (97)	0.76^{NS} (56)	
	LMxR		1.66^{**} (89)	0.86^{NS} (63)	-0.48^{NS} (10)
nP	SFMxR	-0.24^{NS} (33)	0.73^{NS} (97)	0.29^{NS} (56)	
	LMxR		0.25^{NS} (89)	-0.28^{NS} (63)	0.47^{NS} (10)
nP(corr)	SFMxR	1.22^{NS} (33)	-0.80^{NS} (97)	0.33^{NS} (56)	
	LMxR		1.66^{**} (89)	-0.05^{NS} (63)	-0.36^{NS} (10)
CF	SFMxR	0.28^{NS} (33)	-0.58^{NS} (97)	0.83^{NS} (56)	
	LMxR		-0.02^{NS} (89)	-0.58^{NS} (63)	1.17^{NS} (10)
LWT	SFMxR	-0.76^{NS} (23)	0.08^{NS} (88)	0.19^{NS} (55)	
	LMxR		-0.59^{NS} (80)	-0.24^{NS} (59)	-0.60^{NS} (10)
GFW	SFMxR	-0.71^{NS} (33)	0.95^{NS} (94)	-0.02^{NS} (55)	
	LMxR		0.98^{NS} (88)	0.01^{NS} (63)	-0.79^{NS} (10)
CFW	SFMxR	-0.39^{NS} (31)	1.11^{*} (80)	-0.44^{NS} (49)	
	LMxR		-0.32^{NS} (77)	-0.30^{NS} (55)	-0.80^{NS} (9)
YLD	SFMxR	-0.22^{NS} (31)	0.12^{NS} (83)	4.15^{**} (50)	
	LMxR		0.46^{NS} (77)	-0.38^{NS} (55)	-0.79^{NS} (9)
MFD	SFMxR	-0.70^{NS} (31)	0.63^{NS} (83)	-0.77^{NS} (52)	
	LMxR		1.69^{**} (78)	1.38^{*} (57)	-0.72^{NS} (9)
QN_r	SFMxR	3.20^{**} (25)	14.49^{**} (71)	2.51^{**} (27)	
	LMxR		-0.49^{NS} (69)	-0.17^{NS} (34)	
QN_m	SFMxR	-0.44^{NS} (31)	0.86^{NS} (86)	-0.68^{NS} (51)	
	LMxR		2.20^{**} (80)	-0.15^{NS} (57)	-1.31^{NS} (9)
SL_r	SFMxR	-0.18^{NS} (25)	-0.22^{NS} (71)	-0.67^{NS} (27)	
	LMxR		0.27^{NS} (69)	-0.18^{NS} (34)	

TABLE 5.7: continued

Trait	Genotype	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)
SL_m	SFM×R	-0.16^{NS} (31)	-0.12^{NS} (86)	-0.67^{NS} (51)	
	LM×R		0.50^{NS} (80)	0.04^{NS} (57)	-1.14^{NS} (9)
TCN	SFM×R	0.03^{NS} (31)	-0.86^{NS} (86)	-0.18^{NS} (51)	
	LM×R		-0.22^{NS} (80)	-0.56^{NS} (57)	-0.90^{NS} (9)
CPC	SFM×R	-0.49^{NS} (31)	0.49^{NS} (86)	-0.11^{NS} (51)	
	LM×R		-0.63^{NS} (80)	-0.09^{NS} (57)	-1.39^{NS} (9)
CHR_r	SFM×R	-0.73^{NS} (25)	-0.57^{NS} (70)	-0.44^{NS} (27)	
	LM×R		0.58^{NS} (69)	0.16^{NS} (34)	
CHR_m	SFM×R	-0.96^{NS} (33)	-0.68^{NS} (86)	1.12^{NS} (51)	
	LM×R		0.72^{NS} (80)	-0.63^{NS} (57)	4.12^{**} (9)
LUS	SFM×R	-0.90^{NS} (31)	0.45^{NS} (86)	0.83^{NS} (51)	
	LM×R		-0.35^{NS} (80)	1.70^{**} (57)	3.82^{**} (9)
TIP	SFM×R	-0.66^{NS} (31)	-0.37^{NS} (86)	-0.76^{NS} (51)	
	LM×R		0.15^{NS} (80)	0.52^{NS} (57)	-0.75^{NS} (9)
COT	SFM×R	-1.83^{*} (31)	3.76^{**} (86)	-0.27^{NS} (51)	
	LM×R		11.97^{**} (80)	1.57^{*} (57)	-1.50^{NS} (9)
SOU	SFM×R	-1.27^{NS} (31)	-0.79^{NS} (86)	-0.20^{NS} (51)	
	LM×R		-0.41^{NS} (80)	-0.82^{NS} (57)	-0.66^{NS} (9)
HND	SFM×R	-0.50^{NS} (32)	-0.10^{NS} (86)	-0.58^{NS} (51)	
	LM×R		0.45^{NS} (80)	-0.16^{NS} (57)	-0.92^{NS} (9)
GC_r	SFM×R	1.87^{*} (25)	0.69^{NS} (71)	-0.41^{NS} (27)	
	LM×R		0.65^{NS} (69)	0.12^{NS} (34)	
GC_m	SFM×R	0.68^{NS} (32)	-0.08^{NS} (86)	0.09^{NS} (51)	
	LM×R		-0.61^{NS} (80)	-0.01^{NS} (57)	0.00^{NS} (9)
SC_m	SFM×R	-0.71^{NS} (32)	0.04^{NS} (85)	1.57^{*} (48)	
	LM×R		0.31^{NS} (76)	-0.76^{NS} (55)	0.22^{NS} (9)

$*$ P $<$ 0.05
$**$ P $<$ 0.01
NS non-significant

TABLE 5.8: Kurtosis coefficients and their significance using data uncorrected for fixed effects (Upper figure of each pair is SFMxR; lower LMxR)

Trait	Genotype	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)
S/P	SFM	2.89^{**} (33)	0.19^{NS} (97)	0.81^{NS} (56)	
	LMxR		0.65^{NS} (89)	0.41^{NS} (63)	-1.11^{NS} (10)
ln S/P	SFMxR	0.57^{NS} (33)	-0.19^{NS} (97)	0.06^{NS} (56)	
	LMxR		-0.19^{NS} (89)	-0.26^{NS} (63)	-1.16^{NS} (10)
n(P+S)	SFMxR	5.77^{**} (33)	1.94^{**} (97)	1.90^{**} (56)	
	LMxR		1.91^{*} (89)	-0.32^{NS} (63)	1.61^{NS} (10)
n(P+S)corr	SFMxR	0.76^{NS} (33)	-0.58^{NS} (97)	-0.01^{NS} (56)	
	LMxR		1.21^{*} (89)	0.17^{NS} (63)	-0.49^{NS} (10)
nP	SFMxR	-0.16^{NS} (33)	-0.15^{NS} (97)	0.21^{NS} (56)	
	LMxR		-0.57^{NS} (89)	-0.09^{NS} (63)	0.18^{NS} (10)
nP(corr)	SFMxR	1.27^{NS} (33)	-0.79^{NS} (97)	0.04^{NS} (56)	
	LMxR		0.89^{NS} (89)	-0.12^{NS} (63)	-0.36^{NS} (10)
CF	SFMxR	0.85^{NS} (33)	-0.68^{NS} (97)	0.23^{NS} (56)	
	LMxR		-0.10^{NS} (89)	-0.55^{NS} (63)	0.96^{NS} (10)
LWT	SFMxR	-0.86^{NS} (23)	-0.96^{NS} (88)	-0.18^{NS} (55)	
	LMxR		-0.47^{NS} (80)	-0.42^{NS} (59)	-1.05^{NS} (10)
GFW	SFMxR	-0.91^{NS} (33)	1.36^{**} (94)	-0.61^{NS} (55)	
	LMxR		0.14^{NS} (88)	0.42^{NS} (63)	-0.90^{NS} (10)
CFW	SFMxR	-0.49^{NS} (31)	1.53^{**} (80)	-0.68^{NS} (49)	
	LMxR		-0.52^{NS} (77)	0.64^{NS} (55)	0.89^{NS} (9)
YLD	SFMxR	-0.54^{NS} (31)	0.21^{NS} (83)	3.28^{**} (50)	
	LMxR		0.45^{NS} (77)	-0.32^{NS} (55)	-0.75^{NS} (9)
MFD	SFMxR	-0.54^{NS} (31)	0.57^{NS} (83)	-0.71^{NS} (52)	
	LMxR		1.21^{*} (78)	0.86^{NS} (57)	-0.71^{NS} (9)
QN_r	SFMxR	4.65^{**} (25)	17.05^{**} (71)	2.51^{**} (27)	
	LMxR		-0.66^{NS} (69)	-0.10^{NS} (34)	
QN_m	SFMxR	0.29^{NS} (31)	3.07^{**} (86)	-0.33^{NS} (51)	
	LMxR		0.31^{NS} (80)	-0.25^{NS} (57)	-1.43^{NS} (9)
SL_r	SFMxR	0.32^{NS} (25)	-0.04^{NS} (71)	-0.90^{NS} (27)	
	LMxR		-0.44^{NS} (69)	-0.35^{NS} (34)	

TABLE 5.8: continued

Trait	Genotype	F_1 (n)	F_2 (n)	F_3 (n)	F_4 (n)
SL_m	SFMxR	-0.02^{NS} (31)	-0.30^{NS} (86)	-0.16^{NS} (51)	
	LMxR		0.31^{NS} (80)	-0.25^{NS} (57)	-1.18^{NS} (9)
TCN	SFMxR	0.33^{NS} (31)	-0.90^{NS} (86)	-0.47^{NS} (51)	
	LMxR		0.26^{NS} (80)	-0.55^{NS} (57)	-0.91^{NS} (9)
CPC	SFMxR	-0.35^{NS} (31)	0.83^{NS} (86)	0.07^{NS} (51)	
	LMxR		-0.51^{NS} (80)	-0.10^{NS} (57)	-1.37^{NS} (9)
CHR_r	SFMxR	-0.66^{NS} (25)	-0.33^{NS} (70)	-0.61^{NS} (27)	
	LMxR		0.55^{NS} (69)	0.04^{NS} (34)	
CHR_m	SFMxR	-0.86^{NS} (33)	-0.92^{NS} (86)	0.93^{NS} (51)	
	LMxR		0.54^{NS} (80)	-0.19^{NS} (57)	4.13^{**} (9)
LUS	SFMxR	-0.45^{NS} (31)	0.13^{NS} (86)	0.62^{NS} (51)	
	LMxR		-0.04^{NS} (80)	1.98^{**} (57)	4.13^{**} (9)
TIP	SFMxR	-0.70^{NS} (31)	-0.23^{NS} (86)	-0.71^{NS} (51)	
	LMxR		-0.19^{NS} (80)	0.53^{NS} (57)	-0.75^{NS} (9)
COT	SFMxR	-1.89^{*} (31)	4.05^{**} (86)	-0.07^{NS} (51)	
	LMxR		10.92^{**} (80)	1.29^{*} (57)	-1.50^{NS} (9)
SOU	SFMxR	-1.38^{NS} (31)	-0.79^{NS} (86)	-0.21^{NS} (51)	
	LMxR		-0.37^{NS} (80)	-0.97^{NS} (57)	-0.72^{NS} (9)
HND	SFMxR	-0.08^{NS} (32)	-0.23^{NS} (86)	-0.56^{NS} (51)	
	LMxR		0.39^{NS} (80)	0.13^{NS} (57)	-0.62^{NS} (9)
GC_r	SFMxR	1.97^{*} (25)	0.92^{NS} (71)	-0.31^{NS} (27)	
	LMxR		0.41^{NS} (69)	0.27^{NS} (34)	
GC_m	SFMxR	1.39^{NS} (32)	-0.06^{NS} (86)	-0.52^{NS} (51)	
	LMxR		-0.63^{NS} (80)	-0.28^{NS} (57)	-0.01^{NS} (9)
SC_m	SFMxR	-0.47^{NS} (32)	0.11^{NS} (85)	1.00^{NS} (48)	
	LMxR		-0.42^{NS} (76)	-1.09^{NS} (55)	0.17^{NS} (9)

* P < 0.05
** P < 0.01
NS non-significant

TABLE 5.9: Skewness and Kurtosis coefficients and their significance for various fleece and follicle characteristics calculated using data corrected for age, year sampled and birth/rearing rank

Trait	Genotype	Skewness (n)	Kurtosis (n)	Skewness B_1 (n)	Skewness B_2 (n)	Kurtosis B_1 (n)	Kurtosis B_2 (n)
S/P	SFM	0.34^{NS} (39)	0.41^{NS} (39)	0.18^{NS} (69)	0.41^{NS} (63)	-0.54^{NS} (69)	0.74^{NS} (63)
	SFMxR	0.89^{**} (194)	1.24^{**} (194)				
ln S/P	SFM	-0.62^{NS} (39)	1.43^{NS} (39)	-0.25^{NS} (69)	-0.67^{*} (63)	-0.45^{NS} (69)	2.32^{**} (63)
	SFMxR	0.16^{NS} (194)	0.25^{NS} (194)				
n(P+S)	SFM	-0.09^{NS} (39)	-0.91^{NS} (39)	-0.08^{NS} (69)	0.27^{NS} (63)	-0.87^{NS} (69)	0.02^{NS} (63)
	SFMxR	1.31^{**} (194)	3.20^{**} (194)				
n(P+S)corr	SFM	-0.11^{NS} (39)	-0.62^{NS} (39)	0.36^{NS} (69)	0.54^{NS} (63)	0.04^{NS} (69)	0.34^{NS} (63)
	SFMxR	0.18^{NS} (194)	-0.33^{NS} (194)				
nP	SFM	0.18^{NS} (39)	-0.15^{NS} (39)	0.45^{NS} (69)	0.23^{NS} (63)	0.24^{NS} (69)	-0.09^{NS} (63)
	SFMxR	0.58^{**} (194)	0.84^{*} (194)				
nP(corr)	SFM	0.26^{NS} (39)	-0.07^{NS} (39)	0.01^{NS} (69)	0.54^{NS} (63)	0.18^{NS} (69)	0.73^{NS} (63)
	SFMxR	0.11^{NS} (194)	-0.16^{NS} (194)				
CF	SFM	1.20^{**} (39)	2.11^{**} (39)	-0.16^{NS} (69)	-0.10^{NS} (63)	0.85^{NS} (69)	0.03^{NS} (63)
	SFMxR	-0.06^{NS} (194)	0.00 (194)				
LWT	SFM	-1.18^{**} (33)	2.94^{**} (33)	0.05^{NS} (56)	-0.36^{NS} (55)	-0.47^{NS} (56)	-0.08^{NS} (55)
	SFMxR	0.30^{NS} (174)	-0.13^{NS} (194)				

TABLE 5.9: continued

Trait	Genotype	Skewness (n)	Kurtosis (n)	Skewness		Kurtosis	
				B_1 (n)	B_2 (n)	B_1 (n)	B_2 (n)
GFW	SFM	0.97^* (36)	1.04^{NS} (36)	0.40^{NS} (68)	-0.50^{NS} (62)	0.26^{NS} (68)	0.61^{NS} (62)
	SFMxR	0.27^{NS} (190)	1.03^{**} (190)				
CFW	SFM	1.12^{**} (34)	2.32^{**} (34)	0.29^{NS} (64)	-0.23^{NS} (61)	0.07^{NS} (64)	0.21^{NS} (61)
	SFMxR	0.50^{**} (167)	1.40^{**} (167)				
YLD	SFM	0.00^{NS} (37)	-0.30^{NS} (37)	-1.07^{**} (64)	-0.52^{NS} (62)	1.41^* (64)	0.32^{NS} (62)
	SFMxR	0.27^{NS} (171)	2.52^{**} (171)				
MFD	SFM	-0.06^{NS} (37)	-1.03^{NS} (37)	0.04^{NS} (64)	0.92^{**} (62)	-0.39^{NS} (64)	2.61^{**} (62)
	SFMxR	0.29^{NS} (174)	-0.08^{NS} (174)				
QN_r	SFM	-0.43^{NS} (21)	-0.93^{NS} (21)	0.62^* (68)	0.01^{NS} (31)	1.25^* (68)	0.33^{NS} (31)
	SFMxR	1.79^{**} (123)	13.21^{**} (123)				
QN_m	SFM	1.44^{**} (38)	4.36^{**} (38)	-0.05^{NS} (67)	-0.01^{NS} (63)	-0.59^{NS} (67)	-0.29^{NS} (63)
	SFMxR	-0.10^{NS} (176)	0.24^{NS} (176)				
SL_r	SFM	-0.24^{NS} (21)	-0.60^{NS} (21)	-0.46^{NS} (68)	0.80^{NS} (31)	0.84^{NS} (68)	2.57^{**} (31)
	SFMxR	-0.08^{NS} (123)	-0.18^{NS} (123)				
SL_m	SFM	0.16^{NS} (38)	0.07^{NS} (38)	0.21^{NS} (68)	0.67^* (63)	0.04^{NS} (68)	2.68^{**} (63)
	SFMxR	-0.25^{NS} (176)	-0.06^{NS} (176)				

TABLE 5.9: continued

Trait	Genotype	Skewness (n)	Kurtosis (n)	Skewness B$_1$ (n)	Skewness B$_2$ (n)	Kurtosis B$_1$ (n)	Kurtosis B$_2$ (n)
TCN	SFM	-0.21^{NS} (38)	-0.32^{NS} (38)	0.33^{NS} (68)	0.18^{NS} (62)	0.05^{NS} (68)	-0.01^{NS} (62)
	SFMxR	0.44* (176)	0.11^{NS} (176)				
CPC	SFM	-0.25^{NS} (38)	-0.39^{NS} (38)	0.34 (68)	0.16^{NS} (62)	-0.20^{NS} (68)	0.12^{NS} (62)
	SFMxR	0.94 (176)	1.18 (176)				
CHR$_r$	SFM	-0.54^{NS} (21)	-0.35^{NS} (21)	-0.30^{NS} (68)	0.27^{NS} (31)	-1.11^{NS} (68)	-0.27^{NS} (31)
	SFMxR	0.11^{NS} (122)	-0.54^{NS} (122)				
CHR$_m$	SFM	-0.78* (38)	2.69** (38)	-0.25^{NS} (68)	-0.70* (63)	-0.16^{NS} (68)	-0.41^{NS} (63)
	SFMxR	-0.59** (178)	-0.29^{NS} (178)				
LUS	SFM	-0.05^{NS} (38)	-0.76^{NS} (38)	0.71* (68)	-0.08^{NS} (63)	1.55* (68)	-0.32^{NS} (63)
	SFMxR	0.01^{NS} (176)	0.35^{NS} (176)				
TIP	SFM	-0.06^{NS} (37)	-1.34^{NS} (37)	-0.13^{NS} (68)	-0.51^{NS} (63)	-0.25^{NS} (68)	0.54^{NS} (63)
	SFMxR	-0.53** (176)	-0.49^{NS} (176)				
COT	SFM	-0.34^{NS} (37)	0.75^{NS} (37)	-0.75** (68)	-1.26** (63)	-0.72^{NS} (68)	1.18* (63)
	SFMxR	-1.43** (176)	2.89** (176)				
SOU	SFM	-0.29^{NS} (38)	-0.31^{NS} (38)	-0.01^{NS} (68)	0.72* (63)	-1.09^{NS} (68)	-0.02^{NS} (63)
	SFMxR	0.15^{NS} (176)	-0.71* (176)				

Trait	Genotype	Skewness (n)	Kurtosis (n)	Skewness B_1 (n)	Skewness B_2 (n)	Kurtosis B_1 (n)	Kurtosis B_2 (n)
HND	SFM	0.22^{NS} (38)	0.85^{NS} (38)	0.07^{NS} (68)	-0.12^{NS} (63)	-0.25^{NS} (68)	-0.69^{NS} (63)
	SFMxR	-0.32^{NS} (177)	-0.14^{NS} (177)				
GC_r	SFM	0.06^{NS} (21)	-0.47^{NS} (21)	0.40^{NS} (68)	0.37^{NS} (31)	0.53^{NS} (68)	-0.11^{NS} (31)
	SFMxR	-0.05^{NS} (123)	0.69^{NS} (123)				
GC_m	SFM	-1.44^{**} (38)	3.18^{**} (38)	-0.06^{NS} (68)	0.10^{NS} (63)	-0.01^{NS} (68)	-0.36^{NS} (63)
	SFMxR	-0.07^{NS} (177)	-0.01^{NS} (177)				
SC_m	SFM	0.36^{NS} (37)	-0.21^{NS} (37)	-0.09^{NS} (64)	0.25^{NS} (63)	0.19^{NS} (64)	-0.11^{NS} (63)
	SFMxR	-0.61^{**} (173)	1.53^{NS} (173)				

* $P < 0.05$

** $P < 0.01$

NS non-significant

TABLE 5.10: Skewness and Kurtosis coefficients and their significance for various fleece and follicle characteristics calculated using data uncorrected for fixed effects

Trait	Genotype	Skewness (n)	Kurtosis (n)	Skewness		Kurtosis	
				B_1 (n)	B_2 (n)	B_1 (n)	B_2 (n)
S/P	SFM	0.24^{NS} (39)	0.56^{NS} (39)	0.21^{NS} (69)	0.21^{NS} (63)	-0.56^{NS} (69)	0.89^{NS} (63)
	SFMxR	0.78^{**} (194)	1.70^{NS} (194)				
ln S/P	SFM	-0.93^{*} (39)	2.54^{**} (39)	-0.21^{NS} (69)	-0.99^{**} (63)	-0.50^{NS} (69)	3.34^{**} (63)
	SFMxR	0.04^{NS} (194)	0.16^{NS} (194)				
n(P+S)	SFM	-0.43^{NS} (39)	-0.18^{NS} (39)	0.03^{NS} (69)	0.20^{NS} (63)	-0.93^{NS} (69)	0.10^{NS} (63)
	SFMxR	1.14^{**} (194)	1.82^{**} (194)				
n(P+S)corr	SFM	-0.09^{NS} (39)	-0.56^{NS} (39)	0.48^{NS} (69)	0.43^{NS} (63)	0.14^{NS} (69)	0.51^{NS} (63)
	SFMxR	0.23^{NS} (194)	-0.54^{NS} (194)				
nP	SFM	0.83^{*} (39)	0.98^{NS} (39)	0.21^{NS} (69)	0.50^{NS} (63)	-0.19^{NS} (69)	-0.01^{NS} (63)
	SFMxR	0.41^{*} (194)	-0.00^{NS} (194)				
nP(corr)	SFM	0.21^{NS} (39)	-0.39^{NS} (39)	-0.21^{NS} (69)	0.68^{*} (63)	-0.32^{NS} (69)	1.16^{NS} (63)
	SFMxR	0.12^{NS} (194)	-0.40^{NS} (194)				
CF	SFM	0.52^{NS} (39)	0.88^{NS} (39)	-0.21^{NS} (69)	0.38^{NS} (63)	0.17^{NS} (69)	1.08^{NS} (63)
	SFMxR	-0.18^{NS} (194)	-0.21^{NS} (194)				
LWT	SFM	0.03^{NS} (33)	-1.57^{NS} (33)	0.11^{NS} (56)	-0.60^{NS} (55)	-0.63^{NS} (56)	-0.43^{NS} (55)
	SFMxR	0.07^{NS} (174)	-0.95^{NS} (174)				

Trait	Genotype	Skewness (n)	Kurtosis (n)	Skewness		Kurtosis	
				B_1 (n)	B_2 (n)	B_1 (n)	B_2 (n)
GFW	SFM	0.78^* (36)	0.47^{NS} (36)	0.71^{NS} (68)	-0.15^{NS} (62)	0.03^{NS} (68)	0.48^{NS} (62)
	SFMxR	0.45^* (190)	2.34^{**} (190)				
CFW	SFM	0.90^* (34)	1.26^{NS} (34)	0.40^{NS} (64)	-0.21^{NS} (61)	-0.26^{NS} (64)	-0.12^{NS} (61)
	SFMxR	0.88^{**} (167)	1.77^{**} (167)				
YLD	SFM	0.20^{NS} (37)	-0.4^{NS} (37)	-1.21^{**} (64)	-0.42^{NS} (62)	1.56^{**} (64)	-0.03^{NS} (62)
	SFMxR	0.21^{NS} (171)	1.68^{**} (171)				
MFD	SFM	0.23^{NS} (37)	-0.95^{NS} (37)	0.18^{NS} (64)	0.74 (62)	-0.24^{NS} (64)	2.03^* (62)
	SFMxR	0.18^{NS} (174)	0.16^{NS} (174)				
QN_r	SFM	-0.55^{NS} (21)	-0.70^{NS} (21)	0.51^{NS} (68)	-0.01^{NS} (31)	1.39^* (68)	0.48^{NS} (31)
	SFMxR	2.59^{**} (123)	18.43^{**} (123)				
QN_m	SFM	0.96^* (38)	1.02^{NS} (38)	0.14^{NS} (67)	0.11^{NS} (63)	-0.30^{NS} (67)	-0.21^{NS} (63)
	SFMxR	-0.70^{**} (176)	1.80^{**} (176)				
SL_r	SFM	0.23^{NS} (21)	-0.66^{NS} (21)	0.18^{NS} (68)	0.33^{NS} (31)	0.37^{NS} (68)	0.76^{NS} (31)
	SFMxR	0.13^{NS} (123)	-0.08^{NS} (123)				
SL_m	SFM	0.49^{NS} (38)	0.39^{NS} (38)	0.11^{NS} (68)	-0.03^{NS} (63)	-0.39^{NS} (68)	0.92^{NS} (63)
	SFMxR	-0.05^{NS} (176)	-0.17^{NS} (176)				

Trait	Genotype	Skewness (n)	Kurtosis (n)	Skewness B_1 (n)	Skewness B_2 (n)	Kurtosis B_1 (n)	Kurtosis B_2 (n)
TCN	SFM	0.06^{NS} (38)	-0.07^{NS} (38)	0.36^{NS} (68)	0.09^{NS} (62)	-0.06^{NS} (68)	-0.04^{NS} (62)
	SFMxR	0.42^{*} (176)	-0.14^{NS} (176)				
CPC	SFM	-0.35^{NS} (38)	-0.50^{NS} (38)	0.31^{NS} (68)	0.05^{NS} (62)	-0.19^{NS} (68)	0.11^{NS} (62)
	SFMxR	1.51^{**} (176)	1.55^{**} (176)				
CHR_r	SFM	-0.83^{NS} (21)	0.25^{NS} (21)	-0.34^{NS} (68)	0.10^{NS} (31)	-1.15^{*} (68)	-0.30^{NS} (31)
	SFMxR	0.07^{NS} (122)	-0.39^{NS} (122)				
CHR_m	SFM	-1.89^{**} (38)	4.07^{**} (38)	-0.26^{NS} (68)	-1.11^{**} (63)	-0.26^{NS} (68)	0.19^{NS} (63)
	SFMxR	-0.63^{**} (178)	-0.46^{NS} (178)				
LUS	SFM	0.16^{NS} (38)	-0.78^{NS} (38)	0.59^{*} (68)	0.07^{NS} (63)	1.59^{**} (68)	-0.27^{NS} (63)
	SFMxR	-0.18^{NS} (176)	0.43^{NS} (176)				
TIP	SFM	-0.23^{NS} (37)	-1.00^{NS} (37)	-0.26^{NS} (68)	-0.50^{NS} (63)	-0.26^{NS} (68)	-0.68^{NS} (63)
	SFMxR	-0.60^{NS} (176)	-0.40^{NS} (176)				
COT	SFM	-0.79^{*} (37)	0.97^{NS} (37)	-0.80^{**} (68)	-1.70^{**} (63)	-0.65^{NS} (68)	1.95^{**} (63)
	SFMxR	-1.51^{**} (176)	2.93^{**} (176)				
SOU	SFM	-0.18^{NS} (38)	-1.45^{*} (38)	-0.14^{NS} (68)	0.92^{**} (63)	-1.34^{NS} (68)	-0.46^{NS} (63)
	SFMxR	0.54^{**} (176)	-0.67^{NS} (176)				

TABLE 5.10: continued

Trait	Genotype	Skewness (n)	Kurtosis (n)	Skewness B_1 (n)	Skewness B_2 (n)	Kurtosis B_1 (n)	Kurtosis B_2 (n)
HND	SFM	-0.16^{NS} (38)	-0.54^{NS} (38)	0.15^{NS} (68)	-0.74^{*} (63)	-0.26^{NS} (68)	-0.35^{NS} (63)
	SFMxR	-0.41^{*} (177)	-0.18^{NS} (177)				
GC_r	SFM	0.15^{NS} (21)	-0.50^{NS} (21)	0.33^{NS} (68)	-0.43^{NS} (31)	0.60^{NS} (68)	-0.10^{NS} (31)
	SFMxR	-0.14^{NS} (123)	0.97^{NS} (123)				
GC_m	SFM	-0.87^{*} (38)	0.89^{NS} (38)	-0.09^{NS} (68)	-0.24^{NS} (63)	-0.01^{NS} (68)	-0.28^{NS} (63)
	SFMxR	-0.01 (177)	0.33^{NS} (177)				
SC_m	SFM	-0.36^{NS} (37)	-0.82^{NS} (37)	-0.31^{NS} (64)	0.25^{NS} (63)	0.29^{NS} (64)	-0.33^{NS} (63)
	SFMxR	-0.58^{**} (173)	0.23^{NS} (173)				

* $P < 0.05$
** $P < 0.01$
NS   non-significant

5.3.2.1 S/P

For both SFMxR and LMxR groups, the distributions of S/P in the F_1 to F_3 generations were positively skewed. However, skewness disappeared when the data were log transformed. A similar pattern was observed for kurtosis, the data being leptokurtic until log transformation when it conformed to a normal pattern.

In the backcross group there was no significant skewness or kurtosis for S/P. Log transformed data (ln S/P), showed significant negative skewness (B_2, $p<0.05$) and positive kurtosis (B_2, $p<0.01$).

5.3.2.2 n(P+S)

For both genotypes, i.e., SFMxR and LMxR the data showed marked positive skewness. Using n(P+S)corr this skewness became non-significant except in the SFMxR F_1 group and the LMxR F_2 animals.

Positive kurtosis was apparent in each of the F_1 to F_3 generations of the SFMxR animals and in the F_2 group of the LMxR crossbreds. The only group showing leptokurtosis after the data were corrected for skin shrinkage was the LMxR, F_2 generation.

5.3.2.3 nP

In contrast to n(P+S), the skewness increased in the nP(corr) data, the F_1 SFMxR and F_2 LMxR animals being positively skewed. With the exception of the F_2 LMxR generation, there was no apparent kurtosis for nP or nP(corr).

5.3.2.4 MFD

There was skewness in the F_2 SFMxR group ($p<0.05$). The F_2 and F_3 generations of LMxR crossbreds showed positive kurtosis for MFD. The B_2 group showed significant positive skewness and kurtosis ($p<0.01$).

5.3.2.5 QN_r

For all three genotypes, there was significant skewness (see Tables 5.5, 5.6, 5.9 and 5.10). In the SFMxR and BX groups, the data were leptokurtic ($p<0.01$, $p<0.05$ respectively). The significant levels of skewness and kurtosis may reflect the wide variation in numbers of animals per generation in the SFMxR group.

5.3.2.6 TCN

Both TCN and CPC showed positive skewness in the F_2 and F_3 generations of the SFMxR genotype. There was no apparent kurtosis for these traits.

5.3.2.7 COT

COT was positively skewed ($p<0.01$) in the F_2 and F_3 generations of both crossbred genotypes. In the BX animals there was significant negative skewness in the B_1 and B_2 generations ($p<0.01$), but only positive kurtosis in the B_2 ($p<0.01$).

There were also signs of significant positive kurtosis in the F_1 (SFMxR), F_2 (SFMxR; LMxR) and F_3 (LMxR) groups.

5.4 COMPARISON OF VARIANCES OF PARENTAL STRAINS, F_1, F_2 AND BACKCROSSES

Lande (1981) developed a method to estimate minimum gene number which was based on Castle (1921) and Wright (1952).

The estimation equation was:

$$n_E = (\mu_{P2} - \mu_{P1})^2 / (8\sigma^2_s) \le n$$

Where: n_E = the minimum number of effective genetic factors

μ_{P1} and μ_{P2} = the means of the parent populations

σ^2_s = genetic variance

This last term can be estimated in four ways;

1. $\sigma^2_s = \sigma^2_{F2} - \sigma^2_{F1}$

2. $\sigma^2_s = \sigma^2_{F2} - [\frac{1}{2}\sigma^2_{F1} + \frac{1}{4}\sigma^2_{P1} + \frac{1}{4}\sigma^2_{P2}]$

3. $\sigma^2_s = 2\sigma^2_{F2} - \sigma^2_{B1} - \sigma^2_{B2}$

4. $\sigma^2_s = \sigma^2_{B1} + \sigma^2_{B2} - [\sigma^2_{F1} + \frac{1}{2}\sigma^2_{P1} + \frac{1}{2}\sigma^2_{P2}]$

Where:

σ^2_{F1} and σ^2_{F2} = the phenotypic variances of the F_1 and F_2 groups

σ^2_{P1} and σ^2_{P2} = the phenotypic variances of the parental groups

σ^2_{B1} and σ^2_{B2} = the phenotypic variances of the two backcross populations

A computer programme by Angus (1983) based on the model of Lande (1981) was used in the present study to estimate the minimum number of genetic factors controlling fleece and follicle characteristics. The results are given in Table 5.11.

As the present data set has only one backcross population, the second computer routine (σ^2_s from equations 3 and 4), was not valid and was not used. It should also be noted that the programme of Angus (1983) has an error in the routine involving backcross data, such that a different number of genes is obtained each time the same data are entered.

Lande (1981) concluded that if the sample sizes of the parental and F_1 populations were each at least 20 or 30 and those of the F_2 and backcross populations at least 100, then the estimates of n_E would have reasonable accuracy. On these criteria, only the parental (R; SFM) and SFMxR groups have sufficient numbers.

The model (Lande 1981) assumes that the variance of a trait in the F_2 generation will exceed that in the F_1. In the present study this was not the case for most characteristics. Thus the estimates of the minimum number of genetic factors for most traits are negative. n(P+S) and n(P+S)corr seemed to be affected by several genes, while only LWT, GFW, nP and nP(corr) had the low number of estimated genetic factors associated with a major gene. That both liveweight and fleeceweight showed this pattern was surprising as these traits are thought to be controlled by multifactorial inheritance.

Lande's (1981) method was of little value given the nature of the present data i.e., insufficient numbers per group/population. The data met the other criteria of this model. Mayo and Hopkins (1985) tested Lande's method on rat serum dopamine-β-hydroxylase levels and on pasture grass data. The authors expressed concern about the imprecise estimates obtained for traits previously found to be simply inherited. They supported the Castle-Wright theory underlying Lande's (1981) model, but felt that the model did not provide reliable estimates of minimum numbers of genes.

TABLE 5.11: Minimum Number of Genetic Factors

Genotype	Trait	Equation 1	Equation 2
SFMxR	S/P	a	a
LMxR		a	a
SFMxR	ln S/P	a	a
LMxR		a	26.04 ± 79.24
SFMxR	n(P+S)	22.61 ± 94.24	633.70 ± 5719.97
LMxR		6.73 ± 4.92	a
SFMxR	n(P+S)corr	7.61 ± 6.47	a
LMxR		9.60 ± 12.01	a
SFMxR	nP	0.32 ± 0.22	0.77 ± 0.92
LMxR		0.09 ± 0.17	a
SFMxR	nP(corr)	0.12 ± 0.24	0.22 ± 0.56
LMxR		0.10 ± 0.06	0.17 ± 0.14
SFMxR	MFD	a	76.00 ± 187.21
LMxR		a	23.08 ± 35.53
SFMxR	QN	a	a
LMxR		a	a
SFMxR	LWT	0.42 ± 0.21	1.05 ± 0.98
LMxR		0.15 ± 0.12	0.34 ± 0.35
SFMxR	GFW	0.22 ± 0.13	0.49 ± 0.42
LM		0.008 ± 0.00	0.001 ± 0.007

a - estimates of NE were negative as the F_1 variances
were greater than the F_2

5.5 SIMPLE SIBSHIP VARIANCE TESTS FOR THE DETECTION OF MAJOR LOCI

A recent technique developed for detection of major genes uses within sibship means and variances in the following equations:

1. $Y = A + BX$
2. $Y = A + BX^2$
3. $Y = A + BX + BX^2$

where: Y = log within sibship variance for a trait

X = sibship mean for a trait

Fain (1978) proposed this model for use in small families and for human data. Bigham et al (1985) used this method for half-sib families to examine the inheritance of wool bulk.

In the present study, Fain's model was applied to half-sib families of size 3 or larger, within each of the SFMxR and LMxR genotypes. It should be noted that Fain (1978) designed the model for 50 or more sibships and the numbers in the present study were lower:

SFMxR $n = 24$ and LMxR $n = 26$.

Figures 5.29 - 5.34 contain equations based on the above model for both crossbred genotypes, for ln S/P, n(P+S) and nP.

The current results using ln S/P (see figures 5.29 - 5.30) suggest that there is a difference in the mode of inheritance of S/P in the LMxR compared with the SFMxR. In the latter group, S/P appears to be inherited multifactorially but in a recessive manner. In the LMxR, there was an unusual distribution which was difficult to relate to a main gene model. In the LMxR group two families had distinctly higher S/P ratios. This may indicate the presence at one locus of a gene for high S/P at a low frequency. The families showing high S/P are not the same as those showing high nP. This supports the work of Rendel and Nay (1978) who through selection changed nP and S/P independently of each other.

Primary follicle density appears to be controlled by a major gene in the LMxR group (see figures 5.31 - 5.32). This was also suggested in the SFMxR genotype but less strongly as the R^2 for the equation in this group was only 2.4% in comparison with 44.6% in the LMxR.

```
The regression equation is
LNVARlnSP = 1.78 - 0.136 x̄lnSP + 0.0278 xlnSPSQ
SD = 0.005231    R-sq = 4.5%       R-sq(adj) = 0.0%
```



```
LNVARLNS/P
         -
         -
         -
         -
1.6180+        *
         -
         -
         -
         -
1.6160+              *                              *
         -          3                              *
         -           ***
         -          22*
1.6140+              ****
         -               *    *    *2
         -
         -
         -
         +---------+---------+---------+---------+---------+------x̄lnSP
         1.95      2.10      2.25      2.40      2.55      2.70
         N* = 2
```
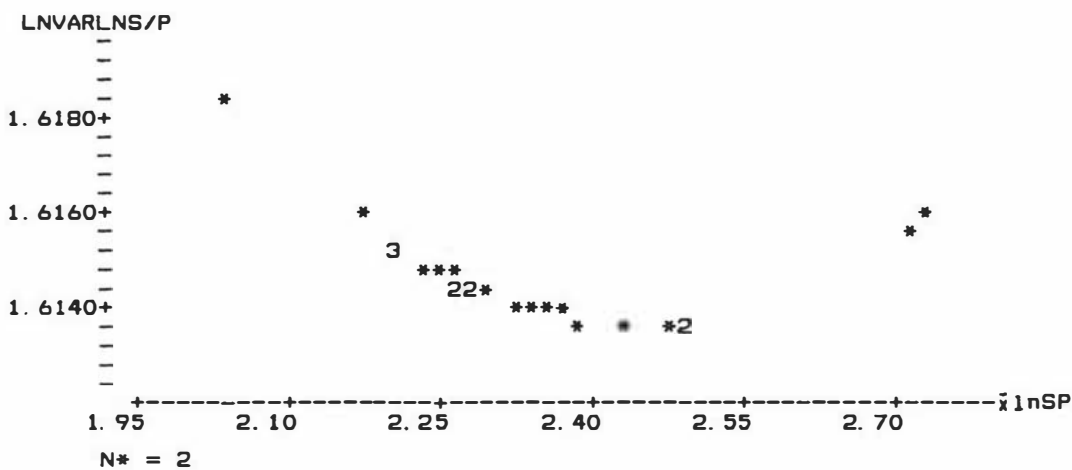
Figure 5.29:   Polynominal regression of the natural
log (ln) variance of ln S/P on the mean
of ln S/P in LMxR

The regression equation is

LNVARlnSP = 1.56 + 0.061 lnSP - 0.0146 lnSPSQ

SD = 0.003745   R-sq = 13.3%
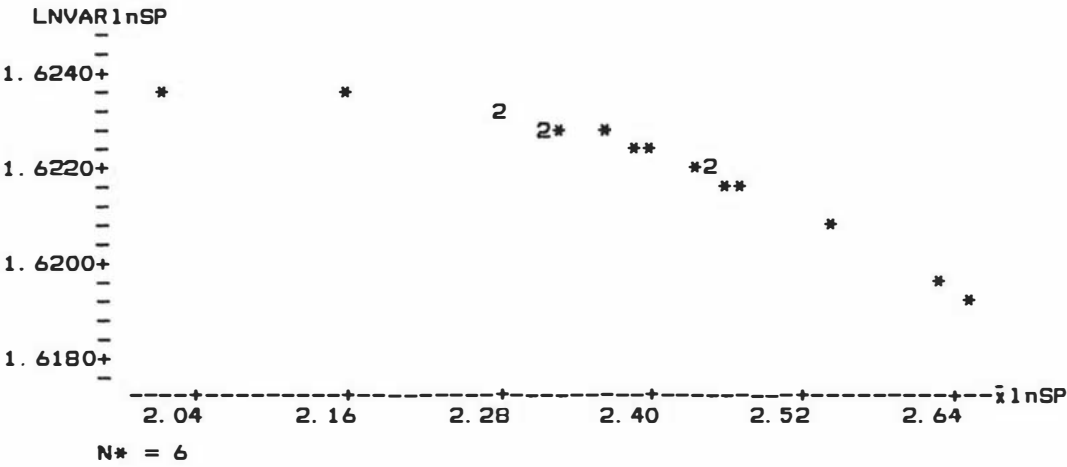
Figure 5.30:   Polynominal regression of the natural
                log (ln) variance of ln S/P on the mean
                of ln S/P in SFMxR

```
    The regression equation is
    LNVARnP = - 42. 5 + 19. 4 xnP - 2. 24 nPSQ
    SD = 0. 9204      R-sq = 44. 6%
```
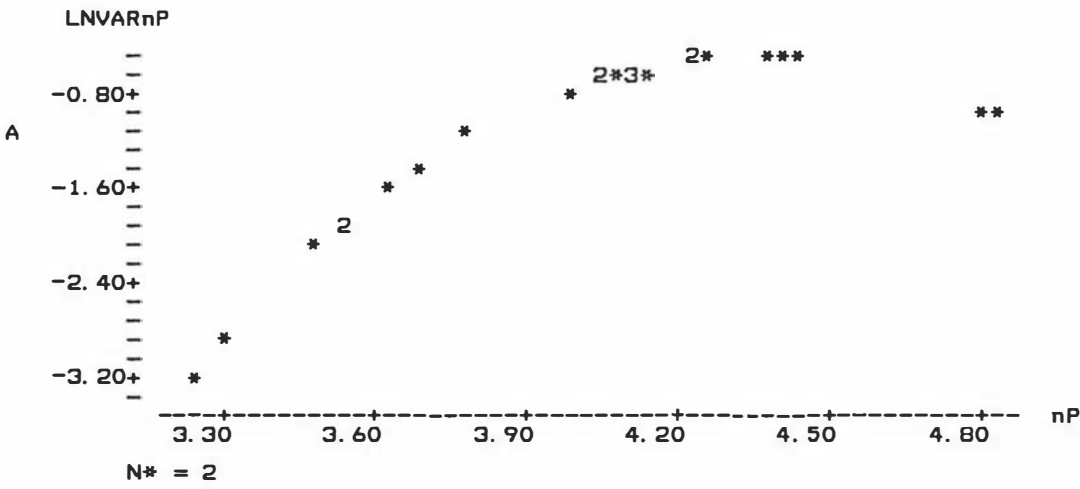

Figure 5.31:   Polynominal regression of the natural
                log (ln) variance of nP on the mean of
                nP for LMxR

281

The regression equation is
LNVARnP = − 7.5 + 2.83 nP − 0.299 nPSQ
SD = 0.7512   R−sq = 2.4%

NVARnP

```
 -0. 80+                                      * *
       -                              **
       -                         *2
       -                       *  2
 -0. 90+                                                    *
       -                                                      *
       -
       -
 -1. 00+            2
       -
       -        *
       -      *
 -1. 10+      *
       -
       -   *
        +---------+---------+---------+----------+---------+------  nP
      3. 50      3. 85      4. 20      4. 55      4. 90      5. 25
       N* = 6
```
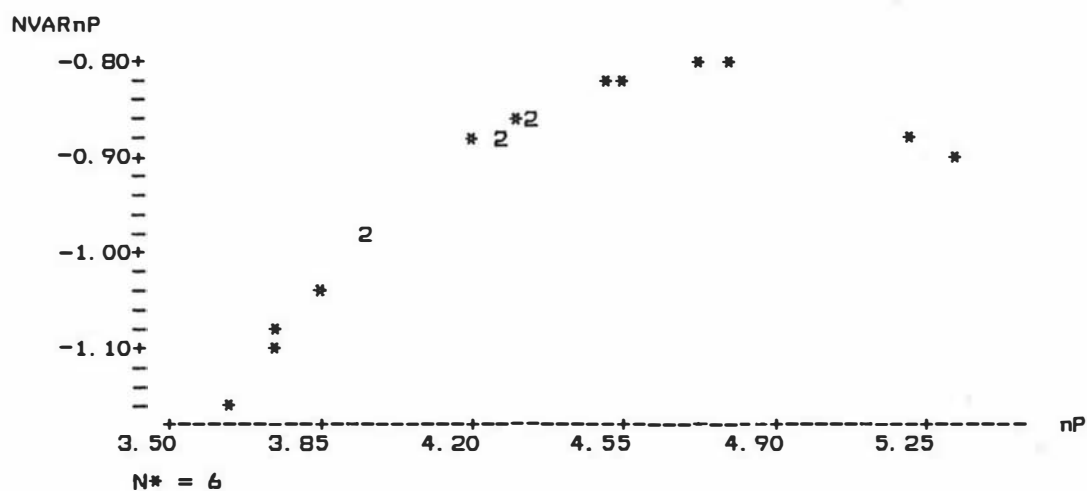
Figure 5.32:   Polynominal regression of the natural
               log (ln) variance of nP on the mean of
               nP for SFMxR

```
The regression equation is
lnVARn(P+S) = 2.43 + 0.027 x̄n(P+S) + 0.00023 n(P+S)SQ


SD = 0.7799       R-sq = 27.0%
```
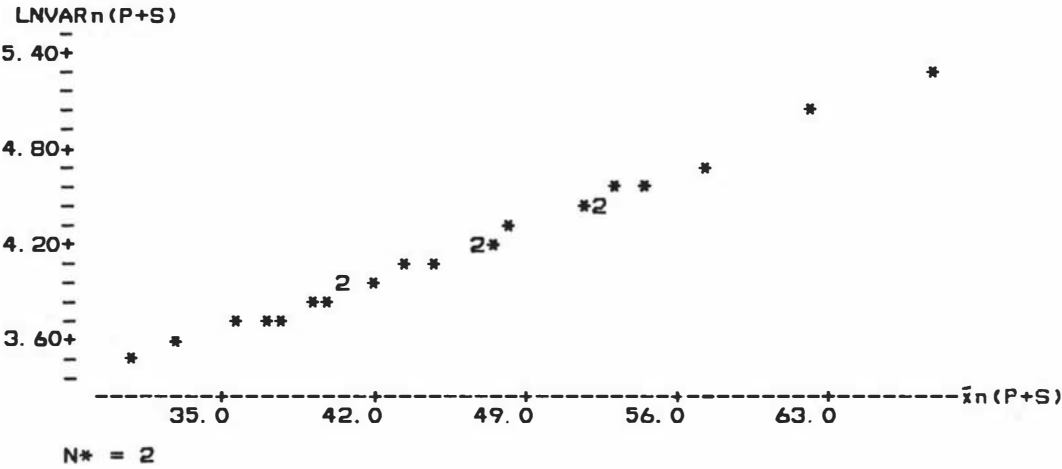

Figure 5.33:   Polynominal regression of the natural
                log (ln) variance of n(P+S) on the mean
                of n(P+S) for LMxR

The regression equation is

LNVARn(P+S) = 0.61 + 0.084 n(P+S) - 0.00029 n(P+S)SQ

SD = 0.6710   R-sq = 48.7%
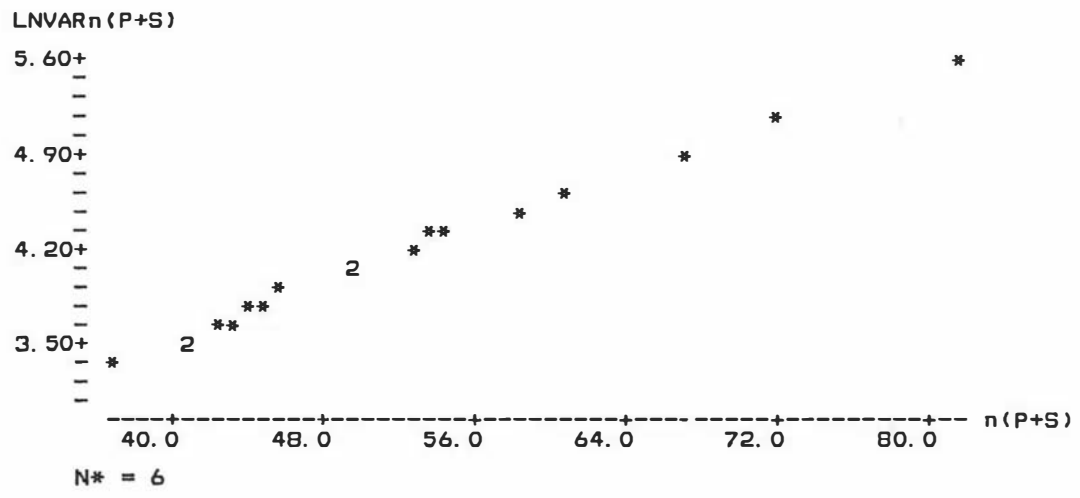
Figure 5.34:   Polynominal regression of the natural
                log (ln) variance of n(P+S) on the mean
                of n(P+S) for SFMxR

The inheritance of n(P+S) appears from figures 5.33 - 5.34 to be multifactorial in both crossbred genotypes, and has some signs of recessive tendencies. That the major gene controlling nP is not evident in this distribution is probably due to the large amount of random noise and high variance for this trait.

5.6 GENERAL DISCUSSION OF METHODS OF MAJOR GENE DETECTION

For most follicle characteristics the frequency distribution results fail to indicate the presence of a major gene. The only sign of genetic segregation, skewness, was apparent only in the S/P data before log transformation. This tends to indicate scale effects rather than the presence of a major gene and illustrates the importance of choice of scale as discussed by Wright (1952) and Falconer (1981). For most analyses with S/P, more consistent results were obtained using the natural log scale.

There was a suggestion of genetic segregation in the n(P+S) data but, as nP and S/P are components of this trait, one would expect major genes to affect one or both of these characteristics as well. Although not evident from the frequency distributions or Bartlett's test results, evidence of a major gene for nP was found when Fain's method was applied.

Evidence of genetic segregation for n(P+S) was noted by Schinckel and Hayman (1960). Using Merino X Border Leicesters, they observed increased variance for n(P+S) in the F_2's vs. the F_1's. The authors suggested that the increased variance for n(P+S) in the F_2 animals was due to the large genetic differences between the parental breeds. They also suggested that this increase in the variance of n(P+S) was clear evidence of the segregation of genetic factors affecting n(P+S), and that the number of follicles per unit area of skin was inherited independently of the ability to produce wool per unit area of skin.

Skewness and kurtosis coefficients have been used as aids to major gene detection by Merat (1968) and Hammond and James (1970). Under Merat's system the data were first tested for homogeneity of family variance and then the g_1 and g_2 statistics calculated in the families with largest and lowest variances. If genes of major effect were present, then the high variance groups should have asymmetric and platykurtic distributions. Merat (1968) also compared the kurtosis coefficient for backcross and parental groups.

For all three genotypes, (SFMxR, LMxR and BX), the lack of significant differences between generations in variances for most follicle and most fleece characteristics suggests the multifactorial mode of inheritance of these traits. It should be noted that the present estimates were within generations and not within families as in the analysis of Merat (1968).

Hammond and James (1970) questionned the sensitivity of these techniques but suggested that they might be useful for traits with moderate heritabilities. The lack of significant skewness and kurtosis for the moderately heritable follicle characteristics is contrary to expectations in the presence of a major gene controlling these traits. Again, intra-family analysis might have clarified the results.

The within familiy analyses gave greatly different results for nP. Using Fain's (1978) techniques there was evidence of a major gene for nP in the LMxR and SFMxR groups. The nP gene frequencies seem to be higher in the LMxR group. These results are supported by the increase in variance for nP, between the F_1 and F_2 generations in the SFMxR group. The lack of significant increase in the between-generation variance in the LMxR group probably reflects the large difference in the F_1 and F_2 generation numbers. Although Fain's (1978) technique, as well as other tests, indicated a multifactorial mode of inheritance for n(P+S), there were small suggestions of genetic segregation in the between-generation frequency distributions.

CHAPTER 6

GENERAL DISCUSSION AND CONCLUSIONS

6.1 ANALYSIS OF FIXED EFFECTS

As noted in Chapter 3, of the three fixed effects examined, age/year born exerted the strongest effect on fleece and follicle characteristics.

The choice of S/P as a criterion for follicle population studies was supported by its insensitivity, relative to n(P+S), to environmental factors. In contrast to much of the published work (Schinckel, 1955a,; Short, 1955a, b; Schinckel and Short, 1961), BRR had little significant effect on any of the follicle characteristics. This suggests that the pre-natal and post-natal conditions provided at Tokanui are adequate to allow follicle development and maturation.

GFW, CFW, LWT, MFD and SL all tended to increase with age and then decline. Since S/P and n(P+S) showed similar patterns, indicating a decline with increasing age in both the number of active follicles and the output per follicle. Data correction for fixed effects provided only small increases in the accuracy of subsequent analyses.

6.2 GENETIC AND PHENOTYPIC PARAMETERS

6.2.1 Repeatabilities and Heritabilities

The differences between the two data sets used to calculate repeatability and heritability estimates must be considered. The repeatability set was a mixed genotype group which had not been corrected for genotype. The data sets created to produce heritability sets were either within genotype or pooled.

The high repeatabilities for most fleece and follicle characteristics support the non-significance of environmental factors, other than age, on these traits. High repeatabilities are generally associated with high heritabilities. This pattern was noted in the present trial for: n(P+S), nP, LWT, MFD, SL_m, TCN and CPC.

Most follicle characteristics are strongly inherited. MFD, SL_m, MFD, TCN and CPC also appear to be influenced by genetic factors. Given the genetic correlations between many of these factors, selection for one should give a concomitant change in other desirable traits.

6.2.2 Genetic and Phenotypic Correlations

S/P was positively correlated genetically and phenotypically with n(P+S). This suggests that the genes controlling S/P also influence n(P+S) and *vice versa*. The environmental correlation between these traits must also be positive. There were significant negative phenotypic correlations between S/P and nP. In contrast, the genetic correlations between these traits were variable, but positive. This suggests that environmental factors may override the postive genetic correlations. These results contrast with those of Rendel and Nay (1978) but may reflect the low number of dam/daughter pairs, the short duration and the different environmental conditions of the present study.

The positive genetic and phenotypic correlations between S/P and GFW and CFW, but negative correlations (both types) between S/P and both SL and MFD, suggest that the genes increasing S/P increase fleeceweight through increases in fibre numbers. The level of the S/P x GFW phenotypic correlations was lower than the genetic correlations. The phenotypic correlations of n(P+S) x GFW were negative although there was a strong positive correlation between S/P and n(P+S).

There was a positive nP x GFW genetic correlation but the equivalent phenotypic correlation was negative. A favourable environment would increase both fleeceweight and liveweight. The increases in liveweight would stretch the skin resulting in lower nP and n(P+S). The suggestion of Rendel and Nay (1978) that concomitant selection for nP and S/P would increase fleeceweight is supported by the genetic correlations between nP x GFW and S/P x GFW. There were high positive genetic and phenotypic correlations between nP and n(P+S). In one genetic pathway to increased fleeceweight the genes increasing nP and S/P are very effective. The importance of nP in the genetic determination of fleeceweight may be more important than previously realized.

The genetic relationships of S/P, nP and n(P+S) with GFW, MFD and SL should be considered in a selection programme. Jackson et al (1975) suggested that selection for increased fleeceweight would lead to increased follicle density. Heydenrych et al (1977) reported little selection response for CFW through for increased S/P. Thei r- results are in line with those of Rendel and Nay (1978). An in-depth review hasbeen published recently (McGuirk et al, 1986) which provides more detail of the results of long-term experiments for fleece and follicle traits in Australian Merinos.

Both S/P and n(P+S) were positively correlated (genetically and phenotypically) with TCN. This suggests that sheep with denser follicles will have more-crimped fleeces.

The positive genetic correlations, MFD x SL, MFD x GFW and SL x GFW suggest that some genes affecting GFW do so through increases in fibre size.

The phenotypic correlations between LWT and GFW, MFD, and SL were all positive. This suggests that conditions which promote increased animal liveweight will also increase GFW through increases in MFD and SL.

The present data suggest that it would not be possible to predict S/P with any accuracy using non-follicular traits.

6.2.3 HETEROSIS

Between generations there was negative heterosis for most follicle characteristics. In the SFMxR, heterosis for nP was positive except between the F_1 and F_2 generations. The highest level of heterosis (although negative), was for n(P+S). High positive heterosis was noted for LWT, GFW and TCN. The mean values for most characteristics increased in succeeding generations, suggesting some directional genetic change.

6.3 MAJOR GENE DETECTION

It should be noted that the present techniques of major gene detection indicate only the possible presence of main genes. Definitive proof will be the identification of sheep having these main genes.

The accuracy of the present analyses would have been improved if the Romneys included as a parental group were linked genetically with the crossbreds. The present study was hampered by the lack of F_1 data, particularly in the LMxRomneys and by the difficulties in collecting data from sufficient closely-related family groups.

The present results suggest that the inheritance of S/P is controlled by at least two, and probably more, loci with high S/P apparently being associated with recessive genes. The negative heterosis found also supports the concept of recessive gene action.

In the crossbreds, S/P showed signs of bimodality and positive skewness and kurtosis. Natural log transformation of S/P removed the bimodality and rendered the skewness non-significant. In the B_2 group there was significant negative skewness and positive kurtosis.

There was a suggestion in both crossbred genotypes of the presence of a main gene influencing nP. Although there was little between-breed variation for nP the within genotype variation in nP was high. The nP frequency distributions of the Romney group indicate that the possible main gene for nP in the crossbreds may come from the Romneys.

The distributions of nP and nP(corr) distributions showed vague signs of bimodality and platykurtosis. In the SFMxR data there was a significant increase in variance between generations. With LMxR there were not sufficient numbers of F_1's for the data to be reliable. Lande's (1981) method suggests that primary follicle density in both crossbred genotypes is controlled by one locus. The use of nP(corr) data gave similar results. The pattern observed using Fain's (1978) technique was consistent with that expected for a major gene. The high heritability and repeatability estimates for nP would be expected in the presence of a main gene.

It has generally been assumed that the correct biological model is that nP and S/P act largely independently of each other and these together determine n(P+S) (Jackson et al, 1975).

Total follicle density equals $\quad$ n(P + S) = nP * (S/P + 1)

If this model is valid then a main gene for nP should have proportionately the same effect on n(P+S) as on nP if the gene does not also affect S/P. Variation in S/P will create extra variation in n(P+S) so it will probably be more difficult to recognize the effect of this gene on n(P+S) than on nP. The frequency distributions, variances and heterosis results along with the regression equations, all suggest a multifactorial mode of inheritance for n(P+S) but with recessive tendencies. Turner (personal communication) stated that the evidence she had considered pointed to multifactorial inheritance of follicle characteristics.

The importance of nP in determining fleeceweight was noted by Jackson et al (1975) and Rendel and Nay (1978). Jackson et al (1975) using canonical analysis proposed three independent pathways of genetic control of fleeceweight: 1. through S/P ratio (controlling n(P+S)); 2. through follicle depth (controlling fibre length) and 3. through either primary or follicle group density (controlling fibre diameter and density) respectively. They suggested that three separately-acting possibly-linked sets of genes were involved.

In the present crossbred flocks, the high heritability estimate and the indication of a major gene for nP suggest that this pathway may be very important in the improvement of fleeceweight particularly if there is selection for fine fibre diameter.

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