A GENETIC EVALUATION OF THE DOHNE MERINO BREED IN SOUTH AFRICA

by

Jan Willem Swanepoel

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Supervisor:	Prof J.B. van Wyk
Co-Supervisors:	Prof S.W.P. Cloete
	Dr G.J. Delport

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Table of contents

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CHAPTER PAGE

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“Yes, Furthermore, I count everything as loss compared to the possession of the priceless privilege of knowing Christ Jesus my Lord and of progressively becoming more deeply and intimately acquainted with Him.”

Phil. 3:8 (The Amplified Bible)

1

History of the Dohne Merino

The Dohne Merino breed is a synthetic dual-purpose (wool and mutton) sheep breed. The breed originated from a cross between German Mutton Merino rams, obtained from the Elsenburg College of Agriculture and South African Merino ewes (Kotze, 1951). The German Mutton Merino was imported to South Africa from Germany in 1932 by the Department of Agriculture.

The development of the breed was always closely related to the Dohne Agricultural Research Station near Stutterheim in the Eastern Cape, hence the name of the breed (McMaster, 1991). This development was initiated and executed by Mr. J.J.J. Kotze at the Dohne research station. The breeding program commenced in 1939 after experiments done by the South African Department of Agriculture. The progeny were interbred and visually selected for rapid lamb growth rate and fine Merino wool under commercial rangeland conditions.

Low fertility and high mortality rates were limitations to Merino sheep farming in the sourveld of the Eastern Cape. Merino sheep of that period also possessed excessive skin folds, resulting not only in high levels of wool production, but also high levels of susceptibility to fleece rot and blow fly strike on account of the excessive skin folds. Furthermore, the selective grazing habits of the Merino demanded higher input costs, as well as more intensive management strategies in order to maintain sustainable woolled sheep farming. Since farm profitability was compromised, farmers envisaged a more extensive farming system, running more adaptable sheep. In terms of higher income, supplementation of returns from wool, by means of higher levels of income from mutton, production formed the primary objective set for a more profitable enterprise. An increased reproduction rate and improved marketability of slaughter lambs, or surplus breeding material, was thought to alleviate the above problem. The Dohne Merino was developed in an effort to fulfil this need.

The Dohne Agricultural Research Station is situated at 27° 28’ longitude and 32° 32’ S. latitude, at an altitude of 1020 m above sea level and 72 km from the coast. It is situated in a summer rainfall area in a mist belt, and is characterized by particularly dry winters and wet, humid summers that are characterized by internal parasites and blowflies, to mention but a few challenges facing sheep breeders in this region.

The Dohne Merino Breed Society was formed in 1966. Since 1974, selection has been done with the aid of performance testing. Comprehensive production records involving all recorded animals being maintained in a computerized flock-recording scheme was introduced *circa* 1985 (Delport, personal communication). Raw on-farm data was collected by breeders, which included wool and weight data. The Breed Society is responsible for handling birth registration and weaning data, while the governmental and nowadays subsidized Agricultural Research Council (ARC) is responsible for performance evaluation, which consisted of testing and routine data manipulation. The Breed Society oversees the final selection and registration of breeding material.

The Dohne Merino Breed Society became well known for their conscientious application of scientific breeding methods in order to establish and improve their breed. They have, however, been extremely reluctant to implement a whole breed BLUP analysis. The Society calculated BLUP breeding values for registered breeders since the 1990’s, but only on a within-flock basis. The grading of animals is however still performed on basis of within-flock indices (or ratios) and breeders primarily rely on this index system. Currently, the Dohne Merino Breed Society is developing structures to enhance the genetic progress of the breed, by changing within-flock genetic evaluations to across-flock genetic evaluations (Delport *et al.* 2003). Sufficient links exist between flocks as a result of the general exchange of breeding material in the Dohne Merino stud industry through the usage of a sire-referencing scheme.

2

General Introduction

The primary goal of animal breeding is to genetically improve production and/or reproduction traits in animal populations, through selection. Snyman & Olivier (2002) confirmed this statement and added that parameter estimates are required to construct a breeding program to genetically improve the economic viability of the sheep breeding enterprise.

Since the introduction of a performance-recording scheme for woolled sheep in South Africa *circa* 1980, recording has been compulsory for all registered Dohne Merino breeders. Performance recording on its own is rather useless, when considering the relatively small contemporary groups and the animal breeding technology currently available.

According to Simm *et al.* (2001) sheep improvement schemes are often hampered by relatively low use of performance recording; relatively small size of recorded flocks and frequent lack of genetic ties to facilitate across-flock genetic evaluations. Atkins *et al.* (1998) argued that the sheep industry, especially the Merino industry in Australia, was slow to adopt an across-flock genetic evaluation, while the other major livestock industries (dairy cattle, beef cattle, meat sheep and pigs) have already developed evaluation schemes. These schemes primarily depend upon on-farm data collection and centralized processing for across-flock predictions of the breeding values of seed-stock animals.

2.1 Breeding value considerations

A sire-referencing scheme for the Dohne Merino stud industry was introduced in 1992, of which the need was highly debatable. According to Simm *et al.* (2001), the creation of a structure to accelerate the rate of genetic improvement is the main goal of sire-referencing schemes. Proof exists that sire-referencing schemes contributed substantially to the rates of genetic progress (Simm *et al.*, 2001). Sire-reference schemes were established to genetically link studs, since there were no other means of comparing animals in different studs or flocks. This method enabled the comparison of animals from different studs or areas through genetic linkage.

Ironically, the necessary genetic links already existed in the Dohne Merino breed upon introduction of sire-referencing. Sire-referencing, however, proved to be an invaluable aid to demonstrate the introduction of BLUP breeding values and across-flock evaluation to Dohne Merino Breeders (Delport, personal communication). Data analyses were initially based on a single-trait sire model, using parameters from Delport & Botha (1994). Since 1996, a single-trait animal model (Delport, unpublished) was used for analysing the sire-referencing scheme as well as individual flocks upon request of breeders. Lagging behind other South African livestock breeds, a complete multiple trait breed analysis was introduced only in 2005.

Animals within a contemporary group are comparable due to the fact that they were subjected to the same environmental conditions. Genetic ties are however required to connect or compare different groups in different environments. Genetic links tie together groups within a flock and also in different flocks, tested at different times. The accuracy of calculated expected progeny differences depends on the number of links established between flocks. It is therefore necessary to have sufficient genetic links to make an across-flock genetic evaluation worthwhile.

2.2 Breeding objectives

Adams & Cronje (2003) stated that there is an increased economic pressure on dual-purpose sheep breeds to grow finer wool, and at the same time, produce more meat. These requirements posed specific challenges to the Dohne Merino.

Combining the abovementioned physiological evidence with information from the only three available genetic studies on the Dohne Merino breed *viz.* Fourie & Heydenrych (1982), Laas (1982) and Delport & Botha (1994), breeding objectives were drastically changed in 1994. According to Londt (personal communication), more emphasis was placed on the reduction of mean fiber diameter (MFD) as well as clean fleece weight (CFW), and an increase in body weight (BW). The ensuing breed policy served to secure the breed's competitive position in South Africa, as well as in the international livestock industry as a progressive dual-purpose breed.

The objectives of this study were: (i) to construct models and estimate genetic parameters, to perform a refined multiple-trait, across-flock, breed analysis; (ii) to assess genetic change; and (iii) to quantify the actual level of inbreeding and investigate the effect of inbreeding depression on yearling body weight and fleece traits in the Dohne Merino breed population.

3

Data and Editing

3.1 Animals

The data used in this study consisted of records from registered Dohne Merino sheep from 97 studs, situated throughout South Africa. Modelling of systematic effects can be problematic due to fluctuations in environmental conditions across years and regions. Different lambing seasons, feeding conditions and management principles were applied in the different studs. The same set of record-keeping guidelines, prescribed by the Dohne Merino Breed Society, was however used by the breeders. The spatial distribution of the breeders contributing data is provided in Figure 3.1. As seen on the figure, the vast majority of breeders were concentrated in three prominent parts of South Africa i.e. Western Cape, Free State and Eastern Cape.

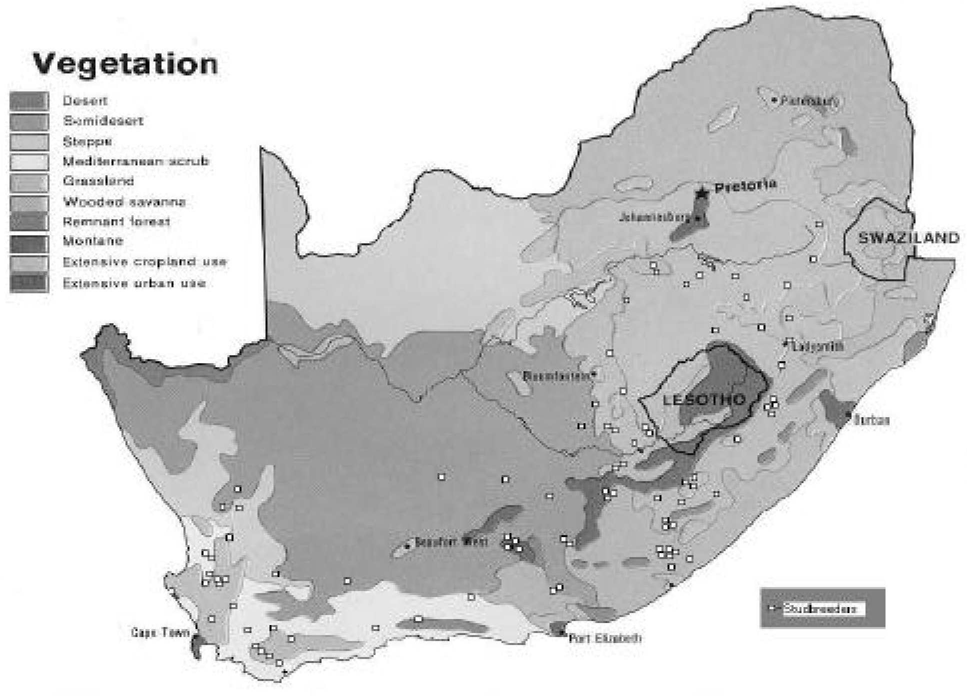

Figure 3.1 Distribution of South African Dohne Merino stud breeders contributing data to the study (2004)

3.2 Data recording

Management guidelines for record keeping prescribed by the Dohne Merino Breed Society are as follows (McMaster, 2000):

Birth	• lambs are tagged • parentage, birth date, birth status and sex are recorded • skipped ewes and stillbirths are recorded
42 days	• live weight and date of weighing are recorded (optional)
100 days	• lambs are weaned • weights and date of weighing are recorded (optional)
4 months	• lambs are judged and shorn to initiate the final test phase
12/14 months	• young animals are weighed and shorn for performance testing
17 months	• final assessment and selection takes place • flock rams are presented for sale • rams for own use and mating are prepared • approved ewes are prepared for mating

Weights are recorded by breeders on-farm. After shearing, the fleece of each individual animal is weighed and a fleece sample is sent to one of the wool testing facilities in South Africa for analysis. The ARC Small Stock Improvement Scheme uses the raw data to do performance testing and calculate within-flock indices. This information is returned to the breeder to use as basis for selection.

The index system as previously used functioned as follows: A within-flock selection index of 85 was regarded as the truncation point for selection at 100 days of age (weaning weight). Only animals with an index of 85 and above could thus be considered for selection. The management guideline for selection at 100 days of age, was optional. The next stage for selection date acquisition was at an age of 12 to 14 months. Data included date of weighing and bodyweight. Thereafter, sheep were shorn and the following recordings were made: date of shearing; greasy fleece weight and clean fleece weight; staple length and fibre diameter. Indices for each trait were then calculated in order to assist in the final selection of animals for stud- or commercial flock purposes.

Since September 2005 selection was based on within flock BLUP of breeding values, derived from data recorded by using the same record keeping guidelines.

3.3 Data editing

One way of compensating for the unpredictable environment of genetic analyses is to assign similarly raised animals to uniform groups, referred to as contemporary groups. A contemporary group is a group of animals of similar breed composition, age and sex that are reared under the same management conditions and have had an equal opportunity to perform. Lofgren & Wood (2001) stated that contemporary groups form the basis for all genetic programs for genetic evaluations and these evaluations depend on all animals in a contemporary group being subjected to similar conditions. The size of each contemporary group must be balanced with uniformity in each group, which is why single sire groups must be avoided. A general rule is to include offspring of at least three sires in each group, with offspring from several litters per sire. The more progeny per sire, the better, as long as they can be managed uniformly.

Contemporary groups in the current study consisted of flock-year-season-sex-management groups (FYSSM). The following limitations have been imposed to these groups:

- Two lambing seasons were created. According to Figure 3.2, which is an indication of the number of animals born in the respective months, two distinct peaks were discernable, one in April and one in September with a clear cut-off point between June and July. January to June was therefore classified as season one or the autumn lambing season and July to December as season two or the spring lambing season.

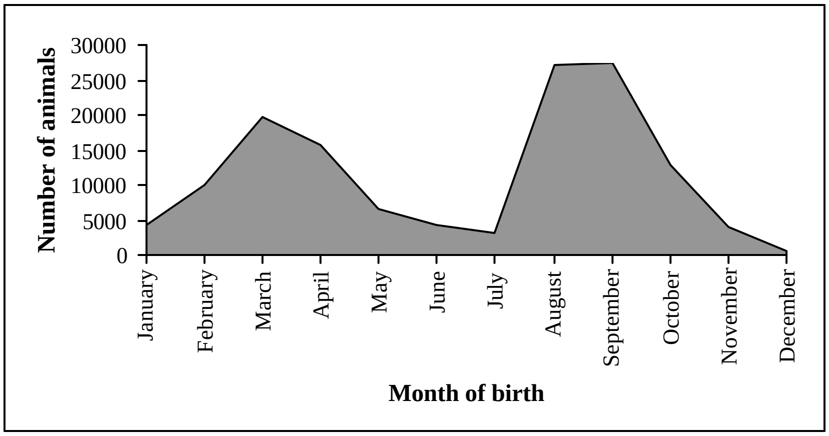

Figure 3.2 The distribution of month of birth for all progeny before editing

- animals without sire and dam identification were omitted
- contemporary groups with less than 10 records were omitted
- range of age at measurement within contemporary groups was limited to 60 days
- progeny of at least two sires must be presented in the contemporary group
- progeny records of sires with fewer than 25 progeny in data set and sires with progeny in only one flock were omitted

Production traits analyzed include: yearling (12 to 14 months) body weight (BW); clean fleece weight (CFW); and mean fibre diameter (MFD). Neither 42 nor 100 day weights were used in this study, since recording of data at these ages was optional. This lead to weaning data being limited and incomplete.

3.4 Data after editing

The official dataset (obtained from the Breed Society) contained 117 331 records with 1 691 sires and 55 826 dams. The edited dataset comprised of 107 389 records for yearling (12 to 14 months) BW, CFW and MFD collected between 1992 and 2004. A summary of the data after editing is presented in Table 3.1. After editing 1 594 contemporary groups (FYSSM) were defined.

Table 3.1 Number of records after editing

	N
No. of records	107 389
No. of sires	1 530
No. of dams	45 178
No. of flocks	97
No. of years	13
No. of seasons	2
No of contemporary groups (FYSSM)	1594

The distribution of body weight (BW) is presented in Figure 3.3. The values ranged from 25 kg to 99 kg, with an average of 50.1 ± 12.3 kg. Gender-specific BW means (± SD) were 55.0 ± 14.1 kg for rams and 43.0 ± 11.0 kg for ewes. Cloete *et al.* (2001) calculated the average yearling BW for an experimental Dohne Merino flock in the Western Cape at 57.9 ± 11.8 kg, 49.8 ± 11.1 kg for Merinos and 65.2 ± 12.6 kg for South African Mutton Merino sheep.

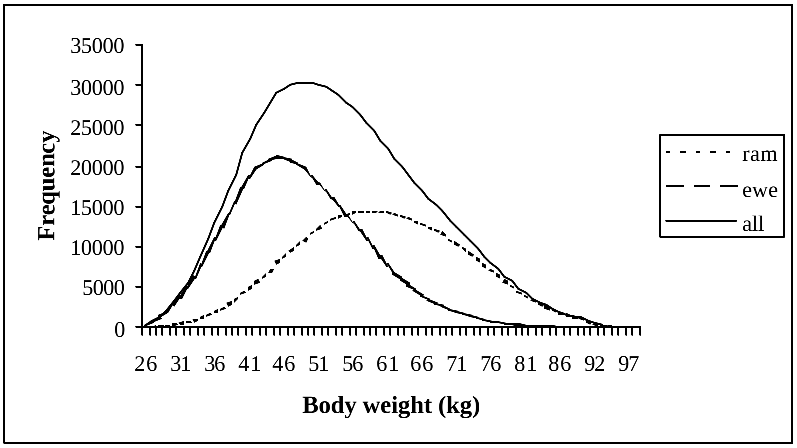

Figure 3.3 Distribution of body weight after editing

The mean estimate for BW calculated by Delport & Botha (1994) for Dohne Merinos was 45.97 kg. The corresponding mean for the Kromme Rhee Dohne Merino nucleus stud was 55.8 ± 10.2 kg (Cloete *et al.*, 1998b).

The distribution of CFW is presented in Figure 3.4. CFW ranged from 0.72 kg to 9.96 kg with an average of 3.12 ± 1.29 kg (Figure 3.5). The average values for rams and ewes were 3.22 ± 1.27 kg and 2.64 ± 1.25 kg respectively. In previous studies (Cloete *et al.*, 1998b; Cloete *et al.*, 2001) the average CFW was 2.1 ± 0.4 kg for

Dohne Merinos, 3.2 ± 0.7 kg for Merinos and 1.6 ± 0.3 kg for South African Mutton Merino sheep (Cloete *et al.*, 2001) with a standardised wool growth period of 183 days.

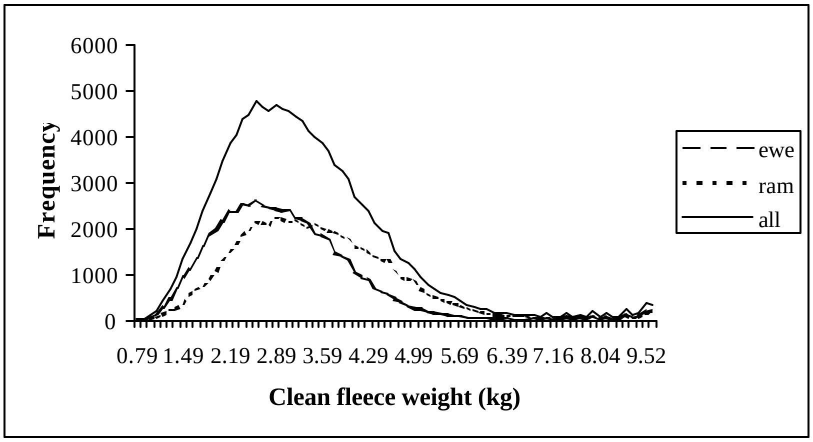

Figure 3.4 Distribution of clean fleece weight after editing

The corresponding mean in the Kromme Rhee Dohne Merino nucleus stud amounted to 1.95 ± 0.39 kg (Cloete *et al.*, 1998b). In the latter study, wool was grown over a period of about 270 days. The average wool production across sexes was calculated to be 2.93 kg. When this weighted mean is adjusted to 183 days, the mean wool production over this period is 1.99 kg, which corresponds to the values obtained by Cloete *et al.* (1998b) and Cloete *et al.* (2001). The mean estimate for CFW calculated by Delport & Botha (1994) for Dohne Merinos was 3.58 kg, which is higher than the current study.

The distribution of MFD is presented in Figure 3.5. The values ranged from 12.7 µm to 26.0 µm with an average of 18.6 µm. The MFD for rams was 19.0 ± 3.4 µm and 17.2 ± 6.2 µm for ewes. The estimate for MFD obtained by Delport & Botha (1994) for Dohne Merinos was 20.9 µm. Studies by Cloete *et al.* (2001) showed that the average value for MFD on Dohne Merinos was 21.8 ± 1.6 µm, 21.9 ± 1.6 µm for Merinos and 23.7 ± 1.5 µm for South African Mutton Merino sheep. The corresponding mean for the Kromme Rhee Dohne Merino nucleus stud was 21.8 ± 1.5 µm (Cloete *et al*, 1998b).

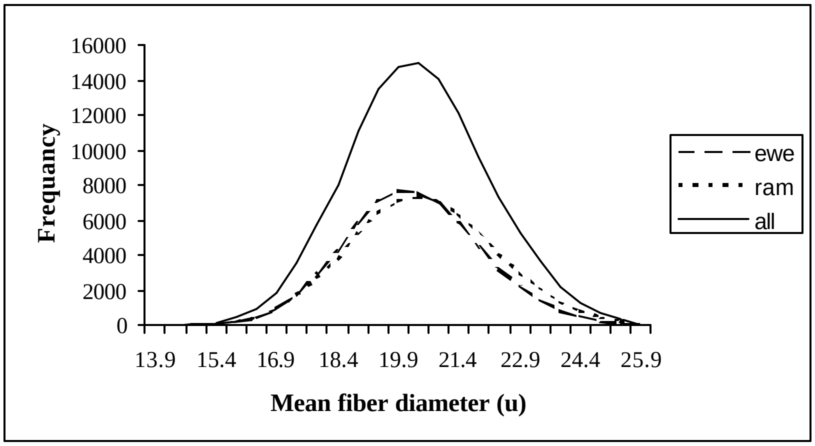

Figure 3.5 Distribution of mean fibre diameter after editing

Coefficients of variation for the production traits were moderate to high, ranging from 8.2% for MFD to 34.0% for CFW (Table 3.2). Cloete *et al.* (2001) calculated the coefficients of variation for the quantitative production traits for Dohne Merino sheep at 20.4% for BW, 19.0% for CFW and 7.3% for MFD.

Table 3.2 Descriptive statistics for yearling body weight and fleece traits in the South African Dohne Merino breed

Trait	n	Mean±SD	CV (%)
Body weight (kg)	107389	48.8±12.3	24.6
Clean fleece weight (kg)	107389	3.12±1.06	34.0
Mean fibre diameter (µm)	107389	19.4±1.6	8.2

n = number of observations; CV = coefficient of variation

Estimates derived by Delport & Botha (1994) for Dohne Merinos were 17.6% for BW, 24.8% for CFW and 8.2% for MFD. A study by Cloete *et al.* (2004) on SA Mutton Merino sheep estimated these values as 7.4% for MFD, 18.5% for BW and 27.0% for CFW. A study on Merinos reported coefficients of variation of respectively 22.3% for BW, 21.1% for yearling CFW and 6.8% for MFD (Cloete *et al.*, 2001). Coefficients of variation below 10% are commonly found for fibre diameter, while more variation is normally found in the other production traits (Olivier *et al.*, 1994; Snyman *et al.*, 1996).

The means for the respective traits in the current study generally corresponded with previous results for the Dohne Merino. Coefficients of variation for the respective traits were much higher than the weighted means calculated by Safari *et al.* (2005) from mostly experimental flocks reported in the literature, as well as results for the Dohne Merino breed.

4

Genetic parameter estimates for yearling body weight and fleece traits

4.1 Introduction

An accurate identification method is required to identify genetically superior animals for selection. The first step, is the development of a suitable statistical model for the estimation of (co)variance components. These estimates are then used to estimate genetic parameters, such as heritability of traits, genetic correlations among traits and to predict breeding values for all animals. The fitting of additional random effects in models is common practice to ensure the increased accuracy of estimates and to optimise selection decisions. Since selection in the Dohne Merino breed takes place under a great variety of environmental conditions, the inclusion of additional random factors, i.e. the sire-flock-year-season interaction (SFYS) and sire-flock interaction (SF) seemed justified, as estimates of variance due to these interactions reflect both interactions and common environmental effects and *vice versa* as stated by Meyer (1987).

Since fleece traits are generally reported to be highly heritable (Safari *et al.,* 2005), provided that directed selection is applied (Rao, 1997), selection for the various wool traits and genetic improvement in wool or dual-purpose sheep breeds are often successful. A study by Cloete *et al.* (2001) showed that woolled sheep are mostly evaluated according to fleece- and live weight traits recorded at yearling age. According to Safari *et al.* (2005) breeding objectives for the sheep breeding enterprise are becoming more complex, since genetic correlations between the traits are not always favourable and correlated responses may largely influence these traits.

The objective of this study was to construct models and estimate genetic parameters for yearling body weight (BW), clean fleece weight (CFW) and mean fibre diameter (MFD) for the South African Dohne Merino sheep breed, with the aim of assisting the breed on embarking on a whole breed across flock BLUP analysis.

4.2 Materials and methods

4.2.1 Data

The edited dataset comprised of 107 389 records for 12-14 month BW, CFW and MFD collected between 1992 and 2004. A detailed description of the data and the editing are presented in Chapter 3.

4.2.2 Statistical analyses

The statistical analysis was divided into three consecutive steps. Firstly, the significance of fixed effects was tested conducting least squares analyses of variance using the GLM procedure of SAS (1994). Effects found to be significant ($P < 0.05$) in these analyses were retained in subsequent analyses. Fixed effects included in the model were flock-year-season-sex-management (FYSSM) (1594 classes), type of birth (singles, multiples), age of dam (2 to 7+ years) and average age (± SD) at measurement fitted as a linear covariate (385 ± 12 days). All the effects were significant ($P < 0.01$) and were retained in the operational model used for subsequent analyses.

The second step was the estimation of (co)variance components for each trait. These were obtained using the ASREML program (Gilmour *et al.*, 2002) fitting single-trait animal models. Random terms were added to the operational model, resulting in eighteen single-trait animal models with various combinations of random effects for each trait. Tests of significance of each random effect were performed using log likelihood ratio tests after adding each random effect (excluding the residual) to the fixed effects model. An effect was considered significant when its inclusion in the model caused a significant increase in the log likelihood. A Chi square distribution for $\alpha = 0.05$ and one degree of freedom were used as the critical test statistic (3.841). The inclusion of the effect was considered significant when -2 times the difference between log likelihoods was greater than the critical value. When differences between log likelihoods were not significant the model with the fewest random effects was chosen. The following single-trait animal models (in matrix notation) were fitted for each trait:

1. $y = Xb + Z_1a + e$
2. $y = Xb + Z_1a + Z_2m + e$ with $\mathrm{cov}(a,m) = 0$
3. $y = Xb + Z_1a + Z_2m + e$ with $\mathrm{cov}(a,m) = A\sigma_{am}$
4. $y = Xb + Z_1a + Z_3pe + e$
5. $y = Xb + Z_1a + Z_2m + Z_3pe + e$ with $\mathrm{cov}(a,m) = 0$
6. $y = Xb + Z_1a + Z_2m + Z_3pe + e$ with $\mathrm{cov}(a,m) = A\sigma_{am}$
7. $y = Xb + Z_1a + Z_4sfys + e$
8. $y = Xb + Z_1a + Z_2m + Z_4sfys + e$ with $\mathrm{cov}(a,m) = 0$
9. $y = Xb + Z_1a + Z_2m + Z_4sfys + e$ with $\mathrm{cov}(a,m) = A\sigma_{am}$
10. $y = Xb + Z_1a + Z_5sf + e$
11. $y = Xb + Z_1a + Z_2m + Z_5sf + e$ with $\mathrm{cov}(a,m) = 0$
12. $y = Xb + Z_1a + Z_2m + Z_5sf + e$ with $\mathrm{cov}(a,m) = A\sigma_{am}$
13. $y = Xb + Z_1a + Z_3pe + Z_3sf + e$
14. $y = Xb + Z_1a + Z_2m + Z_3pe + Z_4sf + e$ with $\mathrm{cov}(a,m) = 0$
15. $y = Xb + Z_1a + Z_2m + Z_3pe + Z_4sf + e$ with $\mathrm{cov}(a,m) = A\sigma_{am}$
16. $y = Xb + Z_1a + Z_3pe + Z_4sfys + e$
17. $y = Xb + Z_1a + Z_2m + Z_3pe + Z_4sfys + e$ with $\mathrm{cov}(a,m) = 0$
18. $y = Xb + Z_1a + Z_2m + Z_3pe + Z_4sfys + e$ with $\mathrm{cov}\ (a,m) = A\sigma_{am}$

where **y** is a vector of observations for yearling body weight, mean fibre diameter or clean fleece weight;

b is a vector of the fixed effects;

a is a vector of direct additive genetic effects;

m is a vector of maternal additive genetic effects;

pe is a vector of maternal permanent environmental effects;

sf is a vector of sire x flock interaction effects;

sfys is vector of sire x flock x year x season interaction effects;

$\mathbf{X}, \mathbf{Z_1}, \mathbf{Z_2}, \mathbf{Z_3}, \mathbf{Z_4}, \mathbf{Z_5}$ is incidence matrices relating the data to the above vectors;

e is a vector of residuals;

A is the numerator relationship matrix and

$s_{\mathbf{am}}$ is the covariance between direct additive genetic and maternal genetic effects.

It was assumed that: $V(a) = As^2_a$; $V(c_{pe}) = Is^2_{pe}$; $V(c_m) = Is^2_m$; $V(c_{sfys}) = Is^2_{sfys}$; $V(c_{sf}) = Is^2_{sf}$; $V(e) = Is^2_e$, with A being the numerator relationship matrix, I an identity matrix; s^2_a, s^2_{pe}, s^2_m, $s^2_{sfys,}$ s^2_{sf} and s^2_e direct genetic variance, ewe permanent environmental and dam variance (half sibs across years), sire-flock-year-season variance and sire-flock variance and environmental (residual) variance respectively.

The following (co)variance estimates and ratios were also calculated:

i. Heritability for the direct additive genetic effect:

$$h^2_a = \sigma^2_a / \sigma^2_p$$

ii. Heritability for the maternal additive effect:

$$h^2_m = \sigma^2_m / \sigma^2_p$$

iii. The genetic correlation between the direct additive and maternal additive genetic effects was estimated as:

$$r_{Gam} = \sigma^2_{am} / (\sigma^2_a + \sigma^2_m)^{½}$$

iv. Permanent environmental variance as proportion of total phenotypic variance:

$$c^2_{pe} = \sigma^2_{pe} / \sigma^2_p$$

v. Sire-flock-year-season (SFYS) variance as proportion of total phenotypic variance:

$$c^2_{sfys} = \sigma^2_{sfys} / \sigma^2_p$$

vi. Sire-flock (SF) variance as proportion of total phenotypic variance:

$$c^2_{sf} = \sigma^2_{sf} / \sigma^2_p$$

Subsequently, after the most significant single-trait models for the different traits were chosen, estimates obtained by single-trait analyses were used as starting values in the three-trait analyses. Different three-trait animal models were fitted according the outcome of the single-trait models. This allowed the calculation of relevant correlations among traits, together with their respective standard errors.

The following three-trait animal models (in matrix notation) were fitted:

1. $y = Xb + Z_1a + e$
2. $y = Xb + Z_1a + Z_2sf + e$
3. $y = Xb + Z_1a + Z_3sfys + e$
4. $y = Xb + Z_1a + Z_4pe + e$
5. $y = Xb + Z_1a + Z_5m + e$
6. $y = Xb + Z_1a + Z_4pe + Z_5m + e$

4.3 Results and discussion

4.3.1 Single-trait analyses

4.3.1.1 Model selection

According to log likelihood ratio tests, the most appropriate model for BW and CFW included both direct and maternal additive genetic effects, permanent environmental effects due to the dam and sire-flock-year-season (SFYS) as random effects. The model with SFYS effects as the only additional random term, except direct animal effects, was found to be superior for MFD. These results are presented in Tables 4.1, 4.2 and 4.3, with the most appropriate models in bold. By taking the highest log likelihood, the smallest error variance and least complex model in consideration the following models were chosen that fitted the traits the best:

$BW = Xb + Z_1a + Z_2m + Z_3pe + Z_4sfys + e$ with $cov(a,m) = A\sigma_{am}$ (Table 4.1)

$CFW = Xb + Z_1a + Z_2m + Z_3pe + Z_4sfys + e$ with $cov(a,m) = A\sigma_{am}$ (Table 4.2)

$MFD = Xb + Z_1a + Z_4sfys + e$ (Table 4.3)

The inclusion of maternal variance (σ^2_m) resulted in the following range of maternal additive variance components for the respective traits: 0.002 to 0.007 for CFW, 0.359 to 1.405 for BW and 0.001 to 0.136 for MFD. If there are strong maternal effects, which are not separately modelled, they can bias heritability estimates. Maternal variance (σ^2_m) improved the log likelihood ratios of the BW and CFW when it was included in the models. Maternal variance ratios had no effect on MFD. Most previous studies on Merino types found maternal genetic variance ratios ranging from 0.01 to 0.15 for BW and from 0.03 to 0.17 for CFW (see estimates summarized from the literature by Cloete *et al.*, 2002).

4.3.1.2 Ratios

The maternal heritability estimates (h^2_m) were lower than direct heritability estimates (h^2_a) for all the models fitted for all the traits (Tables 4.1, 4.2 and 4.3). For MFD maternal heritability (h^2_m) estimates ranged from 0.000 to 0.006, for CFW from 0.010 to 0.042 and for BW from 0.015 to 0.058. These results indicate that maternal effects were still present in BW, to a lesser extent in CFW, and almost completely absent in MFD. These findings are in accordance with results of Snyman *et al.* (1995) in Afrino sheep, which showed that maternal heritability estimates increased up to nine months of age and decreased gradually thereafter. Mortimer & Atkins (1995); Swan & Hickson (1994) and Snyman *et al.* (1996) reported significant additive maternal effects for body weight and small non-significant maternal effects in CFW and MFD. The values obtained by Olivier *et al.* (1998) for an across-flock evaluation of Merino sheep for maternal heritability ranged from 0.03 to 0.04 for MFD, 0.08 to 0.10 for CFW and 0.05 to 0.07 for BW. Van Wyk *et al.* (1994) concluded in a study on Merino sheep that the maternal component could be ignored due to the relative small effect on BW, CFW and MFD. In another study on Merinos, Swan & Hickson (1994) concluded that it is not necessary to consider maternal effects on fleece traits in breeding programs, but maternal genetic effects on BW might be considered.

The estimates of direct heritability (h^2_a) ranged from 0.359 to 0.500 for MFD, 0.145 to 0.239 for CFW and 0.127 to 0.288 for BW respectively. Olivier *et al.* (1998) estimated the direct heritability range for an across stud evaluation of Merino sheep at 0.44 to 0.47 for MFD, 0.28 to 0.40 for CFW and 0.25 to 0.36 for BW when using a range of different models.

Table 4.1 Log likelihoods, (co)variance estimates and ratios calculated for the single-trait models for yearling body weight (BW)

BW	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	**18**
Log Likelihoods	-221080	-220967	-220966	-220955	-220924	-220922	-220969	-220875	-220861	-221043	-220927	-220925	-220918	-220882	-220886	-220836	-220829	**-220812**
Variance Components																		
Total Phenotypic	24.530	24.060	24.050	24.050	23.960	23.970	24.700	24.040	23.990	24.730	24.060	24.010	24.080	23.980	23.930	24.050	23.970	**23.910**
σ^2_e	17.462	18.118	18.164	17.701	17.868	17.806	17.439	18.442	18.757	17.449	18.450	18.843	17.894	18.145	18.459	17.898	18.132	**18.410**
σ^2_a	7.071	4.659	4.564	4.895	4.541	4.662	6.765	3.735	3.056	6.918	3.880	3.042	4.384	3.868	3.227	4.214	3.734	**3.166**
σ^2_m		1.279	1.193		0.509	0.554		1.393	0.872		1.405	0.894		0.523	0.374		0.503	**0.359**
σ_{am}			0.126			-0.121			0.767			0.793			0.459			**0.452**
σ^2_{pe}				1.410	1.040	1.069							1.454	1.112	1.006	1.453	1.117	**0.999**
σ^2_{sh}										0.361	0.328	0.437	0.352	0.336	0.409			
σ^2_{sfys}							0.495	0.473	0.543							0.489	0.479	**0.527**
Variance Ratios																		
a^2	0.288	0.194	0.190	0.204	0.190	0.195	0.274	0.155	0.127	0.280	0.161	0.127	0.182	0.161	0.135	0.175	0.156	**0.132**
	0.008	0.009	0.010	0.009	0.009	0.011	0.008	0.010	0.010	0.008	0.011	0.012	0.009	0.010	0.012	0.009	0.010	**0.011**
m^2		0.053	0.050		0.021	0.023		0.058	0.036		0.058	0.037		0.022	0.016		0.021	**0.015**
		0.004	0.006		0.004	0.005		0.004	0.005		0.004	0.005		0.005	0.005		0.005	**0.004**
c^2_{pe}				0.059	0.043	0.045							0.060	0.046	0.042	0.060	0.047	**0.042**
				0.004	0.005	0.005							0.004	0.005	0.005	0.004	0.005	**0.005**
sh^2										0.015	0.014	0.018	0.015	0.014	0.017			
										0.002	0.002	0.002	0.002	0.002	0.002			
$sfys^2$							0.020	0.020	0.023							0.020	0.020	**0.022**
							0.002	0.002	0.002							0.002	0.002	**0.002**
r_{am}			0.054			-0.075			0.470			0.481			0.418			**0.424**
			0.062			0.076			0.100			0.113			0.156			**0.142**

Table 4.2 Log likelihoods, (co)variance estimates and ratios calculated for the single-trait models for yearling clean fleece weight (CFW)

CFW	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	**18**
Log Likelihoods	23180.8	23223.8	23236.8	23222.0	23243.0	23267.2	23343.5	23374.1	23373.1	23266.6	23297.8	23305.1	23326.1	23333.3	23333.1	23384.3	23399.0	**23401.2**
Variance Components																		
Total Phenotypic	0.238	0.236	0.237	0.236	0.235	0.237	0.240	0.237	0.237	0.240	0.236	0.236	0.236	0.236	0.236	0.236	0.236	**0.236**
σ^2_e	0.181	0.184	0.181	0.182	0.182	0.177	0.182	0.186	0.186	0.183	0.188	0.189	0.185	0.187	0.186	0.184	0.185	**0.183**
σ^2_a	0.057	0.047	0.053	0.046	0.045	0.054	0.052	0.038	0.038	0.052	0.036	0.034	0.037	0.034	0.036	0.038	0.036	**0.039**
σ^2_m		0.006	0.002		0.003	0.005		0.006	0.007		0.007	0.006		0.002	0.003		0.002	**0.003**
σ_{am}			-0.007			-0.009			0.000			0.001			-0.010			**-0.002**
σ^2_{pe}				0.008	0.006	0.008							0.009	0.007	0.008	0.009	0.007	**0.008**
σ^2_{sh}										0.005	0.005	0.005	0.005	0.005	0.003			
σ^2_{sfys}							0.006	0.006	0.006							0.006	0.006	**0.006**
Variance Ratios																		
a^2	0.239	0.197	0.224	0.197	0.189	0.229	0.215	0.160	0.161	0.215	0.154	0.145	0.155	0.146	0.152	0.160	0.152	**0.166**
	0.008	0.009	0.012	0.008	0.008	0.012	0.008	0.010	0.012	0.008	0.010	0.014	0.009	0.010	0.014	0.009	0.009	**0.012**
m^2		0.025	0.042		0.012	0.023		0.027	0.028		0.030	0.026	0.022	0.010	0.011		0.010	**0.013**
		0.003	0.006		0.003	0.005		0.004	0.005		0.004	0.005	0.002	0.004	0.005		0.004	**0.004**
c^2_{pe}				0.033	0.024	0.034							0.038	0.032	0.032	0.036	0.030	**0.032**
				0.003	0.004	0.004							0.004	0.004	0.004	0.004	0.004	**0.004**
sh^2										0.020	0.020	0.021		0.021	0.021			
										0.002	0.002	0.003		0.002	0.003			
$sfys^2$							0.025	0.025	0.025							0.026	0.026	**0.025**
							0.002	0.002	0.002							0.002	0.002	**0.002**
r_{am}			-0.298			-0.502			-0.016			0.101			-0.099			**-0.227**
			0.048			0.058			0.086			0.115			0.138			**0.101**

Table 4.3 Log likelihoods, (co)variance estimates and ratios calculated for the single-trait models for yearling mean fibre diameter (MFD)

MFD	1	2	3	4	5	6	**7**	8	9	10	11	12	13	14	15	16	17	18
Log likelihoods	-63393.3	-63389.5	-63368.7	-63391.1	-63388.9	-63380.8	**-63258.0**	-63257.4	-63257.8	-63308.0	-63308.3		-63306.8	-63297.9	-63328	-63264.9	-63272.6	-63264.7
Variance Components																		
Total Phenotypic	1.337	1.334	1.346	1.333	1.332	1.348	**1.343**	1.342	1.340	1.348	1.348		1.345	1.345	1.304	1.340	1.339	1.342
σ^2_e	0.712	0.717	0.688	0.714	0.717	0.676	**0.715**	0.718	0.720	0.716	0.716		0.718	0.718	0.788	0.717	0.718	0.712
σ^2_a	0.625	0.609	0.673	0.611	0.604	0.688	**0.602**	0.595	0.590	0.607	0.607		0.595	0.595	0.469	0.589	0.588	0.600
σ^2_m		0.007	0.012		0.006	0.009		0.003	0.003		0.000			0.000	0.000		0.001	0.136
σ_{am}			-0.027			-0.038			0.002						0.000			-0.005
σ^2_{pe}				0.009	0.005	0.014							0.007	0.007	0.021	0.007	0.006	0.007
σ^2_{sh}										0.025	0.025		0.025	0.025	0.027			
σ^2_{sfys}							**0.026**	0.026	0.026							0.026	0.026	0.026
Variance Ratios																		
a^2	0.467	0.457	0.500	0.458	0.454	0.510	**0.448**	0.444	0.440	0.450	0.450		0.443	0.442	0.359	0.440	0.439	0.447
	0.008	0.009	0.016	0.009	0.010	0.017	**0.009**	0.010	0.017	0.009	0.009		0.010	0.010	0.001	0.009	0.010	0.017
m^2		0.006	0.009		0.004	0.006		0.002	0.002		0.000			0.000	0.000		0.001	0.001
		0.003	0.003		0.003	0.003		0.002	0.003		0.002			0.000	0.000		0.002	0.002
c^2_{pe}				0.006	0.004	0.010							0.005	0.005	0.016	0.005	0.005	0.006
				0.003	0.003	0.004							0.003	0.003	0.003	0.003	0.003	0.004
sh^2										0.019	0.019		0.019	0.019	0.021			
										0.002	0.002		0.002	0.002	0.002			
$sfys^2$							**0.020**	0.019	0.019							0.020	0.019	0.019
							0.002	0.002	0.002							0.002	0.002	0.002
r_{am}			-0.302			-0.491			0.048						0.000			-0.171
			0.079			0.126			0.219						0.000			0.330

Table 4.4 Estimates of variance components and ratios (SE in brackets) obtained by three-trait analysis for yearling body weight (BW), clean fleece weight (CFW) and mean fibre diameter (MFD)

		Models					
	Trait	1	2	3	4	5	6
Log likelihood		-252582	-252387	**-252209**	-252429	-252482	-252389
	BW	24.560	24.750	**24.730**	24.16	24.14	23.43
σ^2_p	CFW	0.238	0.240	**0.240**	0.237	0.2367	0.2343
	MFD	1.337	1.348	**1.343**	1.337	1.337	1.337
	BW	17.410	17.390	**17.380**	17.920	17.620	17.810
σ^2_e	CFW	0.181	0.183	**0.182**	0.183	0.182	0.182
	MFD	0.713	0.717	**0.716**	0.713	0.713	0.713
	BW	7.150	7.012	**6.856**	4.997	5.552	4.811
σ^2_a	CFW	0.057	0.052	**0.058**	0.048	0.052	0.046
	MFD	0.623	0.605	**0.600**	0.624	0.624	0.624
	BW		0.350				
σ^2_{sf}	CFW	-	0.004	-	-	-	-
	MFD		0.026				
	BW			**0.487**			
σ^2_{sfys}	CFW	-	-	**0.006**	-	-	-
	MFD			**0.027**			
	BW				1.239		0.807
σ^2_m	CFW	-	-	-	0.006	-	0.005
	MFD				-		-
	BW					0.971	0.629
σ^2_{pe}	CFW	-	-	-	-	0.004	0.002
	MFD					-	-
	BW	0.291 (0.008)	0.283 (0.008)	**0.277 (0.008)**	0.207 (0.009)	0.230 (0.009)	0.205 (0.009)
h^2_a	CFW	0.239 (0.008)	0.217 (0.008)	**0.216 (0.008)**	0.203 (0.008)	0.218 (0.008)	0.198 (0.008)
	MFD	0.466 (0.008)	0.449 (0.009)	**0.447 (0.009)**	0.467 (0.008)	0.466 (0.008)	0.467 (0.008)
	BW				0.051 (0.004)		0.034 (0.004)
h^2_m	CFW	-	-	-	0.026 (0.003)	-	0.023 (0.003)
	MFD				-		-

4.3.2 Three-trait analyses

4.3.2.1 (Co) variance components

The (co)variance components and ratios obtained from the six different three-trait models with the most appropriate model (in bold) are displayed in Tables 4.4 and 4.5 respectively.

According to the best log likelihood, the most appropriate three-trait model consisted of only the direct additive and SFYS effects to be included as random traits. The results of the model considered being the most appropriate are displayed in Table 4.6.

Table 4.5 Estimates (SE in brackets) of genetic (below diagonal) and phenotypic (above diagonal) correlations obtained by three-trait analyses for yearling body weight (BW), clean fleece weight (CFW) and mean fibre diameter (MFD).

Model	Trait	BW	CFW	MFD
1	BW	-	0.3165 (0.0033)	0.1307 (0.0038)
	CFW	0.0773 (0.0230)	-	0.1803 (0.0037)
	MFD	0.1034 (0.0183)	0.1458 (0.0193)	-
2	BW	-	0.3188 (0.0034)	0.1291 (0.0039)
	CFW	0.0550 (0.0255)	-	0.1798 (0.0038)
	MFD	0.0938 (0.0192)	0.1343 (0.0211)	-
3	**BW**	-	**0.3179 (0.0034)**	**0.1293 (0.0039)**
	CFW	**0.0501 (0.0257)**	-	**0.1799 (0.0037)**
	MFD	**0.0989 (0.0194)**	**0.1388 (0.0210)**	-
4	BW	-	0.3127 (0.0033)	0.1319 (0.0038)
	CFW	-0.1173 (0.0324)	-	0.1812 (0.0037)
	MFD	0.1216 (0.0213)	0.1599 (0.0207)	-
5	BW	-	0.3181 (0.0033)	0.1315 (0.0038)
	CFW	0.0939 (0.0261)	-	0.1809 (0.0037)
	MFD	0.1122 (0.0204)	0.1543 (0.0201)	-
6	BW	-	0.3200 (0.0035)	0.1339 (0.0038)
	CFW	-0.0816 (0.0328)	-	0.1821 (0.0037)
	MFD	0.1222 (0.0216)	0.1633 (0.0210)	-

Table 4.6 Estimates (SE in brackets) of variance components and ratios, and direct heritability (on diagonal), genetic (below diagonal) and phenotypic (above diagonal) correlations obtained by three-trait analysis for yearling body weight (BW), clean fleece weight (CFW) and mean fibre diameter (MFD)

	BW	CFW	MFD
Variance components			
Phenotypic	24.730	0.240	1.343
Residual	17.380	0.182	0.716
Direct additive	6.856	0.058	0.600
Sire x flock x year x season	0.487	0.006	0.027
Variance ratios			
Direct heritability (SE)	0.277 (0.008)	0.216 (0.008)	0.447 (0.009)
Sire- flock-year-season	0.020 (0.002)	0.024 (0.002)	0.020 (0.002)
Correlation estimates & ratios			
BW	0.277 (0.008)	0.318 (0.003)	0.129 (0.004)
CFW	0.050 (0.026)	0.216 (0.008)	0.180 (0.004)
MFD	0.100 (0.019)	0.139 (0.021)	0.447 (0.009)

4.3.2.2 Heritability estimates

The heritability of BW, heritability was estimated as 0.277 (0.008) from the three-trait analysis. This value is within the range of other published values for the Dohne Merino. Corresponding variance ratios (SE) were published by Cloete *et al.* (1998b) for the Kromme Rhee Dohne flock (0.24 (0.06)). Fourie & Heydenrych (1982), Delport & Botha (1994) and Cloete *et al.* (2001) calculated slightly higher values i.e. 0.37 (0.17), 0.35 (0.09) and 0.33 (0.07) respectively. The value compared fairly well with the weighted mean reported by Badenhorst & Olivier (1991) (0.22 (0.07)) for the Afrino; Brash *et al.* (1992) (0.22 (0.11)) for the Border Leicester; Brash *et al.* (1992) (0.25 (0.08)) for the Corriedale breed; Brash *et al.* (1994a) (0.24 (0.07)) for the Border Leicester; Cloete *et al.* (2001) (0.30 (0.07)) for the South African Mutton Merino and Cloete *et al.* (2004) (0.23 (0.05)) for the South African Mutton Merino. Safari *et al.* (2005) derived a weighted heritability estimate of 0.31 (0.03) for dual-purpose sheep parameters obtained from the literature.

The heritability for CFW was 0.216 (0.008), which is also lower, but comparable with the value calculated by Fourie & Heydenrych (1982) (0.25 (0.15)). Delport & Botha (1994) and Cloete *et al.* (2001) estimated these values at 0.29 (0.08) and 0.28 (0.06), respectively for Dohne Merino sheep. Other estimates were 0.30 (0.08) for Afrino sheep (Badenhorst & Olivier, 1991); 0.29 for Merinos (Olivier *et al.,* 1994); 0.29 (0.07) for Corriedale sheep (Brash *et al.*, 1994b) and 0.27 (0.04) (Snyman *et al.*, 1998a), 0.29 (0.02) (Snyman *et al.*, 1998a) and 0.28 (0.10) (Cloete *et al.*, 2002) for Merino sheep. The averaged value derived by Safari *et al.* (2005) from literature values was 0.31 (0.04) for dual-purpose sheep, which also is somewhat higher than the calculated value in the present study.

A heritability of 0.447 (0.009) was estimated for MFD. This estimate is within the range of other published values for Dohne Merinos. Some of these values are 0.6 (0.2) by Fourie & Heydenrych (1982)); 0.37 (0.09) by Delport & Botha (1994); 0.43 (0.07) by Cloete *et al.* (1998b) and 0.61 (0.06) by Cloete *et al.* (2001). A wide range of estimates for fibre diameter have been published, some of these are 0.48 (0.07) for Merino sheep (Mortimer & Atkins, 1995); 0.39 (0.09) for Afrino sheep (Badenhorst & Olivier, 1991); 0.18 (0.08) for Coopworth sheep (Brash *et al.*, 1994c); 0.44 (0.05) for Merino sheep (Swan & Hickson, 1994); 0.63 for Merino sheep (Olivier *et al.*, 1994); 0.63 (0.01) for Merino sheep Cloete *et al.* (1998a); 0.59 (0.08) for Merino sheep (Cloete *et al.,* 2001); 0.67 (0.05) for South African Mutton Merino sheep (Cloete *et al.,* 2004) and 0.57 (0.05) derived from the literature for dual purpose sheep (Safari *et al*,. 2005).

4.3.2.3 Correlations

The genetic correlation estimated between BW and CFW (0.050 (0.026)) was below the mean derived from numerous literature values. This implies that selection for a higher BW would not affect CFW. Cloete *et al.* (2004) found that the genetic correlation between BW and CFW for South African Mutton Merinos, also a dual-purpose breed (wool and mutton), was lower in comparison to the values obtained for Merino sheep, a wool breed. The authors concluded that the genetic relationship between the two traits might be lower for dual-purpose sheep, like the Dohne Merino, than primarily wool breeds. Other recorded values (SE) were –0.13 (0.22) for Afrino sheep (Badenhorst & Olivier, 1991); –0.009 (0.036) for Afrino sheep (Snyman *et al.*, 1998b); 0.13 (0.13) for SA Mutton Merino sheep (Cloete *et al.*, 2004) and 0.28 (0.04) for Merino sheep (Cloete *et al.*, 2002).

Low genetic correlations of BW with CFW and MFD suggest that wool traits may not be compromised by selection for meat production. According to the review by Safari *et al.* (2005), the majority of published values were generally positive and moderate in magnitude. Studies by Badenhorst & Olivier (1991) on Afrino sheep; Brash *et al.* (1994b) on Corriedale sheep; Brash *et al.* (1994c) on Coopworth sheep; Snyman *et al.* (1998b) on Afrino sheep; Cloete *et al.* (2002) on Merino sheep and Cloete *et al.* (2004) on South African Mutton Merino sheep reported respective estimates of -0.07 (0.21); -0.02 (0.16); -0.20 (0.24); -0.05 (0.03); 0.17 (0.04) and 0.22 (0.10) for this genetic correlation.

MFD and CFW were genetically positively related to each other (0.139 (0. 021)), implying that selection for CFW, without taking MFD into consideration, could result in wool increasing in diameter. This value is slightly lower than other published values. A comparable value for Dohne Merino sheep published by Delport & Botha (1994) was 0.17 (0.20). Other values for Merino sheep were 0.12 (0.26) by James *et al.* (1990), 0.26 (0.03) by Cloete *et al.* (1998a) and 0.31 (0.03) by Cloete *et al.* (2002). Brash *et al.* (1994b) estimated a value of 0.29 (0.15) for Corriedale sheep and Cloete *et al.* (2004) 0.38 (0.08) for South African Mutton Merino sheep.

The phenotypic correlation between BW and CFW was estimated as 0.318 (0.003), which accords with other published values. Safari *et al.* (2005) derived a corresponding weighted phenotypic correlation of 0.35 from literature values from woolled sheep. Other estimates were 0.30 (0.02) for Corriedale sheep (Brash *et al.*, 1994b) and 0.37 (0.02) for Merino sheep (Cloete *et al.*, 2002). Higher values were published by Cloete *et al.* (1998a) for Merino sheep (0.49 (0.01)) and 0.49 (0.04) for South African Mutton Merino sheep (Cloete *et al.*, 2004). Very low (0.143 (0.02)) and negative (-0.009 (0.036)) correlations were estimated for two different groups of Afrino sheep by Snyman *et al.* (1998b).

The phenotypic correlation between BW and MFD was 0.129 (0.004). This value corresponds to other published values: (0.10) for Afrino sheep (Badenhorst & Olivier, 1991); 0.01 (0.20) for Corriedale sheep (Brash *et al.*, 1994b); 0.022 (0.023) for Afrino sheep (Snyman *et al.*, 1998b); 0.17 (0.04) for Merino sheep (Cloete *et al.*, 2002); 0.19 (0.05) for the South African Mutton Merino (Cloete *et al.*, 2004) and an estimate of 0.13 for woolled sheep derived from the literature in the review of Safari *et al*. (2005).

The estimated value for the phenotypic correlation between MFD and CFW was 0.180 (0.004). Delport and & Botha (1994) derived a comparable estimate of 0.10 for Dohne Merino sheep. Other values obtained from previous studies were 0.20 (0.02) for Merino sheep (Cloete *et al.*, 1998a); 0.163 (0.023) for Afrino sheep (Snyman *et al.*, 1998b); 0.16 (0.03) for Merino sheep (Hill *et al.*, 2001) and 0.20 (0.06) for the South African Mutton Merino (Cloete *et al.*, 2004). Higher values were obtained by Badenhorst & Olivier (1991) for Afrino sheep (0.25); 0.34 (0.04) for Corriedale sheep (Brash *et al.*, 1994b); 0.26 for Merino sheep (Swan & Hickson, 1994); 0.25 (0.03) for Merino sheep (Cloete *et al.*, 2002) and 0.25 for woolled sheep in general (Safari *et al.* 2005).

4.4 Conclusions

The heritability estimates of BW and CFW were lower while the MFD estimate was within the range of literature values.

Direct genetic correlations of BW, CFW and MFD were positive, which suggest that selection for bigger and heavier sheep would generally lead to a broader MFD and higher CFW. Because these correlations are fairly low the subsequent correlated response of direct selection for body weight on fleece traits should be small and *vice versa*.

The present study supports the contention of Cloete *et al.* (2004) that the genetic relationship of live weight traits with fleece traits in dual-purpose sheep breeds might be slightly lower than that of primarily wool breeds. Further work on this topic is thus required.

5

Genetic and environmental trends

5.1 Introduction

Sheep breeding enterprises have to be dynamic in implementing changes to meet the changing demands of consumers, changing environments and economic realities.

Breeding programs must be evaluated on a regular basis in order to determine their effectiveness. Genetic trends indicate the amount of genetic improvement over time, or lack thereof, in a population. Environmental trends can be derived for the assessment of management performance, allowing breeders to determine the effectiveness of management interventions in the flock. Moreover, a study by Wilson & Willham (1986) also indicated that environmental trends could provide important information to the commercial breeder on management effects and / or climatic changes.

Accurate genetic parameters for a breed are required before changes are made to selection criteria. To determine the effectiveness of genetic selection, genetic trends in the population under consideration need to be monitored.

It is widely accepted that the most effective way of separating genetic and environmental effects is by using an appropriate BLUP animal model that incorporates all known relationships in the population. Breeding values derived from such analyses can be averaged within birth years and used to depict genetic trends.

The purpose of this study was to assess genetic change in BW, CFW and MFD in the Dohne Merino breed.

5.2 Materials and methods

5.2.1 Data

The data, which comprised of 103 632 records for 12-14 month BW, CFW and MFD collected between 1992 and 2003 were used for analysing genetic, phenotypic and environmental trends. Data obtained for 2004 were incomplete and not suitable for use in this chapter. A detailed description of the full dataset and editing is presented in Chapter 3.

5.2.2 Statistical analyses

5.2.2.1 Breeding values

Direct breeding values were calculated for each trait by using the data from the most appropriate three-trait mixed model analyses that included direct additive and SFYS effects as random. Although maternal genetic effects were found to be significant in some single-trait analyses (BW and CFW), maternal variances were small and would not have a marked effect on the trends. Breeding values were obtained as a by-product from the three-trait analysis used in the estimation of (co)variance components for traits by ASREML (Gilmour *et al.*, 2002) (see Chapter 4).

5.2.2.2 Genetic trends

Genetic trends were calculated as the regression of average predicted breeding values on year of birth.

5.2.2.3 Environmental trends

There are different ways of defining and computing environmental trends. The most common way is to regress the year-season solution on the year of birth. This, however, does not represent the total environmental effect, since adjustments are made for known non-genetic effects. The environmental trend was calculated by subtracting the averaged breeding value from the unadjusted phenotypic value within birth years.

5.3 Results and discussion

5.3.1 Phenotypic and environmental trends

Environmental trends (b), standard errors (SE) and R^2 values for the years 1992 to 1996 and 1996 to 2003 are provided in Table 5.1. The two regression coefficients for each trait resulted from the fact that the environmental trends for the respective traits showed a distinct change in environmental trend from 1996. In all cases the environmental trend increased from 1992 to 1996 and decreased from 1996 to 2003.

Table 5.1 Regression coefficients (b), standard errors (SE) and R^2 values for environmental values of body weight (BW), clean fleece weight (CFW) and mean fibre diameter (MFD) for the years 1992 to 1996 and 1996 to 2003

		1992 - 1996	1996 - 2003
Body weight (BW) (kg)	b	0.230	-0.306
	SE	0.623	0.119
	R^2	0.043	0.525
Clean fleece weight (CFW) (kg)	b	0.126	-0.083
	SE	0.032	0.015
	R^2	0.839	0.840
Mean fibre diameter (MFD) (µm)	b	1.014	-0.147
	SE	0.177	0.041
	R^2	0.916	0.685

The phenotypic and environmental trends for yearling BW, CFW and MFD between 1992 and 2003 are presented in Figures 5.1, 5.2 and 5.3.

According to Figure 5.1 the regression coefficient for the environmental trend of BW indicated an increase from 1992 to 1996 (0.230 ± 0.623; $P > 0.05$), where after the regression coefficient decreased (-0.306 ± 0.119; $P > 0.05$). The R^2 values obtained for BW was 0.043 from 1992 to 1996 and 0.525 from 1996 to 2003. This indicates a poor fit for the first five years and a better fit for the last eight years. A low phenotypic value for BW was recorded in 1993 (45.8 kg). An increase to 49.3 kg took place from 1992 to 1996, where after BW gradually decreased to 47.1 in 2001. In 2003 the phenotypic value for BW was 48.7 kg.

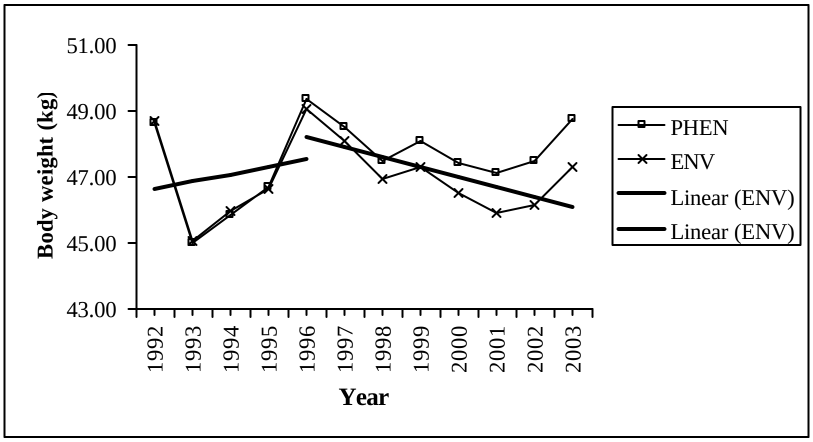

Figure 5.1 Annual mean phenotypic and environmental values (linear trends) for body weight

The mean phenotypic value of CFW gradually increased to 3.08 kg in 1996 and then decreased to 2.45 kg in 2003 (Figure 5.2). The environmental trend for CFW accordingly declined from 1996. The regression coefficient (0.126 ± 0.032; $P < 0.05$) for the first five years shows an increase from 1992 to 1996 and a decrease for the period from 1996 to 2003. The R^2 values for the environmental trend from 1992 to 1996 for CFW was 0.923, suggesting that 92% of the variation of the environmental values for CFW was associated with birth years, there after the R^2 value was 0.840.

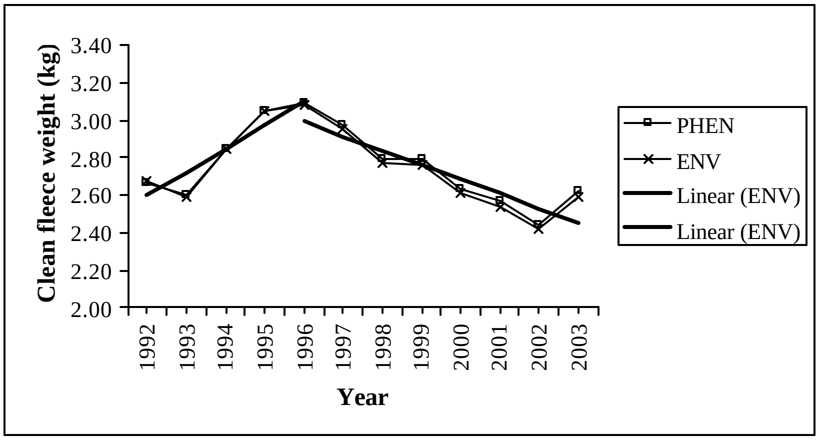

Figure 5.2 Annual mean phenotypic and environmental values for clean fleece weight and linear regressions

The regression coefficient for MFD (Figure 5.3) inclined with 1.014 ± 0.177 (P > 0.05) from 1992 to 1996, which indicates that the environmental value for this trait increased over the five years. From 1996 to 2003 the regression coefficient was negative (-0.147 ± 0.041) indicating that the environmental trend declined during this time.

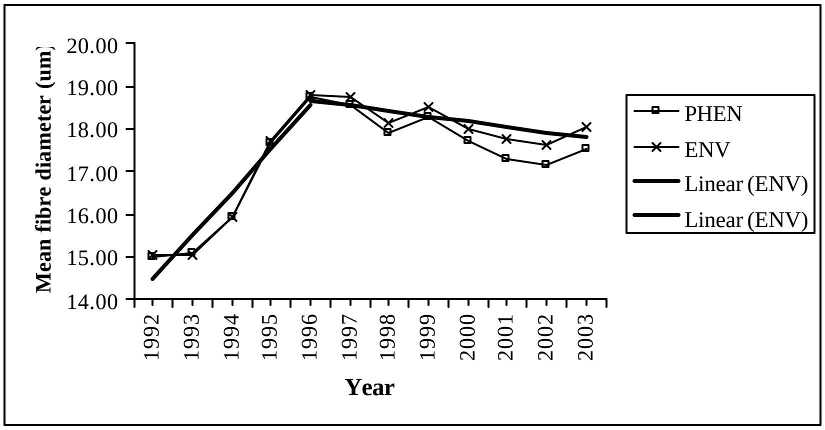

Figure 5.3 Annual mean phenotypic and environmental values for mean fibre diameter

The R^2 values for 1992 to 1996 and 1996 to 2003 were 0.92 and 0.69 respectively suggesting that 92% and 69% of the variation of the environmental values for MFD was associated with birth years. The phenotypic trend of MFD increased sharply from 1992 to 1996 to 18.72 µm, where after the value declined slowly with 0.19 µm annually to 17.19 µm in 2004.

South Africa experienced drier than average years, especially in 1995 and 2000 (Fouche, personal communication) possibly causing environmental deterioration. The changes in economic conditions over the past 10 years increased pressure on farmers. This might have resulted in farmers cutting on input costs by for example providing less supplements etc. also resulting in the decline in the environmental trend.

5.3.2 Genetic trends

According to Table 5.2 the linear regressions produced good fits for the genetic trends as indicated by relatively high R^2 values (0.82-0.97).

Table 5.2 Regression coefficients (b), standard errors (SE) and R^2 values for breeding values for body weight (BW), clean fleece weight (CFW) and mean fibre diameter (MFD). Figures in brackets are expressed relative to the overall phenotypic means provided in Table 3.2

Trait	b	SE	R^2
BW	0.1542 (0.33)	0.0079	0.974
CFW	0.0035 (0.12)	0.0005	0.819
MFD	-0.0514 (-0.28)	0.0054	0.900

The linear regressions depicting genetic trends for yearling BW, CFW and MFD between 1992 and 2003 are presented in Figures 5.4, 5.5 and 5.6. The average direct breeding value for BW showed a slight increase from 1992 to 2003 (R^2=0.974) annually, or 0.27% of the overall phenotypic mean with a regression coefficient of 0.154 ± 0.008.

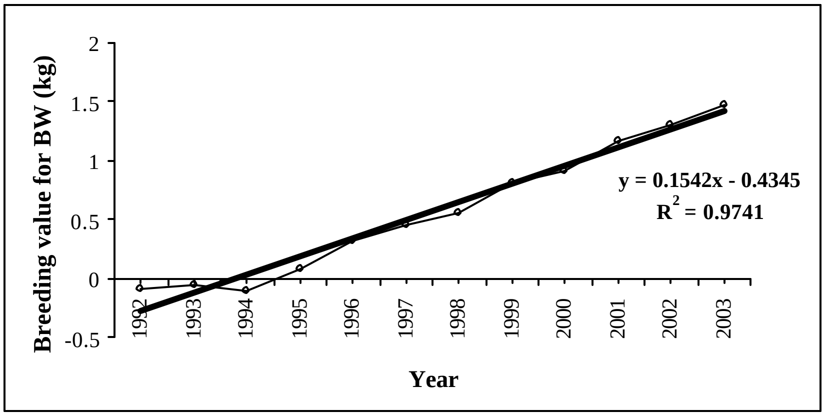

Figure 5.4 Annual mean breeding values and linear regression for body weight (BW)

In a study conducted by Cloete *et al.* (1998b) the genetic improvement in BW of the Kromme Rhee Dohne Merino nucleus flock amounted to 0.145 kg per annum (R^2=0.85). Olivier *et al.* (1995) calculated the genetic trend in Merinos of the Grootfontein stud for BW at 0.205 kg per annum (R^2 =0.82) from 1966 to 1984 and at 0.631 kg per annum (R^2=0.94) from 1985 to 1991. During the latter period, the selection objective was to increase BW and to decrease MFD while keeping CFW constant. During this period, replacements were selected on BLUP of breeding values.

The regression coefficient for CFW was 0.0035 ± 0.0005 (Table 5.2), or 0.1% relative to the overall phenotypic mean. According to the regression coefficient, there was constant change in the desired direction, albeit slow at only about 0.1% per annum. The genetic value increased over the years by a mere 0.004 kg per annum (R^2=0.819). Cloete *et al.* (1998b) calculated the genetic change in the Kromme Rhee Dohne Merino stud for CFW to be 0.016 kg annually (R^2=0.96).

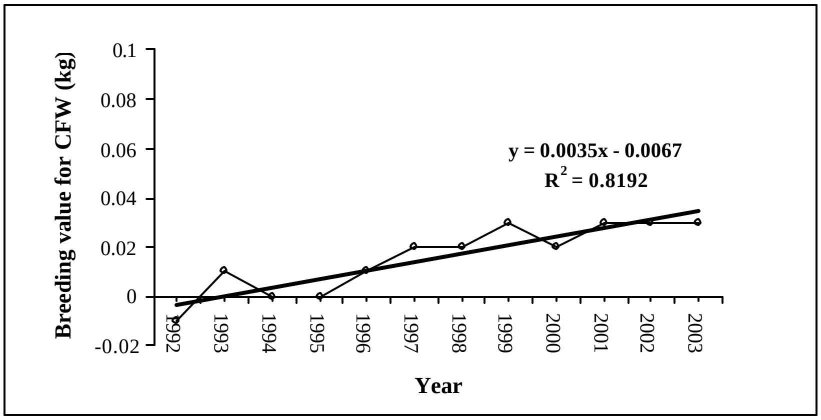

Figure 5.5 Annual mean breeding values and linear regression for clean fleece weight (CFW)

The estimated direct additive breeding value for MFD gradually decreased from 1992 to 2003 with 0.47 µm overall, which amounts to -0.039 µm per annum (R^2=0.90) (Figure 5.6). The acquired response amounted to approximately 0.2% of the overall phenotypic mean. Cloete *et al*. (1998b) found the genetic change of MFD in the Kromme Rhee Dohne Merino nucleus flock to be slower at -0.011 µm per annum. The decrease in average MFD breeding values (Figure 5.6) is a result of selection for finer fibres in the breed, as prompted by premiums paid for finer wool from 1996. This new selection pressure applied caused the reduction in the phenotypic value of MFD in the breed.

In a study on Merino sheep of the Grootfontein stud, Olivier *et al.* (1995) found that the genetic trend for MFD was 0.027 µm per annum (R^2=0.55) in a positive direction for the period from 1966 to 1984.

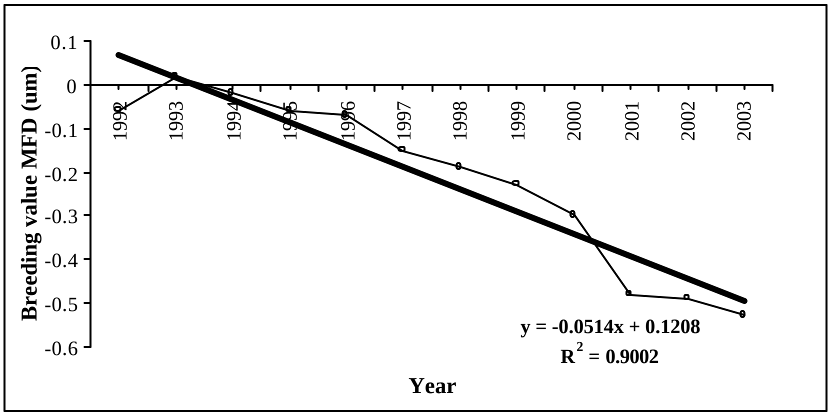

Figure 5.6 Annual mean breeding values and linear regression for mean fibre diameter (MFD)

In the period from 1985 to 1991, when selection using the BLUP of breeding values was implemented and an objective of reducing MFD was strived for, the realised genetic change amounted to –0.157 µm per annum (R^2=0.84).

5.4 Conclusions

The selection objective favoured by the Dohne breeders' participating in the study was to increase BW, while reducing MFD. CFW obviously received less emphasis than the former two traits. This selection objective is driven by economic realities, and is shared by other major wool sheep breeds in South Africa. In the breed analysis of the Merino breed, Olivier *et al.* (2004) found that the genetic trend for BW amounted to 0.24 kg per annum, or approximately 0.5% of the overall phenotypic mean. The response in CFW amounted to -0.007 kg, or approximately 0.2% of the overall phenotypic mean. MFD was reduced at a rate of 0.063 micron per year, or approximately 0.3% of the overall phenotypic mean. It is evident that both Breed Societies share the same basic breeding objective. Although it could be argued that the realised responses could be faster when it is compared to experimental populations (where single-trait selection was practiced in many cases), it is reassuring that the Dohne Merino Breed Society is making progress in the desired direction. The responses has to be seen as satisfactory if it is considered that the data were obtained from individual breeders, in all probability differing markedly in their perceptions of the ideal replacement animal.

6

Inbreeding

6.1 Introduction

The accumulation of inbreeding and the resulting consequences thereof has long been a concern in animal breeding, due to its deleterious effect on additive genetic variance as well as on phenotypic values (Falconer & McKay, 1996). The primary consequence of inbreeding at the farm level is inbreeding depression. Inbreeding impairs growth, production, health, fertility and survival. This concern has become more serious in present-day animal breeding, in which selection responses are maximized by the use of animal model best linear unbiased predictors (BLUP) of breeding values. The use of these breeding values alone may result in more closely related selection candidates, with increased levels of inbreeding since they share most of their familial information (Fernandez & Toro, 1999). Nevertheless, the net effect of inbreeding in a selection program will depend on the magnitude of the selection response relative to the possible depression and rate of accumulation of inbreeding.

Depending on whether genetic gain and inbreeding depression compensate for each other, the level of inbreeding of the animals may need to be accounted for during selection process. Recent advances in genetic selection programs have greatly increased the annual response to selection, but rates of inbreeding have likewise increased substantially (Weigel, 2001).

The purpose of this study was to quantify the actual level of inbreeding and to investigate the effect of inbreeding depression on yearling body weight and fleece traits in the Dohne Merino population.

6.2 Materials and methods

6.2.1 Data

All available pedigree data, which comprised of 266 268 records (302 169 animals) for the period 1975 to 2003 were used for calculating individual inbreeding coefficients. The original pedigree file included animals with only one parent, since these animals might also contribute to the inbreeding coefficients. Animals without parents were omitted. The bigger dataset was used to create as many as possible links between animals to calculate the inbreeding coefficients as accurately as possible. Data obtained for 2004 was incomplete and not suitable for use in this chapter. The Dohne Merino Breed Society employs a strategy of upgrading F3 commercial animals, for which no pedigrees are supplied, to the studs. The number of animals entering the dataset in this manner may lead to under estimation of inbreeding and might therefore have an influence in the outcome of this study.

6.2.2 Statistical analyses

Firstly all known relationships from the entire dataset were used to calculate the individual inbreeding coefficients using the MTDFNRM program of Boldman *et al.* (1995). The rate of inbreeding (?F) was estimated as the difference between the individual inbreeding (F_t) and the inbreeding of the parents (F_{t-1}) divided by ($1-F_{t-1}$) (Falconer & McKay, 1996).

Inbreeding depression was estimated as the regression of performance (corrected for fixed effects) on the individual and dam inbreeding coefficients, fitting an animal model. Linear coefficients were estimated using the ASREML program (Gilmour *et al*. 2002) fitting single-trait animal models.

The generation interval was calculated as the average actual age of the parents when the progeny were born.

6.3 Results and discussion

The number of animals and their average inbreeding coefficients from 1975-2003 are presented in Table 6.1. According to Table 6.1 only 18.67% of all the animals were inbred to some extent. No animals born before 1980 were inbred.

Table 6.1 Data description

	n	%	Level of inbreeding
Total number of animals	302169	100.00	0.64
Non inbred	245768	81.33	0.00
Inbred	56401	18.67	3.43
Number of animals without sires	35901	11.88	-
Number of animals without dams	37026	12.25	-

When all the animals in the study were considered, the average inbreeding coefficient was 0.64%, compared to an average inbreeding of 3.43% for inbred animals (Table 6.1). Figure 6.1 shows the annual proportion (%) of inbred animals from 1980 to 2003. The proportion of inbred animals increased from 0% in 1980 to 38% in 2003. The percentage of inbred animals in 2003 might be an alarming matter. The maximum individual inbreeding coefficient of animals born in 2003 was 32.0% while 3.2% of these animals had an inbreeding coefficient higher than 10%. After 1984 the maximum individual inbreeding coefficients were 25.0% or higher. Since 1992 an annual average of 373 animals had an inbreeding coefficient higher than 10% (Table 6.2).

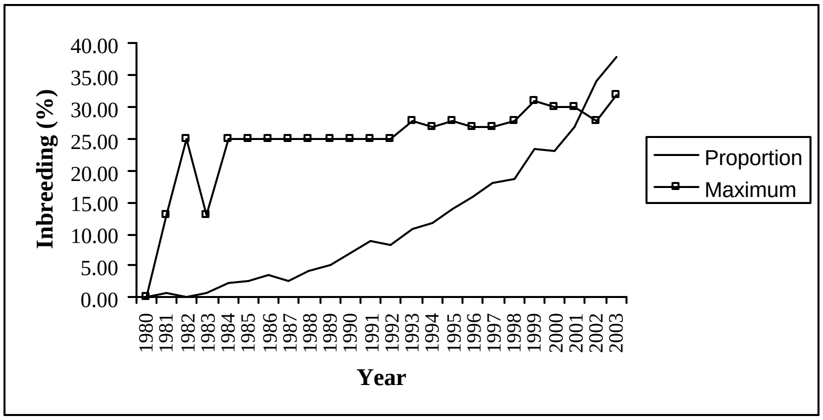

Figure 6.1 Annual mean and maximum individual levels of inbreeding with the line depicting the regression of inbreeding coefficient on birth year

Table 6.2 shows a summary of the total number of animals, the proportion of inbred animals, the annual average and standard deviation (SD) and number of animals with inbreeding above 10% from 1980 to 2004.

Table 6.2 Number of animals (total, inbred) and proportion of inbred animals, the annual average (SD) and number of animals with inbreeding above 10% from 1980 to 2004.

	Animals			Inbreeding		
Year	Total	Inbred	% Inbred	Annual average	Standard deviation	Number above 10%
1980	599	0	0.00	0.0000	0.000	0
1981	792	7	0.88	0.0011	0.000	7
1982	1161	2	0.17	0.0003	0.000	2
1983	1283	8	0.62	0.0004	0.000	1
1984	2041	47	2.30	0.0013	0.000	8
1985	2706	74	2.73	0.0016	0.000	10
1986	4125	153	3.71	0.0014	0.000	16
1987	5328	138	2.59	0.0011	0.000	21
1988	6760	293	4.33	0.0013	0.000	16
1989	8310	426	5.13	0.0025	0.000	70
1990	10167	701	6.89	0.0030	0.000	58
1991	10696	944	8.83	0.0032	0.000	65
1992	14630	1220	8.34	0.0033	0.000	101
1993	16210	1778	10.97	0.0037	0.000	121
1994	16651	1994	11.98	0.0040	0.011	148
1995	20044	2832	14.13	0.0046	0.013	211
1996	20174	3208	15.90	0.0052	0.016	250
1997	21346	3899	18.27	0.0063	0.019	340
1998	21601	4036	18.68	0.0059	0.018	318
1999	22281	5211	23.39	0.0079	0.022	478
2000	23237	5381	23.16	0.0079	0.023	484
2001	22400	5997	26.77	0.0099	0.028	614
2002	22702	7778	34.26	0.0122	0.029	737
2003	20853	7896	37.87	0.0122	0.028	675
2004*	4754	2375	49.96	0.0166	0.031	185

* Incomplete data
F = Inbreeding coefficients; SD = standard deviation

The accumulated average inbreeding for the 24 years from 1980 to 2003 was 1.22%. With an average generation interval of 3.5 years, it was calculated that the period from 1980 to 2003 involved approximately 6.57 generations. Inbreeding therefore seemed to accrue at 0.186% per generation.

According to Figure 6.2, the rate of inbreeding constantly increased from 1980 to 2003 in the Dohne Merino breed. The regression coefficient of the average rate of inbreeding on birth year was derived as 0.00016 ± 0.00003 (R^2=0.73) for 1980 to 1994 and 0.00036 ± 0.00006 (R^2=0.84) for 1995 to 2003. The inbreeding coefficients were very low and did not differ significantly from zero ($P < 0.01$). From about 1994 the increase in inbreeding seemed to accelerate. This appearance might be associated with superior sires being used more widely or possibly because pedigree information was better. The annual average rate of inbreeding was 0.002%. In 2003 the rate of inbreeding was 0.006%. Nicholas (1989) suggested that inbreeding rates of up to 0.5% per year should be acceptable in animal breeding programs. It appears that rates of inbreeding in this breed (0.002% annually) are well below the critical levels cited by the latter author and consideration of additional methods to avoid inbreeding is not necessary at the present time (Figure 6.2).

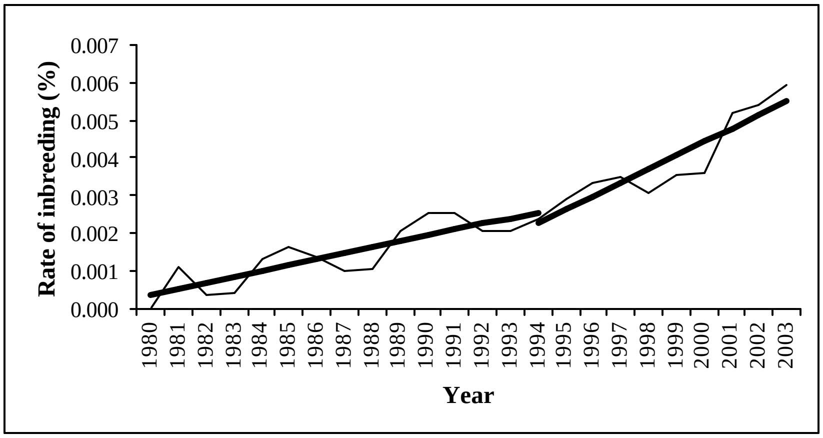

Figure 6.2 Mean rate of inbreeding (? F) within birth year (1980-2003)

According to Table 6.3 there were no significant ($P > 0.05$) effects of inbreeding depression. The high standard errors made any inference on the estimates speculative and would thus not be further discussed.

The values for regression coefficients of BW stated in a review by Lamberson & Thomas (1984) ranged between -0.266 and -0.025. In a study by MacKinnon

(2003), the effects of lamb or dam inbreeding varied for MFD, and none of the regressions were significantly different from zero.

Table 6.3 Regression coefficients (b ± SE) for the different traits on individual inbreeding coefficients of animal and/or dam for a 1% change in inbreeding.

Trait	Animal		Dam	
	b	P	b	P
Body weight	-0.2145 ± 0.5516	0.7204	0.1277 ± 0.8796	0.6258
Clean fleece weight	-0.0673 ± 0.0549	0.2162	0.0906 ± 0.0876	0.3722
Mean fibre diameter	0.0008 ± 0.1233	0.4870	0.0122 ± 0.1966	0.7336

P > 0.05 = non-significant

A review by Lamberson & Thomas (1984) showed little effect of inbreeding on fleece weight, but effects were more prominent in Merino sheep than in other range sheep. According to MacKinnon (2003) it seems that individual inbreeding does not have a large effect on the quality of the fleece, but may slightly decrease fleece weight.

6.4 Conclusions

The average level of inbreeding in the Dohne Merino sheep breed, with data at disposal for this study was low (0.64). The percentage of animals that were inbred to some extent increased to a high (38%) in 2003, while the average level of inbreeding in that year was still very low (1.22%). It appears that rates of inbreeding in the breed (0.002% per year) are well below the critical levels (0.5% per year) and consideration of additional methods to avoid inbreeding is not necessary at the present time. A possible reason for the low levels of inbreeding might be related to the pattern of exchange of breeding material between studs and by introducing commercial F3 animals to studs. Based upon relatively low levels of inbreeding and lack of evidence of significant inbreeding depression in the three traits studied, it is hypothesized that other production and reproduction traits should not be affected deleteriously.

7

General conclusions

The accuracy and validity of results from scientific analyses might often be interpreted in more ways than one. Care should thus be taken in being too assertive when drawing conclusions. Taking this into careful consideration, the following conclusions were made regarding this study:

The observed coefficients of variation were higher than most published values. This may indicate some extra scope for selection, which is a very positive outcome of this study. Alternatively, it could simply be a function of more phenotypic variation, because the animals were maintained on diverse properties and under widely divergent managerial regimes.

Estimates of phenotypic and genetic parameters were refined to facilitate accurate three-trait breeding value predictions of the South African Dohne Merino breed. The significance of the sire-flock-year-season effect for all traits suggests that the inclusion of some form of a genotype by environmental interaction be further investigated for inclusion in national evaluations. Maternal genetic variances declared between 1.0% to 4.2% and 1.6% to 5.8% of the respective overall phenotypic variances for CFW and BW. It could thus be reasoned that it did not declare a sufficient proportion of the overall phenotypic variation to be of value in the practical selection of replacements. Olivier *et al.* (1994) also found that the maternal components could be ignored in selection and genetic studies on Merino sheep.

Heritability estimates for all traits ranged from moderate to high according to the levels set by Turner & Young (1969), and should respond to direct selection.

Estimates of the genetic parameters for CFW, MFD and BW at 12-14 months were generally lower than those obtained in literature. The low genetic correlation between BW and MFD may be an indication that selection on wool quality may be practiced without compromising mutton production traits. The genetic correlations between BW and CFW and between CFW and MFD were positive, but generally lower than published values. Values for the phenotypic correlations are well within the range of previously published estimates.

All traits were favourably affected by current selection procedures, but genetic improvement was comparatively slow to what is attainable in theory. Selection over the years resulted in an improvement of 0.145 kg per annum relative to the overall phenotypic mean for BW. MFD was correspondingly reduced very slowly by -0.011 µm. The emphasis on CFW was much less and genetic progress was accordingly affected. Genetic gains in the desired direction can be markedly accelerated if selection decisions are based on BLUP of breeding values. This statement was confirmed in a study by Olivier *et al.* (1995).

The level of inbreeding in the Dohne Merino population is very low (0.64%), with a relatively high proportion of animals with zero inbreeding (1980 to 2003) (> 80%). The percentage of animals that were inbred to some extent increased to a high (38%) in 2003, while the average level of inbreeding in that year was still very low (1.22%). The average rate of inbreeding for the breed over the 23 years of the study was 0.002% per year, which is well below critical levels. Based upon relatively low levels of inbreeding and lack of evidence of significant inbreeding depression in the three traits studied, it is hypothesized that other production and reproduction traits should not be affected deleteriously. In general the results suggest that inbreeding at present is not a problem in the South African Dohne Merino breed.

In recent years, breeding programs put much emphasis on keeping CFW constant, while reducing MFD. However, more than half of Dohne Merino offspring are slaughtered at weaning age, since income from meat is becoming increasingly important (This statement refers to weaning weight which could not be analysed in this study). It is therefore recommended that the recording of weaning weight should be made compulsory. Further study on the trait and effects is needed.

Abstract

Genetic (co)variances for yearling body weight (BW), clean fleece weight (CFW) and mean fibre diameter (MFD) in the SA Dohne Merino population were estimated using records of 107 389 animals recorded between 1992 and 2004. The data include records of 1 530 sires and 45 178 dams. An animal model with direct and maternal additive, maternal permanent and temporary environmental effects was fitted for all traits. Sire-flock (SF) and sire-flock-year-season (SFYS) was included as additional random effects. Fixed effects were (FYSSM) (1594 classes), type of birth (singles, multiples), age of dam (2 to 7+ years) and average age (± SD) at measurement fitted as a linear covariate (385 ± 12 days). Estimates obtained by single-trait analyses were used as starting values in three-trait analyses.

The direct genetic heritability estimates for FD, CFW and BW obtained from the three-trait analysis were 0.447 (0.009), 0.216 (0.008) and 0.277 (0.008) respectively. The genetic correlations were 0.050 between BW and CFW, 0.100 between BW and FD and 0.139 between FD and CFW. The phenotypic correlations were 0.318 between BW and CFW, 0.129 between BW and FD and 0.180 between FD and CFW. Direct genetic correlations of BW, CFW and MFD were positive, which suggest that selection for bigger and heavier sheep would generally lead to a stronger MFD and higher CFW. Because these values are very low the subsequent effect of this phenomenon would be that the effect of selection for body traits on fleece traits would be very small and *vice versa*.

Genetic trends were calculated using the annual average breeding value estimates (EBV) for each trait. According to the genetic trends derived, the selection policy followed did cause genetic change in the traits studied, even though it was slow.

The level of inbreeding (F) in the South African Dohne Merino sheep population is very low. The proportion of animals that was inbred to some extent increased from 0% (average F=0) in 1980 to 38% in 2003 (average F=1.22%). No significant inbreeding depression on BW, CFW and MFD could be found. In general the results suggest that inbreeding at present is not a serious problem in the South African Dohne Merino breed.

Keywords: Dohne Merino sheep; clean fleece weight; fibre diameter; body weight; genetic parameters; genetic-, phenotypic- and environmental trends; inbreeding

Opsomming

‘n Analise van die Dohne Merino skaapras in Suid Afrika is gedoen. Die data dateer vanaf 1992 tot 2004. Genetiese parameters van onderskeidelik groei- en woleienskappe vir 12 tot 14 maande oue diere is beraam. Veseldikte (VD), skoon vaggewig (SVM) en liggaamsgewig (LM) inligting van 107 389 diere wat 1 530 vaars en 45 178 moers insluit, was beskikbaar vir ontledings. Benewens direkte genetiese-, maternale genetiese- en omgewingseffekte, is vaar-kudde en vaar-kudde-jaar-seisoen effekte as addisionele toevallige effekte ingesluit. Die waardes wat bereken is uit enkel-eienskap analises is gebruik as beginwaardes vir die drie-eienskap analises.

Die beraamde direkte oorerflikhede van die drie-eienskap analises was 0.447 (0.009) vir VD, 0.216 (0.008) vir SVM en 0.277 (0.008) vir LM. Die genetiese korrelasies tussen LM en SVM was 0.050, 0.100 tussen LM en VD en 0.139 tussen VD en SVM. Die fenotipiese korrelasies tussen LM en SVM was 0.318, 0.129 tussen LM en VD en 0.180 VD en SVM. Genetiese korrelasies tussen LM, SVM en VD was positief, wat ‘n aanduiding is dat seleksie vir ‘n groter dier kan lei tot sterker wol en ‘n swaarder vag. Omdat hierdie waardes baie laag is, sal die gevolglike gekorreleerde effek van seleksie vir groei-eienskappe op woleienskappe baie laag wees en *vice versa*.

Genetiese tendense is verkry deur die gemiddelde voorspelde teelwaarde (VTW) per jaar vir elke eienskap te bereken. Uit die genetiese tendense is dit duidelik dat seleksie gebaseer op teeltdoelwitte, daargestel deur die Genootskap, wel genetiese vordering in al drie eienskappe getoon het , alhoewel vordering baie stadig was.

Die vlak van inteling in die Suid Afrikaanse Dohne Merino populasie is tans laag. Produksie en reproduksie vlakke sal dus nie negatief deur inteling beinvloed word nie. Die persentasie diere wat tot ‘n sekere mate ingeteel is, het gestyg van 0%

(gemiddelde F=0%) in 1980 tot 38% (gemiddelde F=1.22%) in 2003. Geen betekenisvolle inteeltverval kon gevind word nie. Die resultate dui daarop dat inteling tans nie ‘n ernstige probleem in die Suid Afrikaanse Dohne Merino skaapras is nie.

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I hereby declare that the dissertation submitted by me in fulfilment of the requirements of a Masters in Agriculture at the University of the Free State, is my own independent work and has not previously been submitted by me at another university or faculty. I furthermore cede copyright of the dissertation to the University of the Free State.

Jan Willem Swanepoel