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# **THE GENETIC BASIS OF GESTATION LENGTH IN BONSMARA CATTLE**

by

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Dissertation submitted to the Faculty of Natural and Agricultural Sciences,

Department of Animal, Wildlife and Grassland Sciences,

University of the Free State,

In partial fulfilment of the requirements for the degree

**MAGISTER SCIENTIAE AGRICULTURAE**

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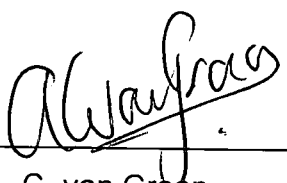
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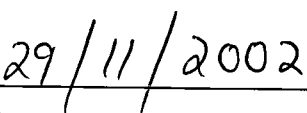
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## Declaration

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## Preface

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# Chapter 1

## General introduction

### 1.1 Introduction

The essence of beef breeding is to produce a constant supply of high quality edible meat for the consumer. In order to achieve this the breeder must produce a calf crop every year. Therefore, the reproduction performance in a herd must be high. Trenkle & Willham (1977) estimated reproduction traits to be economically five times more important than production traits. Age at first estrus, breeding or calving, number of services per conception, service or calving interval, gestation length, calving ease, calving or pregnancy rate and calving date are considered female fertility traits (Meyer *et al.*, 1990). All these traits have an influence on the reproduction of the herd. In this study the genetic basis of gestation length in the Bonsmara breed of South Africa is investigated.

### 1.2 The physiology of gestation length

Frandsen (1981) refers to gestation as the condition of a female while her young are developing within her uterus. Gestation starts at fertilization of the ovum and lasts until the birth of the offspring. Normal gestation lengths vary substantially among farm species (Table 1.1).

Table 1.1 Gestation lengths of different farm species (Frandsen, 1981)

Species	Gestation Length		
	Minimum	Maximum	Mean
Mare	323	341	336
Cow	274	291	282
Ewe	140	160	150
Sow	110	116	114

Many studies have been conducted on the physiology of gestation. Frandson (1981) reports three basic stages of gestation, viz. fertilization, implantation and parturition. Fertilization is when the spermatozoon penetrates the ovum. In the implantation stage the new embryo becomes established at a developmental site on the endometrium in the uterus, where it will then develop and become a foetus. The final stage is parturition, which is the act of giving birth to the young. Gestation length is terminated at parturition. The intriguing question is now, what causes the onset of parturition at the end of gestation? Several factors appear to be involved in the initiation of parturition, particularly changes in hormone levels, as measured in the maternal blood plasma (Frandson, 1981). Frandson (1981) and Van Rensburg (1983) reported that it had long been accepted that the foetus is involved and it could influence the duration of gestation. There is also little doubt that a stage is reached when the nutritional demands of the growing foetus become more than what the placenta can cope with. Frandson (1981) stated that the time of parturition was dependent on the functional activity of the foetus' pituitary and adrenal glands. If the foetus' adrenals are removed (i.e. foetus adrenalectomy) while still in the uterus, gestation is prolonged (Frandson, 1981). This indicates that the foetus' hypothalamus-pituitary-adrenal axis is deeply involved in the termination of gestation.

### **1.3 (Co)variances and literature values**

According to the personal opinion of Dr. K. Anderson of North American Limousin Foundation the primary advantages of a shorter gestation length were:

- 1) Most beef producers in North America (and other extensive beef producing regions) begin their breeding season on a fixed date; the "small " increase in postpartum interval is exactly represented by the difference in gestation length. Genetically, at the extreme, this range is between eight and nine days, as expressed by the full range in

gestation length as expected progeny difference (EPD), but is less for most animals because the standard deviation of gestation length expected progeny difference is about plus or minus one day (i.e. two day range for slightly over 60% of the animals). Thus improved rebreeding performance (Dr. K Anderson – personal communication).

- 2) Because of the genetic correlation between gestation length and birth weight, the longer the gestation the heavier the birth weight. Thus if gestation length is shorter there will be a decrease in birth weight and that is associated with a subtle improvement in caving ease, primarily for first calf heifers (Dr. K. Anderson – personal communication.)
- 3) Although the genetic correlation between gestation length and weaning is essentially zero, earlier born (older) calves weigh more on a fixed weaning date because of being older at weaning (i.e. equal to the preweaning average daily gain of animals times the number of days of age) (Dr K. Anderson – personal communication).

Like all continuously expressed traits, gestation length is under both genetic and environmental control (Reynolds *et al.*, 1990). It has a direct effect on dystocia through its correlation with birth weight. Herring (1996) reported that in Hereford and Angus cows the correlation between gestation length and dystocia were 0.25 and 0.10 respectively. He also reported that as gestation length increased, birth weight increased by 0.30 (0.14kg) to 0.80 (0.36kg) pounds per day of gestation. Reynolds *et al.* (1980) also found in their study that, for each one-day increase in gestation length, birth weight increased by an average of 0.25 to 0.30 kg, depending on the variables in the model. Brinks (1995) reported that birth weight increased by 0.15 kg for each day longer in gestation. However, calves gained 0.97 kg more from birth to weaning and weighed 0.82 kg more in actual weaning weight for each day shorter in gestation, due to being older at weaning.

In the study of Meyer *et al.* (2000) it was found that gestation length in Holsteins ranked third in importance among factors that affect stillbirth rates for all levels of dystocia. Laird & Hunter (1977) suggested that AI organizations survey and publish the mean gestation length of their bulls and that breeders, where necessary, modify their prepartum feeding. Sex and breed of sire had significant effects on gestation length and birth weight (Bech Andersen *et al.*, 1976; Laird & Hunter, 1977; Browning *et al.*, 1995). Foote (1981) also reported that breed of sire affected gestation length significantly. Shorter gestation lengths and lighter birth weights were observed for multiple births in cattle (Davis *et al.*, 1989; Davis & Bishop, 1992).

Gestation length, both treated as a trait of the calf (foetus) and as a trait of the dam, was investigated in the current study. Data was analysed using both univariate and multivariate procedures in order to obtain genetic and phenotypic parameters for gestation length and birth weight. A multivariate evaluation is the methodology of choice to evaluate animals on more than one traits of economic importance, which may be phenotypically and genetically related, since it accounts for the relationships amongst them (Henderson & Quaas, 1976). Multivariate models account simultaneously for the heritabilities and correlations of the two or more traits. It requires the simultaneous estimation of a considerable number of parameters (Meyer, 1994). With the availability of increased computing power, multivariate analyses, using an animal model have become standard practice in the quantitative animal-breeding world.

Literature overview of heritability estimates and mean gestation lengths are presented in Table 1.2.

Table 1.2 Heritability estimates and mean gestation lengths for some cattle breeds

Breed	Number of Animals	Heritability $\pm$ Standard Error	Mean Gestation Length $\pm$ Standard Deviation	Reference	Year
Holstein	1522	0.73	282.3	Fisher & Williams	1978
Cross breed	4639	0.78 $\pm$ 0.003	285.8	Cundiff <i>et al.</i>	1986
Simmental	71461	0.38	284.3 $\pm$ 5.52	Wray <i>et al.</i>	1987
Simmental	4345	0.24	288.1	Kemp <i>et al.</i>	1988
Holstein	52862	0.33	281.3 $\pm$ 6.00	Nadarajah <i>et al.</i>	1989
Beef cross breeds	4322	0.48 $\pm$ 0.07	284.9 $\pm$ 4.0	Baker <i>et al.</i>	1990
Braunvieh	227686	0.46	288.5	Hagger & Hofer	1990
Holstein	55284	0.41	281.9	Hagger & Hofer	1990
Simmental	236692	0.50	286.6	Hagger & Hofer	1990
Ayrshire	5561	0.012	282 $\pm$ 5.0	Moore <i>et al.</i>	1990
Dairy Breeds	1240	0.24 $\pm$ 0.10	262	Simerl <i>et al.</i>	1991
Beef Breeds	7536	0.46 $\pm$ 0.6	288	Gregory <i>et al.</i>	1995,a
Beef Breeds	7767	0.45 $\pm$ 0.6	281	Gregory <i>et al.</i>	1995,b
Beef Breeds	Unknown	0.30	Unknown	Amer <i>et al.</i>	1998
Beef-Dairy Crosses	88135	0.32 $\pm$ 0.03	285 $\pm$ 5.0	McGuirk <i>et al.</i>	1998
Holstein	75685	0.45 $\pm$ 0.02	280.9 $\pm$ 5.0	McGuirk <i>et al.</i>	1999

The objectives of this study were to investigate genetic and phenotypic parameters of gestation length as well as correlations with birth weight. Breeding value predictions, based on mixed model solutions, were also calculated for gestation length and birth weight where after the genetic trend for gestation length and birth weight determined.

## **Chapter 2**

### **Genetic and phenotypic parameter estimates of gestation length and birth weight in Bonsmara cattle treated as traits of the calf**

#### **2.1 Introduction**

The phenotypic and genetic correlations between gestation length and birth weight are well documented in the literature (Burfening *et al.*, 1978; Fisher *et al.*, 1978; Bourdon *et al.*, 1982; Kemp *et al.*, 1988; Haggard *et al.*, 1990; Gregory *et al.*, 1995a and Gregory *et al.*, 1995b). Increased cases of dystocia are usually associated with an increase in gestation length and birth weight (Burfening *et al.*, 1981 and Cundiff *et al.*, 1986). Nadarajah *et al.* (1989) reported that dystocia in cows led to extensive calf losses, production of weak calves and enormous veterinary expenses. The impaired reproductive performance of cows that had calving problems also led to additional economic losses (Price *et al.*, 1978). It is therefore necessary to consider the inclusion of these traits in a selection program. The objectives of this chapter are to investigate the phenotypic and genetic basis of gestation length and birth weight, as well as the relationship between the two traits, both treated as traits of the calf.

#### **2.2 Materials and methods**

##### **2.2.1 Data description**

A total number of 33147 records of the Bonsmara cattle breed in South Africa were available for this study. All measurements were recorded in the National Beef Cattle Improvement Scheme. In order to accurately determine gestation

length, only animals with artificial insemination dates and birth dates were used in the study.

Data was available for the period 1989 to 2000. The observations coded as follows were excluded from the data:

- Animals with calving problems (1.12%)
- Animals with 14 and more offspring (0.04%)
- Multiple births
- Embryo births
- Abortion
- Abortion after seven months
- Still born
- Died after birth
- Destroyed

Further to this the following edits were also preformed: Records had to have a gestation length as well as a birth weight measurement. Duplicate records were also eliminated. Herds with less than 20 records in the data set were also not used in the analysis. All the contemporary groups (made up of herd x year x season) with less than five animals per group were eliminated. After editing, 26962 records remained in the analysis.

The two traits investigated in this study were gestation length and birth weight. Gestation length was calculated as the birth date minus the artificial insemination date. Birth weight was measured within three days of birth. All records outside three standard deviations from the mean were eliminated.

A comparison of the data used in the present study and those for the 2000 International Bonsmara BLUP analysis are presented in Table 2.1. Numbers used in this study only represents 26% of the data due to the low usage of

artificial insemination in the breed. The mean progeny per sire is almost double when artificial insemination is used. It is also clear from the ratio of dams per sire that there were three times more dams per sire in the present study than in the 2000 International Bonsmara BLUP analysis, including that AI-sires are more widely used on the cow population compared to natural service sires.

*Table 2.1 Comparison of data used in this investigation (present study; only A.I.) and the 2000 International Bonsmara BLUP analysis (includes natural mating as well as A.I.)*

	<b>Present study</b>	<b>Bonsmara breed</b>
Number of herds	273	1039
Number of animals	26962	516049
Number of sires	321	10740
Mean progeny per sire	84	48
Number of dams	18185	186491
Mean progeny per dam	2	3
Ratio of dams per sire	1:57	1:17

### **2.2.2 Statistical analysis**

PROC GLM (SAS, 1996) was used to determine the importance of the possible non-genetic sources on the traits under investigation. The following fixed effects were initially included in the model: herd x year x season ("HYS") (1126 levels) which was concatenated from; herd (273 levels), year (12 levels), season (2 levels) and sex. Van der Westhuizen (1997) stated that the fitting of age of dam (in days) as a covariable (linear and/or quadratic) rather than as a fixed effect avoids the danger of arbitrary decisions on age groups and this could be of particular significance in cases where genetic evaluation is based on data collected over divergent managerial systems or different environmental circumstances resulting in differences in mating (due to the particular management practice). The inclusion of age of dam as a covariable seems to be in agreement with researchers in Australia and New Zealand (Swalve, 1993 and



Meyer, 1994). The curvilinear relationship between age of dam and birth weight is the result of cows reaching their peak in mothering ability at an age of between six and ten years of age (Van der Westhuizen, 1997). This is why the linear and quadratic regressions of dam age were also included as covariates.

REML VCE 4.2.5 of Groeneveld (1998) was used for both the univariate and bivariate analyses. In order to determine the model that fitted the data best, a univariate analysis was performed. The inclusion and exclusion of the appropriate random effects in six different models took maternal genetic or permanent environmental (maternal) effects, a combination thereof and the covariance between effects into account as described by Meyer (1992). The most comprehensive alternative model, as described by Meyer (1992), that could be fitted to estimate (co)variance components for gestation length and birth weight can be described as follows in matrix notation:

$$y = Xb + Z_1a + Z_2m + Z_3c + e$$

where

- y = a vector of records for gestation length and birth weight
- X = a known incidence matrix relating observations to fixed effects
- b = a vector of fixed effects consisting of HYS, sex, age of dam (linear regression) and age of dam (quadratic regression)
- Z<sub>n</sub> = known incidence matrices relating observations to random effects
- a = a random vector of the additive genetic effects
- m = a random vector of the maternal genetic effects
- c = a random vector of the permanent maternal environmental effects
- e = a random vector associated with residual error

Only four of the six basic models of Meyer (1992) could be analysed, as the REML VCE 4.2.5 programme of Groeneveld (1998) automatically includes the correlation between the direct and maternal effects. The first model (Model 1) used for the analysis, can be described as a simple animal model with the animals' direct genetic effects as the only random effect, ignoring any maternal influences. Model 2 included permanent maternal environmental effect, fitted as an additional random effect and uncorrelated with all other effects in the model. Model 3 attributed all maternal effects to the genotype of the dam, fitting the maternal genetic effect as a second random effect for each animal with the same relationship structure as the direct additive genetic effects. In this model, direct and maternal effects were correlated. The most comprehensive model (model 4) included both a permanent maternal environmental and a genetic maternal effect and also accounted for the genetic correlation between direct and maternal effects. Model 5 was the same as model 3; the only difference being that a sire x herd interaction was also fitted as an additional random effect in the model. This was done to test for the possibility of heterogeneity of variance over herds.

The decision of what model would describe the data the best can be based on an estimate of the likelihood. The most suited model is determined by comparing the value of the log-likelihood of each model, expressed as a deviation from the model with the highest log-likelihood value. Significance is tested by multiplying the differences by  $-2$  and comparing it to a Chi-squared statistic test with one degree of freedom (Swalve, 1993).

Phenotypic variances were estimated for each trait as follows (Wilham, 1972):

$$\sigma_p^2 = \sigma_a^2 + 1.5\sigma_{am} + 0.5\sigma_m^2 + \sigma_e^2$$

where

$\sigma_p^2$	=	phenotypic variance
$\sigma_a^2$	=	direct additive variance
$\sigma_{am}$	=	covariance between direct and maternal
$\sigma_m^2$	=	maternal variance
$\sigma_e^2$	=	residual variance

"Total heritability" (Meyer, 1992) was also estimated as:

$$h_T^2 = (\sigma_a^2 + 0.5\sigma_m^2 + 1.5\sigma_{am}) / \sigma_p^2$$

where

$h_T^2$	=	total heritability
$\sigma_a^2$	=	direct additive variance
$\sigma_m^2$	=	maternal variance
$\sigma_{am}$	=	covariance between direct and maternal
$\sigma_p^2$	=	phenotypic variance

A bivariate analysis of gestation length and birth weight was performed, using the most suitable model for each trait. Cameron (1993) reported that the genetic variance and covariance estimates using multitrait REML methodology result in unbiased estimates of the genetic correlation, because they allow the fitting of more realistic models.

### 2.2.3 Correlated response

In the National Beef Cattle Improvement Scheme only birth weight is generally recorded and not gestation length. Supposing selection is carried out for lower

birth weight, the improvement in gestation length can be calculated as a correlated response. Correlated response can be calculated as follows:

$$CR_y = i h_x h_y r_g \sigma_{py}$$

where

$i$	=	intensity of selection
$h_x$	=	square root of the heritability of birth weight
$h_y$	=	square root of the heritability of gestation length
$r_g$	=	the genetic correlation between gestation length and birth weight
$\sigma_{py}$	=	the phenotypic standard deviation of gestation length

(Falconer, 1989)

Expected improvement by indirect selection can also be compared with the expected change if selection was carried out directly for gestation length. The comparison is made from the ratio of the two expected responses:

$$\frac{CR_y}{R_y} = \frac{i_x r_g h_x}{i_y h_y}$$

where

$\frac{CR_y}{R_y}$	=	The effectiveness of indirect selection for gestation length by selecting for birth weight. If the same selection intensity is assumed for both gestation length and birth weight the correlated response will be $h_x r_g$ .
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(Falconer, 1989)

## 2.3 Results and discussion

### 2.3.1 General statistics

The effect of calving season on number of calvings is presented in Figure 2.1. There were over a thousand calvings per month, with only January and February having less than a thousand on average. Two seasonal peaks can be observed around May and October, due to different management practices.

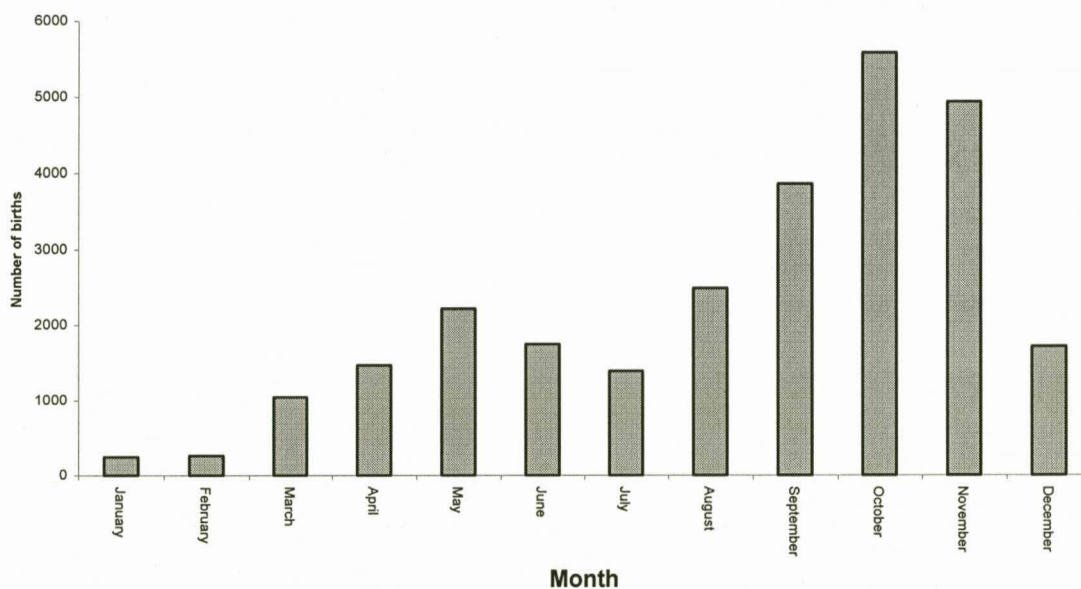


Figure 2.1 Number of calves born per month

Table 2.2 General statistics of gestation length and birth weight and a comparison between the birth weights in the present study and the animals in the 2000 Bonsmara BLUP analysis

Variable	Present study		Bonsmara breed
	Gestation length	Birth weight	Birth weight
Number of animals	26962	26962	516049
Minimum	266	21	15
Maximum	307	51	65
Mean	286.4	35.9	35.6
Variance	42.95	22.97	23.49
Std Dev	6.6	4.8	4.8
Std Error	0.04	0.03	0.01
Coeff of Variation	2.29	13.37	13.61

Table 2.3 The mean and standard deviations of gestation length and birth weight for Bonsmara calves within sex and a comparison between the birth weights in the present study and the animals in the 2000 International Bonsmara BLUP analysis

	Present study		Bonsmara breed
	Gestation length (days)	Birth weight (kg)	Birth weight (kg)
Male	287.0 ± 6.5	36.8 ± 4.7	36.7 ± 4.9
Female	285.7 ± 6.6	34.8 ± 4.6	34.6 ± 4.6

Only herds with animals subjected to artificial insemination were used in the present study for analysis (Table 2.2). This constitutes only 5% of the Bonsmara breed. The mean gestation length is  $286.4 \pm 6.6$  days. This is higher than the value of 282 days reported by Frandson (1981). Only birth weight statistics could be compared between the data of the present study and those of the Bonsmara breed, as gestation length cannot be calculated for the rest of the breed. The

mean, variance, standard deviation, standard error and coefficient of variation of birth weight of this investigation were similar to those of the Bonsmara breed. The minimum birth weight for the present study was 6kg heavier than that of the Bonsmara breed and the maximum was 14kg lighter than that of the Bonsmara breed. Birth weight estimates were also within the same range of literature values (Burfening *et al.*, 1978 for Simmental; Bourdon & Brinks, 1982 for Red Angus, Angus and Hereford; Scholtz *et al.*, 2000 for Bonsmara). Wilson *et al.*, 1976 for Chianina, Fisher & Williams, 1978 for Holstein and Reynolds *et al.*, 1990 for Crossbreeds reported higher values for birth weight, while Reynolds *et al.*, (1980) for Crossbreeds reported lower values. In Table 2.3 the differences between male and female animals is presented for gestation length and birth weight. Male animals had on average a nearly two day longer gestation length and were on average two kilograms heavier than female animals.

Figures 2.2 and 2.3, respectively, present the frequency distribution of gestation length and birth weight of the observations in the present study.

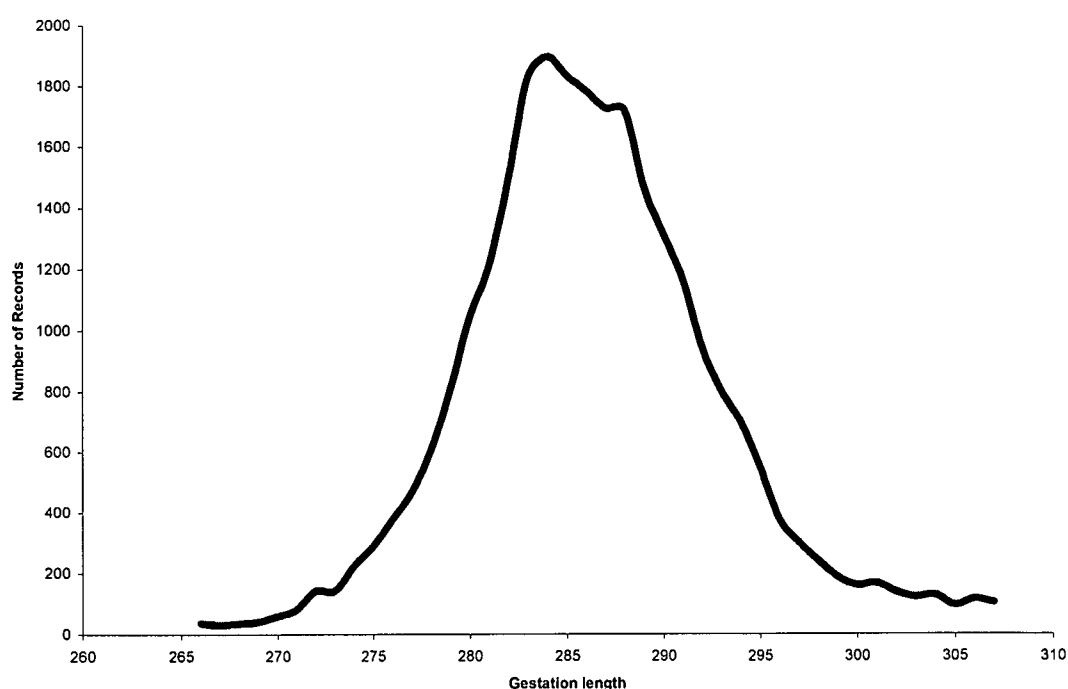


Figure 2.2 Frequency distribution of gestation length

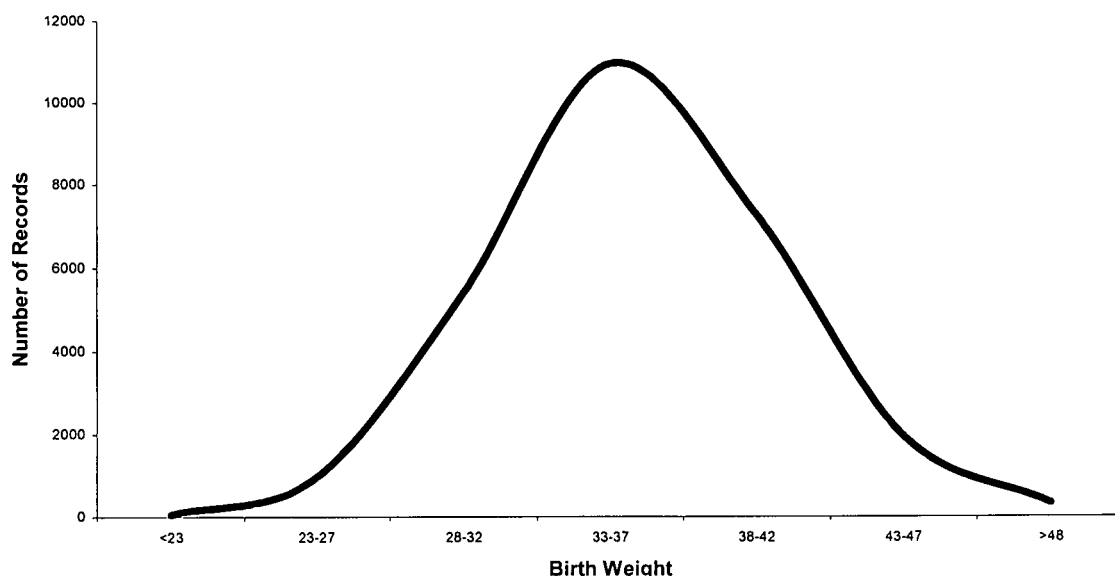


Figure 2.3 Frequency distribution of birth weight

The frequency distributions of gestation length (Figure 2.2) and birth weight (Figure 2.3) are positively skewed to the right with skewness values of 0.34 and 0.12 respectively. Using the Tabachnick & Fidell (1996) test for significance of skewness, it was determined that the data was significantly skewed. Kurtosis characterises the relative peakedness or flatness of the distribution. Kurtosis values of 0.72 and 0.11 were estimated for gestation length and birth weight. The positive values indicate a relatively peaked distribution. Kurtosis was found to be significant (Tabachnick & Fidell, 1996). Although the distribution were skewed and peaked in this study, the data were treated as if it was normally distributed in order to estimate genetic (co)variances.

The phenotypic correlation between gestation length and birth weight was moderate and positive (0.22). This is also in agreement with the studies of Burfening *et al.* (1978) and Kemp *et al.* (1988). The Aberdeen-Angus Cattle Society (Web site, 2002), The British Belgian Blue Cattle Society (Web site,



2002) and The British Limousin Cattle Society (Web site, 2002) also published a phenotypic correlation of 0.24 between the two traits. Fisher & Williams (1978), Bourdon & Brinks (1982), Hagger & Hofer (1990) and Gregory *et al.* (1995) reported higher values than the present study.

Factors influencing gestation length and birth weight are presented in Tables 2.4 and 2.5 respectively. All non-genetic factors included in the model had a highly significant influence on the two traits. Gregory *et al.* (1991) and Newman *et al.* (1993) also reported that the age of the dam influence gestation length significantly.

*Table 2.4 Analysis of variance of gestation length treated as a trait of the calf*

Source	Df	MS	F-Value
HYS	1135	210.1131	6.04***
Sex	1	10584.0692	304.22***
Age of dam (linear)	1	3234.0613	92.96***
Age of dam (quadratic)	1	1842.0672	52.95***
Error	25885	34.791	

Df=degrees of freedom, MS=mean squares, \*\*\*P<0.001, R<sup>2</sup>=0.22, CV=2.0

*Table 2.5 Analysis of variance of birth weight treated as a trait of the calf*

Source	Df	MS	F-Value
HYS	1135	130.4996	8.26***
Sex	1	25883.2191	1639.00***
Age of dam (linear)	1	15620.5527	989.14***
Age of dam (quadratic)	1	11020.9291	697.88***
Error	25885	15.7921	

Df=degrees of freedom, MS=mean squares, \*\*\*P<0.001, R<sup>2</sup>=0.34, CV=11.08

### 2.3.2 (Co)variance components and genetic parameters

#### i) Univariate analysis

##### a) Gestation length

Table 2.6 presents the genetic (co)variance estimates for gestation length, for the five different models used in this study. The direct heritability estimates vary between 0.45 and 0.30, while the maternal heritability estimates vary between 0.09 and 0.06. Model 3 (direct heritability of 0.39 and a maternal heritability of 0.09) was the most suited model, because it had the highest log-likelihood value and it differs significantly from the other models (Swalve, 1993). A negative genetic correlation of  $-0.25$  was also estimated between the genetic effects. This is in agreement with a correlation of  $-0.27$  obtained by Nadarajah *et al.* (1989), while Doyle *et al.* (1995) reported a higher negative genetic correlation of  $-0.40$ . All the correlations between the direct and maternal effects were negative. Other researchers that reported heritabilities (direct) in the same range as the present study were Wray *et al.* (1986), Azzam *et al.* (1987), Wray *et al.* (1987), Nadarajah *et al.* (1989) and Cundiff *et al.* (1998). Higher heritabilities (direct) that vary between 0.48 and 0.73 were reported by Burfening *et al.* (1978), Fisher & Williams (1978), Barlow & O'Neill (1980), MacNeil *et al.* (1984) and Doyle *et al.* (1995). Lower heritabilities that vary from 0.11 to 0.25 were reported by Laird & Hunter (1977), Kemp *et al.* (1988), Moore *et al.* (1990), Simerl *et al.* (1991) and Silva *et al.* (1992).

Sire x herd interaction was only tested with the model (Model 3), which fitted the data best. The log-likelihood of the model (Model 5), where by the sire x herd interaction was included, was significantly worse than Model 3 ( $P < 0.01$ ).

Table 2.6 Estimates of (co)variance components and genetic parameters for gestation length treated as a trait of the calf

Parameter	Model 1	Model 2	Model 3	Model 4	Model 5
$\sigma_a^2$	16.882	14.669	14.265	14.474	10.995
$\sigma_m^2$			3.196	2.593	2.308
$\sigma_{am}$			-1.700	-1.759	-0.120
$\sigma_c^2$		1.562		0.859	
$\sigma_e^2$	20.716	20.791	21.255	20.820	22.521
$\sigma_p^2$	37.598	35.460	34.568	33.952	34.490
$h^2$	0.449± 0.016	0.396± 0.018	0.385	0.391	0.299
$m^2$			0.086	0.070	0.063
$r_{am}$			-0.252	-0.287	-0.024
$c^2$		0.042± 0.008		0.023	
$h^2_T$	0.447	0.414	0.385	0.387	0.347
Log-L	73617.489	73600.738	125135.534	125132.221	125064.063
$\Delta$ Log-L	-51518.045**	-51534.796**	0	-3.313**	-71.471**
$\sigma^2(s_h)$					1.120
$c^2(s_h)$					0.030

$\sigma_a^2$  = direct additive genetic variance;  $\sigma_m^2$  = maternal additive genetic variance;  $\sigma_{am}$  = direct-maternal genetic covariance;  $\sigma_c^2$  = maternal environmental variance;  $\sigma_e^2$  = error variance;  $\sigma_p^2$  = phenotypic variance;  $h^2$  = direct heritability;  $m^2$  = maternal heritability;  $r_{am}$  = direct-maternal genetic correlation;  $c^2$  = permanent environmental effect;  $h^2_T$  = total heritability; Log-L = log-likelihood;  $\Delta$  Log-L = log-likelihood expressed as deviation from the model with the highest value;  $\sigma^2(s_h)$  = sire x herd interaction variance;  $c^2(s_h)$  = sire x herd variance as a proportion of total variance; \*\* = significantly different from 0 ( $P < 0.01$ ).

## b) Birth weight

Table 2.7 presents the genetic (co)variance estimates and parameters for birth weight. The direct heritabilities vary between 0.46 and 0.24, while the maternal heritabilities vary between 0.11 and 0.10. The log-likelihood values clearly demonstrate that Model 3 was the most suited model, because it had the highest value and it differs significantly from the other models (Swalve, 1993). A direct heritability of 0.24 and a maternal heritability 0.11 were obtained. This is in agreement with literature values obtained by Meyer (1992) for birth weight. Literature estimations vary considerably. A lower direct heritability of 0.19 was estimated by Kemp *et al.* (1988), while Simerl *et al.* (1991), Johnson *et al.* (1992), Meyer *et al.* (1993), Waldron *et al.* (1993) and Cundiff *et al.* (1998) reported higher values that vary between 0.30 and 0.58. Meyer *et al.* (1993) estimated maternal heritabilities for birth weight in Herefords of 0.22 and in Wokalups of 0.08, while Waldron *et al.* (1993) reported a maternal heritability of 0.07. The genetic correlation obtained in this study between the direct and maternal heritability for birth weight was low and negative (-0.06). A positive genetic correlation in Herefords (0.06) and Wokalups (0.14) were reported by Meyer *et al.* (1993), while Johnson *et al.* (1992) reported negative values (-0.12 and -0.13).

The log-likelihood value obtained for sire x herd interaction (Model 5) in this study was significantly worse than Model 3 ( $P < 0.01$ ).

Table 2.7 Estimates of (co)variance components and genetic parameters for birth weight treated as a trait of the calf

Parameter	Model 1	Model 2	Model 3	Model 4	Model 5	Bonsmara breed
$\sigma_a^2$	8.136	6.275	3.891	3.952	3.058	4.72
$\sigma_m^2$			1.820	1.570	1.699	1.46
$\sigma_{am}$			-0.155	-0.184	0.171	-0.280
$\sigma_c^2$		0.990		0.334		
$\sigma_e^2$	9.388	9.742	10.987	10.846	11.231	8.760
$\sigma_p^2$	17.524	16.017	14.878	16.877	14.882	
$h^2$	0.464± 0.015	0.369± 0.005	0.235	0.239	0.185	0.310
$m^2$			0.110	0.095	0.103	0.090
$r_{am}$			-0.058	-0.074	0.075	
$c^2$		0.058±0.005		0.020		
$h^2_T$	0.464	0.392	0.307	0.264	0.245	
Log-L	69917.835	69881.299	121376.815	121373.989	121323.899	
$\Delta$ Log-L	-51458.980**	-51495.516**	0	-2.826	-50.090**	
$\sigma^2(s_h)$					0.396	
$c^2(s_h)$					0.024	

$\sigma_a^2$  = direct additive genetic variance;  $\sigma_m^2$  = maternal additive genetic variance;  $\sigma_{am}$  = direct-maternal genetic covariance;  $\sigma_c^2$  = maternal environmental variance;  $\sigma_e^2$  = error variance;  $\sigma_p^2$  = phenotypic variance;  $h^2$  = direct heritability;  $m^2$  = maternal heritability;  $r_{am}$  = direct-maternal genetic correlation;  $c^2$  = permanent environmental effect;  $h^2_T$  = total heritability; Log-L = log-likelihood;  $\Delta$  Log-L = log-likelihood expressed as deviation from the model with the highest value;  $\sigma^2(s_h)$  = sire x herd interaction variance;  $c^2(s_h)$  = sire x herd variance as a proportion of total variance; Bonsmara breed = (co)variance and genetic parameters of the 2000 International Bonsmara BLUP analysis; \*\* = significantly different from 0 ( $P < 0.01$ ).

## ii) Bivariate analysis

Model 3 was used in the bivariate analyses of both gestation length and birth weight. The (co)variances for gestation length and birth weight were estimated and are presented in Table 2.8.

Table 2.8 (Co)variance matrices of gestation length and birth weight treated as traits of the calf. Variances are depicted on the diagonal and covariances above the diagonal

Residual Variance		
	Gestation length	Birth weight
Gestation length	21.329	1.951
Birth weight		11.011

		Maternal		Direct	
		Gestation length	Birth weight	Gestation length	Birth weight
Maternal	Gestation length	3.152	1.389	-1.697	-0.548
	Birth weight		1.882	-1.348	-0.204
Direct	Gestation length			14.199	2.962
	Birth weight				3.842

The variances of the univariate analyses of gestation length and birth weight (Table 2.6 and 2.7) corresponded well with those of the bivariate analysis (Table 2.8). The direct-maternal covariances of gestation length and birth weight are negative and are in the same order for both the univariate (Table 2.6 and 2.7)

and bivariate (Table 2.8) analyses. Bennett & Gregory (2001) reported a direct variance value of 16.16, which is fractionally higher than in this study (14.20) for gestation length. The (co)variances were used to estimate the heritabilities as well as the genetic correlations between gestation length and birth weight (Table 2.9).

*Table 2.9 Corresponding ratios for gestation length and birth weight treated as traits of the calf. Heritabilities are depicted on the diagonal and genetic correlations above the diagonal*

		Maternal		Direct	
		Gestation length	Birth weight	Gestation length	Birth weight
Maternal	Gestation length	0.085	0.570	-0.254	-0.157
	Birth weight		0.114	-0.261	-0.076
Direct	Gestation length			0.384	0.401
	Birth weight				0.232

The maternal genetic correlation (0.57) and direct genetic correlation (0.40) between gestation length and birth weight (Table 2.9) were the only positive correlations. These values were higher than those of Gregory *et al.* (1995a), Gregory *et al.* (1995b) and Bennett & Gregory (2001). Hagger & Hofer (1990), The Aberdeen Angus Cattle Society (Web site, 2002), The British Belgian Blue Cattle Society (Web site, 2002) and The British Limousin Cattle Society (Web site, 2002) all reported higher genetic correlations than in the present study. The estimated direct heritability of 0.38 for gestation length was higher than the values ranking between 0.01 and 0.32 reported by Moore *et al.* (1990), McGuirk *et al.* (1998), The Aberdeen Angus Cattle Society (Web site, 2002), The British Belgian Blue Cattle Society (Web site, 2002) and The British Limousin Cattle Society (Web site, 2002). Baker *et al.* (1990), Hagger & Hofer (1990), Gregory *et al.* (1995a), Gregory *et al.* (1995b), McGuirk *et al.* (1999) and Bennett & Gregory

(2001) reported higher direct heritabilities (0.41 to 0.59) for gestation length than in the present study.

The direct and maternal heritabilities for birth weight were estimated as 0.23 and 0.11 respectively. The weighted mean values for heritability estimates (Koots *et al.*, 1994) are different for direct (0.31) and in agreement for maternal (0.14) when compared to the present study. Estimated values for heritability of birth weight in this study are in the same range as those summarised by Mohiuddin (1993). Maternal heritability is also in agreement with Meyer (1994) and Van der Westhuizen (1997). A higher maternal heritability of 0.19 was reported by Meyer (1993). The direct heritabilities of 0.58, 0.34 and 0.38 of Meyer (1993), Meyer (1994) and Van der Westhuizen (1997) were also higher than in the present study. The correlation between the maternal and direct heritabilities (-0.08) was negative and low. This is in contrast with the values of -0.57 and 0.33 obtained by Meyer (1993) and Meyer (1994).

### **2.3.3 Correlated response**

The improvement of performance in a trait, other than the one in which selection was carried out, can be predicted by using the heritability of each trait and the genetic correlation between the two traits (Falconer, 1989). Gestation length is seldom recorded in the South African National Beef Cattle Improvement Scheme, however birth weight is. Through the correlated response of indirect selection for gestation length on birth weight, the effectiveness of change of gestation length could be determined by this means:



$$\begin{aligned}
\frac{CR_y}{R_y} &= \frac{i_x r_g h_x}{i_y h_y} \\
&= \frac{(0.401) (\sqrt{0.232})}{(\sqrt{0.384})} \\
&= 0.312
\end{aligned}$$

The same selection intensity for both gestation length ( $i_y$ ) and birth weight ( $i_x$ ) was assumed. If the correlated response on gestation length was larger than the direct selection on birth weight, which is not the case in the present study, it would be better to select indirectly for gestation length through the direct selection on birth weight. The effectiveness of indirect selection is 31%, compared to selection directly on gestation length.

## 2.4 Conclusion

The heritabilities of the bivariate analysis indicate that gestation length is highly heritable. The direct heritability of 0.38 suggests that it is mostly the direct genetic effect of the calf that is the primary influence on the length of gestation. In contrast with the direct heritability, the maternal heritability was lower at (0.09). The inclusion of sire x herd interaction was non-significant and was therefore ignored in the bivariate analysis. The direct heritability (0.24) for birth weight was also higher than the maternal heritability (0.10). This is also an indication that birth weight is more under the influence of the direct genetic effects of the calf, although there is a sizeable maternal effect as well. The estimated genetic correlations indicate that indirect selection for shorter gestation length is possible by selecting against higher birth weight. The effectiveness is, however, only 0.31.

## Chapter 3

# Genetic and phenotypic parameter estimates of gestation length and birth weight in Bonsmara cattle treated as traits of the dam

### 3.1 Introduction

Beef producers need to take informed culling, mating and management decisions in order to make a profit (Robinson *et al.*, 1989). One area affected by these decisions is the fertility in the herd. Gestation length may be one of the fertility traits that has some potential for selection (Nadarajah *et al.*, 1989). Wray *et al.* (1987) stated that some breeders might select directly to reduce gestation length in order to lengthen the postpartum interval to the breeding season, thus allowing the dam more time to return to oestrus and increase the likelihood of becoming pregnant. Sagebiel *et al.* (1973) reported that maternal effects on gestation length were found to be significant. This indicates that the foetus is not always responsible for the variation of gestation length. The objectives of this chapter were to determine the (co)variance components and the genetic parameters of gestation length and birth weight as well as the relationship between them both, if treated as traits of the dam.

### 3.2 Materials and methods

#### 3.2.1 Data description

The same data sets, as described in Chapter 2 were used for this study. In Table 3.1 the number of calves per dam is presented. A total of 13054 dams had only calved once. This was nearly 50% of the whole data set. There was only one dam that had ten calves.

Table 3.1 Number of calvings per dam in the present study

Number of calves	Number of dams
1	13054
2	3069
3	1146
4	530
5	213
6	96
7	53
8	17
9	6
10	1

### 3.2.2 Statistical analysis

The following repeatability model was fitted for both gestation length and birth weight (Mrode, 1996):

$$y = Xb + Za + Wpe + e$$

where

- y = vector of observations for the  $i$ -th trait which are gestation length or birth weight.
- b = vector of fixed effects for the  $i$ -th trait which includes sex, HYS and age of dam (linear and quadratic)
- a = vector of random animal effects for the  $i$ -th trait, which includes "AI-sire"
- pe = vector of random permanent environmental effects and non-additive genetic effects for the  $i$ -th trait
- e = vector of random residual effect for the  $i$ -th trait

X, Z and W were incidence matrices relating records for the  $i$ -th trait of the fixed animal, random animal and permanent environmental effects respectively.

The four models used in Chapter 2, as described by Meyer (1992), were also used for the univariate and bivariate analyses of gestation length and birth weight. "AI-sire" was included in the models as a random effect to test for its significance. An additional model (Model 5), the same as Model 3, was also fitted with the only difference being that a sire x herd interaction, fitted as a random effect, was included. This was done to test for the possibility of heterogeneity of variance over herds.

Log-likelihood tests were carried out to determine the most suitable model to analyse the data. The same models that were used to analyse gestation length were used to analyse birth weight. The only differences in the models were the sources of non-genetic variation (See Table 3.2 and Table 3.3).

### **3.2.3 Correlated response**

Expected correlated genetic superiority in gestation length, when selection is on birth weight, depends on the genetic correlation between the two traits and their heritabilities (Van Vleck *et al.*, 1987). Thus, the relative selection progress for gestation length by selection for birth weight is compared by the ratio of the two expected responses. Using the heritabilities and genetic correlation estimated when the traits were treated as traits of the dam, the same estimations were done as in Chapter 2.

### 3.3 Results and discussion

#### 3.3.1 General statistics

Table 3.2 Analysis of variance of gestation length treated as a trait of the dam

Source	Df	MS	F-Value
Sex	1	2824.0389	90.89***
HYS	1101	147.1021	4.73***
AI- sire	306	165.7239	5.33***
Birth weight	1	31906.1871	1026.91***
Age of dam (linear)	1	628.5569	20.23***
Error	22344	31.070	

Df=degrees of freedom, MS=mean squares, \*\*\*P<0.001, R<sup>2</sup>=0.32, CV=1.94

Table 3.3 Analysis of variance of birth weight treated as trait of the dam

Source	Df	MS	F-Value
Sex	1	17838.00179	1230.46***
HYS	1101	83.32782	5.75***
AI-sire	306	41.66255	2.87***
Gestation length	1	14378.79143	991.84***
Age of dam (linear)	1	9478.69012	653.84***
Age of dam (quadratic)	1	6836.18314	471.56***
Error	22343	14.4970	

Df=degrees of freedom, MS=mean squares, \*\*\*P<0.001, R<sup>2</sup>=0.40, CV=10.64

The effects of sex of calf and "HYS" were significant sources of variation (P<0.001) in gestation length and birth weight. Age of dam (linear) was only significant for gestation length. Both age of dam (linear) and age of dam (quadratic) were found to be significant sources of variation in birth weight. Gregory *et al.* (1991) and Newman *et al.* (1993) also reported that age of dam

significantly affected gestation length. "AI-sire" was also a significant source of variation ( $P < 0.001$ ).

### 3.3.2 (Co)variance components and genetic parameters

#### (i) Univariate analysis

Estimation of (co)variance components and genetic parameters for gestation length and birth weight, together with the log-likelihood values for each analysis, are presented in Table 3.4 and 3.5. In the univariate analysis for gestation length (Table 3.4), Model 3 was the most suited model, because it had the highest log-likelihood value, but there was no significant difference between Model 3 and Model 4 (Swalve, 1993). In such a case the simplest model, Model 3 was used. The direct heritability was 0.14 and maternal heritability was 0.02. The maternal heritability was very low. Burfening *et al.*, 1981; Bourdon & Brinks, 1982 and MacNeil *et al.*, 1984 all reported higher direct heritabilities for gestation length. Maternal heritability in this investigation was also lower than the value of 0.09 of Burfening *et al.* (1981). The correlation between the direct and maternal effects was low and negative. Burfening *et al.* (1981) reported a higher value of  $-0.38$  for the genetic correlation between direct and maternal.

As described in section 3.2.2 a sire x herd interaction was also investigated. The log-likelihood value obtained through this analysis is significantly worse than those in Model 3 ( $P < 0.01$ ). This implies that sire x herd interaction had no significant effect on the analysis.

The effect of "AI-sire" was fitted as a random effect in all the models, as described in section 3.2.2. The  $c^2_{\text{AI-sire}}$  - value (0.09) for "AI-sire" obtained through this analysis was small, but it was higher than the maternal heritability of 0.02 (Model 3).

### a) Gestation length

Table 3.4 Estimates of (co)variance components and genetic parameters for gestation length treated as a trait of the dam

Parameter	Model 1	Model 2	Model 3	Model 4	Model 5
$\sigma_a^2$	4.878	4.412	4.759	4.713	4.687
$\sigma_m^2$			0.737	0.704	0.700
$\sigma_{am}$			-0.539	-0.526	-0.510
$\sigma_c^2$		0.459		0.075	
$\sigma_e^2$	26.852	26.717	26.659	26.643	23.375
$\sigma_p^2$	31.639	31.129	30.978	30.919	27.647
$h^2$	0.137±0.007	0.127±0.009	0.137	0.135	0.135
$m^2$			0.021	0.020	0.020
$r_{am}$			-0.288	-0.289	-0.282
$c^2$		0.013±0.007		0.002	
$h^2_T$	0.1513	0.1417	0.1394	0.1383	0.1545
Log-L	40591.725	40589.799	62829.823	62829.784	62791.033
$\Delta$ Log-L	-22238.098**	-22240.024**	0	-0.039	-38.790**
$\sigma^2(s_h)$					0.909
$c^2(s_h)$					0.026
$\sigma^2_{(AI-sire)}$	3.201	3.203	3.194	3.194	2.575
$c^2_{(AI-sire)}$	0.092±0.008	0.092±0.008	0.092	0.092	0.074

$\sigma_a^2$  = direct additive genetic variance;  $\sigma_m^2$  = maternal additive genetic variance;  $\sigma_{am}$  = direct-maternal genetic covariance;  $\sigma_c^2$  = maternal environmental variance;  $\sigma_e^2$  = error variance;  $\sigma_p^2$  = phenotypic variance;  $h^2$  = direct heritability;  $m^2$  = maternal heritability;  $r_{am}$  = direct-maternal genetic correlation;  $c^2$  = permanent environmental effect;  $h^2_T$  = total heritability; Log-L = log-likelihood;  $\Delta$  Log-L = log-likelihood expressed as deviation from the model with the highest value;  $\sigma^2(s_h)$  = sire x herd interaction variance;  $c^2(s_h)$  = sire x herd variance as a proportion of total variance;  $\sigma^2_{AI-sire}$  = variance due to the AI-sire;  $c^2_{AI-sire}$  = AI-sire variance as a proportion of total variance; \*\* = significantly different from 0 ( $P < 0.01$ ).

## b) Birth weight

Table 3.5 Estimates of (co)variance components and genetic parameters for birth weight treated as a trait of the dam

Parameter	Model 1	Model 2	Model 3	Model 4	Model 5	Bonsmara breed
$\sigma_a^2$	2.541	2.423	2.325	2.282	2.320	4.72
$\sigma_m^2$			0.099	0.077	0.102	1.46
$\sigma_{am}$			0.088	0.088	0.089	-0.280
$\sigma_c^2$		0.129		0.072		
$\sigma_e^2$	12.206	12.177	12.220	12.203	12.065	8.760
$\sigma_p^2$	14.747	14.600	14.727	14.656	14.569	
$h^2$	0.165±0.007	0.157±0.009	0.151	0.148	0.150	0.310
$m^2$			0.006	0.005	0.007	0.090
$r_{am}$			0.183	0.211	0.182	
$c^2$		0.008±0.007		0.005		
$h^2_T$	0.172	0.166	0.170	0.167	0.172	
Log-L	37464.830	37464.040	59710.672	59710.455	59669.582	
$\Delta$ Log-L	-22245.842**	-22246.632**	0	-0.217	-41.090**	
$\sigma^2(s_h)$					0.378	
$c^2(s_h)$					0.024	
$\sigma^2_{(AI-sire)}$	0.675	0.675	0.677	0.676	0.503	
$c^2_{(AI-sire)}$	0.044±0.005	0.044±0.005	0.044	0.044	0.033	

$\sigma_a^2$  = direct additive genetic variance;  $\sigma_m^2$  = maternal additive genetic variance;  $\sigma_{am}$  = direct-maternal genetic covariance;  $\sigma_c^2$  = maternal environmental variance;  $\sigma_e^2$  = error variance;  $\sigma_p^2$  = phenotypic variance;  $h^2$  = direct heritability;  $m^2$  = maternal heritability;  $r_{am}$  = direct-maternal genetic correlation;  $c^2$  = permanent environmental effect;  $h^2_T$  = total heritability; Log-L = log-likelihood;  $\Delta$  Log-L = log-likelihood expressed as deviation from the model with the highest value;  $\sigma^2(s_h)$  = sire x herd interaction variance;  $c^2(s_h)$  = sire x herd variance as a proportion of total variance;  $\sigma^2_{AI-sire}$  = variance due to the AI-sire;  $c^2_{AI-sire}$  = AI-sire variance as a proportion of total variance; Bonsmara breed = (co)variance and genetic parameters of the 2000 International BLUP analysis; \*\* = significantly different from 0 ( $P < 0.01$ ).



As with gestation length, Model 3 fitted the data best for the analysis of birth weight as demonstrated by the log-likelihood value (Swalve, 1993). The direct heritability was 0.15 and the maternal heritability was 0.01. The direct heritability obtained in this study was lower than that obtained by Burfening *et al.* (1981), Bourdon & Brinks (1982) and MacNeil *et al.* (1984). Burfening *et al.* (1981) reported a maternal heritability of 0.10, which was much higher than that obtained in the present study. All the correlations, including the correlation between direct and maternal, were positive. This was in contrast with the analysis of gestation length. A negative genetic correlation between direct and maternal for birth weight of -0.24 was also reported by Burfening *et al.* (1981).

The value of the log-likelihood of Model 5, which includes the sire x herd interaction, was worse than those of Model 3 ( $P < 0.01$ ). This implies no specific interaction for sire x herd in this dataset.

"AI-sire" was fitted as a random effect in all the models as described in section 3.2.2. The  $c^2_{\text{AI-sire}}$  value for "AI-sire" (0.04) was small but it was higher than the maternal heritability of 0.01 (Model 3).

## **(ii) Bivariate analysis**

The results of the bivariate analysis are presented in Table 3.6 and 3.7. In the bivariate analysis "AI-sire" was included as a random effect.

Table 3.6 (Co)variance matrices of gestation length and birth weight treated as traits of the dam. Variances are depicted on the diagonal and covariances above the diagonal.

Residual Variance		
	Gestation length	Birth weight
Gestation length	27.624	3.409
Birth weight		12.647

		Maternal		Direct	
		Gestation length	Birth weight	Gestation length	Birth weight
Maternal	Gestation length	0.628	-0.142	-0.549	-0.092
	Birth weight		0.046	-0.083	0.067
Direct	Gestation length			5.417	1.562
	Birth weight				2.644

AI-sire		
	Gestation length	Birth weight
Gestation length	3.568	0.711
Birth weight		0.807

From Table 3.6 it is clear that the variances were lower than when the traits were treated as traits of the calf (Table 2.8). All the variances corresponded well between the univariate (Table 3.4 and 3.5) and bivariate (Table 3.6) analyses of gestation length and birth weight. The covariances for gestation

length and birth weight were in the same order for both the univariate analysis (Table 3.4 and 3.5) and bivariate analysis (Table 3.6).

*Table 3.7 Corresponding ratios of gestation length and birth weight treated as traits of the dam. Heritabilities are depicted on the diagonal and genetic correlations above the diagonal*

		Maternal		Direct	
		Gestation length	Birth weight	Gestation length	Birth weight
Maternal	Gestation length	0.017	-0.832	-0.298	-0.071
	Birth weight		0.003	-0.166	0.192
Direct	Gestation length			0.148	0.413
	Birth weight				0.163

AI-sire		
	Gestation length	Birth weight
Gestation length	0.097	0.419
Birth weight		0.050

The positive genetic correlation between direct and maternal for birth weight (0.19) is in contrast with that in Chapter 2, which was low and negative (-0.08). The genetic correlation between direct and maternal for gestation length was negative and higher (-0.30) than the results from the analysis done in Chapter 2 of -0.25 (Table 2.9). The direct genetic correlation (0.41) between gestation length and birth weight, and the correlation between birth weight direct and birth weight maternal (0.19), were the only positive correlations (Table 3.7). The direct genetic correlation between gestation length and birth weight of 0.41, when treated as a trait of the dam, was largely the same as the correlation of 0.40 when it was treated as a trait of the calf. Maternal heritabilities for gestation length (0.02) and birth weight (0.003) were very low to negligible. The direct heritabilities of 0.15 and 0.16 for gestation

length and birth weight were also lower than those when treated as traits of the calf. Robinson (1996) reported that the additional information from using two traits was again thought to have resulted in improved estimates, given the relatively high estimates of correlations between parameters for each trait. In this investigation it was not the case.

### 3.3.3 Correlated response

The improvement of performance in a trait other than the one in which selection was carried out can be predicted using the heritability of each trait and the genetic correlation between the two traits (Falconer, 1989). Gestation length is not generally recorded in the South African National Beef Cattle Improvement Scheme, but birth weight is. Using the correlated response of indirect selection for gestation length on birth weight it is possible to see how much improvement of gestation length by this means has been effected.

$$\begin{aligned}\frac{CR_y}{R_y} &= \frac{i_x r_g h_x}{i_y h_y} \\ &= \frac{(0.413) (\sqrt{0.163})}{(\sqrt{0.148})} \\ &= 0.433\end{aligned}$$

The same selection intensity in both gestation length ( $i_y$ ) and birth weight ( $i_x$ ) is assumed. The values are in the same range as those estimated when the traits were treated as traits of the calf.

### 3.4 Conclusion

In this investigation all the heritabilities were smaller than those in Chapter 2. The direct heritabilities for gestation length and birth weight were 0.15 and 0.16 respectively. The maternal heritabilities were 0.02 and 0.003 for gestation length and birth weight. The maternal heritabilities were low to negligible. This is also an indication that the direct genetic effect controls gestation length genetically. Thus the traits must be analysed as traits of the calf and not of the dam. The genetic correlation between gestation length and birth weight was positive (0.41). This is very favourable, as selection against birth weight (higher) will also result in a shorter gestation length. But it is better to select direct for gestation length because the correlated response on indirect selection is 0.43. Therefore 57% less progress will be made per generation interval, than with the use of direct selection for gestation length.

## **Chapter 4**

### **Estimated breeding values and genetic trends for gestation length and birth weight in Bonsmara cattle**

#### **4.1 Introduction**

The true genetic value of an animal is never known; therefore breeding values are predicted (Henderson, 1975). The purpose of predicting an animal's breeding value (EBVs) is to identify genetically superior animals. The estimated breeding values can be used to make breeding decisions in beef breeders' selection programmes. Estimated breeding values are more accurate than the indices (ratios) that are currently being used in the National Beef Cattle Improvement Scheme. The breeding value is predicted from an analysis of all the information that is available on the animal, both its individual performance and that of its relatives. The genetic trend depicts the genetic change of the breed over the birth years. The aim of this study was to predict the breeding values (EBVs) for gestation length and birth weight using mixed model methodology and subsequently describe the genetic trends for these traits.

#### **4.2 Materials and methods**

##### **4.2.1 Data description**

A sub set off data from the Bonsmara breed was used to predict breeding values (EBVs) and genetic trends for gestation length and birth weight. A total of 26962 records that had been collected between 1989 and 2000 were available for the predictions and are described in Chapter 2.

### **4.2.2 Statistical analysis**

The breeding value predictions and genetic trends for gestation length and birth weight were calculated using the variance and covariance components presented in Chapter 2. The year 1990 was fitted as the base year, meaning the average EBV for gestation length and birth weight for animals born in 1990 were set to zero. Accuracies were also determined based on the method of Meyer (1989) for obtaining approximate reliabilities. The reliability for each animal is derived from the corresponding diagonal element in the mixed model equations (MME), adjusting for selected off-diagonal coefficients.

## **4.3 Results and discussion**

### **4.3.1 Estimated breeding values**

#### **(i) Gestation length**

Direct and maternal breeding values for gestation length (in days) were predicted. The frequency distributions of the direct and maternal breeding values are presented in Figure 4.1 and 4.2.

The frequency distribution of the direct breeding values for gestation length was negatively skewed to the left as the estimated skewness value of  $-0.32$  indicates. The test of Tabachnick & Fidell (1996) showed that the skewness was significant. A kurtosis value of  $0.40$  indicated that the distribution was also significantly peaked as estimated through the test for significance of Tabachnick & Fidell (1996). These values can range between  $10$  and  $-10$ . The frequency distribution of the maternal breeding values were not evenly or normally distributed and covered a range from  $-2$  to  $2.5$  with a significantly positive skewness to the right ( $0.29$ ) and was flat ( $-0.24$ ). Some individual EBVs are presented in Appendix A (artificial insemination bulls) and Appendix B (selected animals). In both lists the highest and lowest EBVs are listed for each trait.

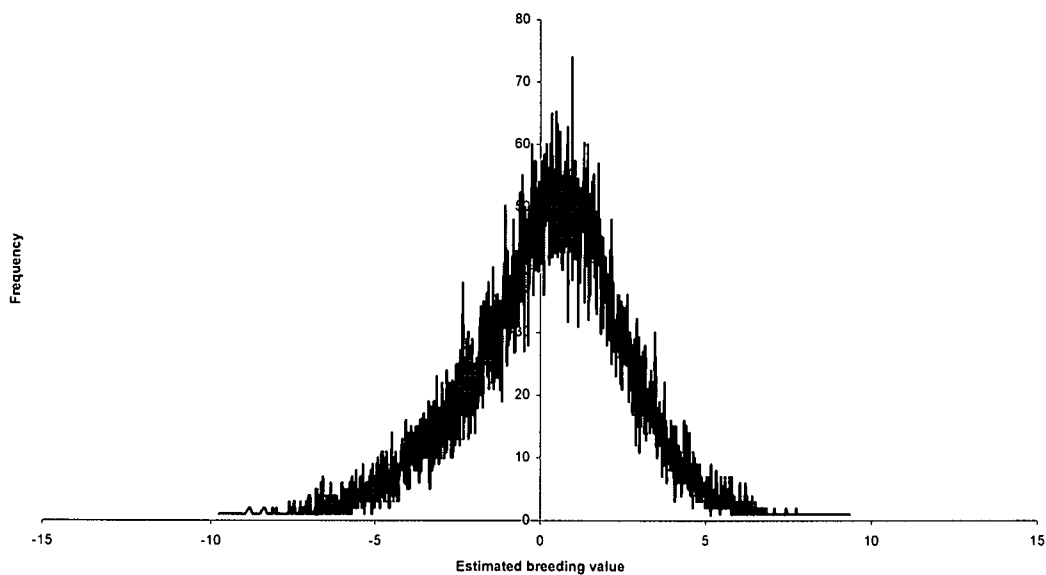


Figure 4.1 *Frequency distribution of direct estimated breeding values of gestation length treated as a trait of the calf*

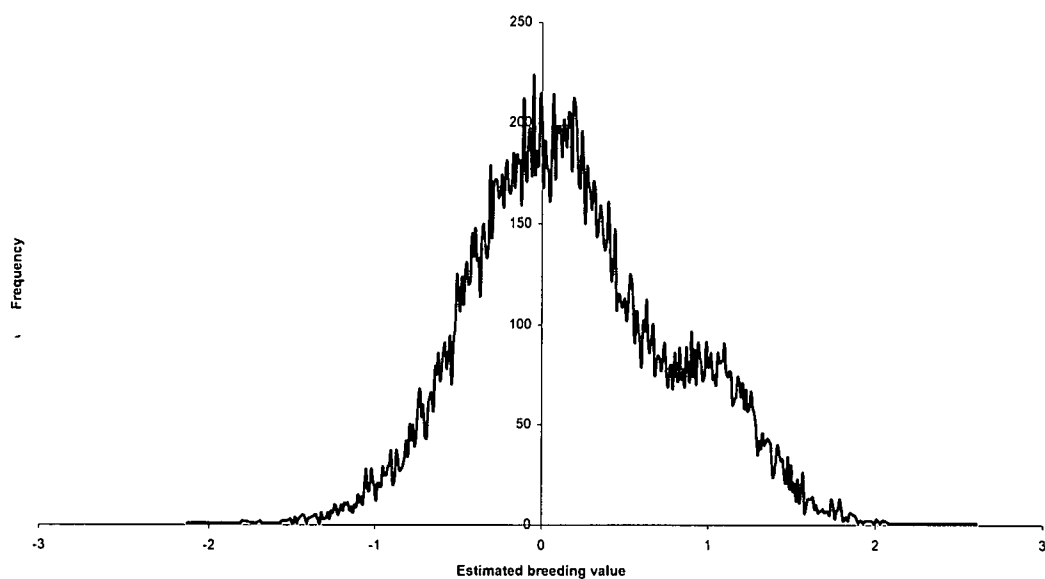


Figure 4.2 *Frequency distribution of maternal estimated breeding values of gestation length treated as a trait of the calf*



### **4.3.2 Genetic trends**

#### **(i) Gestation length**

The genetic trend for gestation length is presented in Figure 4.3. Both direct and maternal trends are presented in this figure. The  $R^2$  - values (coefficient of determination) are the estimated proportion of the variance that could be attributed to the linear regression. The values in Figure 4.3 (both direct and maternal  $R^2$  - values) are very low and thus the linear regression line does not fit or explain the data very well. In spite of the low  $R^2$  - values, the linear regression shows a trend even though there was no direct selection for gestation length. In Chapter 2 it was shown that a correlated response on indirect selection for gestation length through direct selection on birth weight could be expected. The direct gestation length breeding value trend is in a negative direction, showing that gestation length was becoming shorter, probably as a correlated response to selection for lower birth weight. Over 12 years the average direct gestation length breeding value had decreased slightly by 0.30 days. Maternal gestation length breeding values were however becoming more positive. This is a result of the negative correlation between direct and maternal values for gestation length.

#### **(ii) Birth weight**

The genetic trends for the direct breeding values of birth weight are presented in Figure 4.4, while the genetic trends for the maternal breeding values are presented in Figure 4.5. In both cases (direct and maternal) the  $R^2$  - values of the regressions fitted on the trend, in the present study were lower than the  $R^2$  - values for the Bonsmara breed. This could be due to fewer numbers in the present study compared to the National data basis. The genetic trends (both direct and maternal) for the present study and those of the breed were in opposite directions. The possible explanation for this could be that all the bulls used for artificial insemination were highly selected for specific traits, for example, birth weight. Selection for lower birth weight is a clear criterion,

because of its genetic correlation with dystocia. Most of the bulls used for artificial insemination were bulls with below average breeding values (EBVs) for birth weight. In the extensive South African beef industry, natural mating is mostly practised, with a small selected group of females been artificially inseminated. Mating records of the Bonsmara cattle breed reveal in this respect that only 33147 records from a total of over half a million apply to artificial insemination – i.e. 6.4%. This could explain the differences in the genetic trends between recordings used in this study and those of the breed.

Figure 4.5 presents the genetic trend for the maternal breeding values of birth weight. A negative genetic correlation exists between the direct and maternal effects (Figures 4.4 and 4.5). Lykings *et al.* (2000) reported that predicted maternal breeding values together with direct breeding values for birth weight could be used in selection programmes to influence birth weights and reduce calving difficulty.

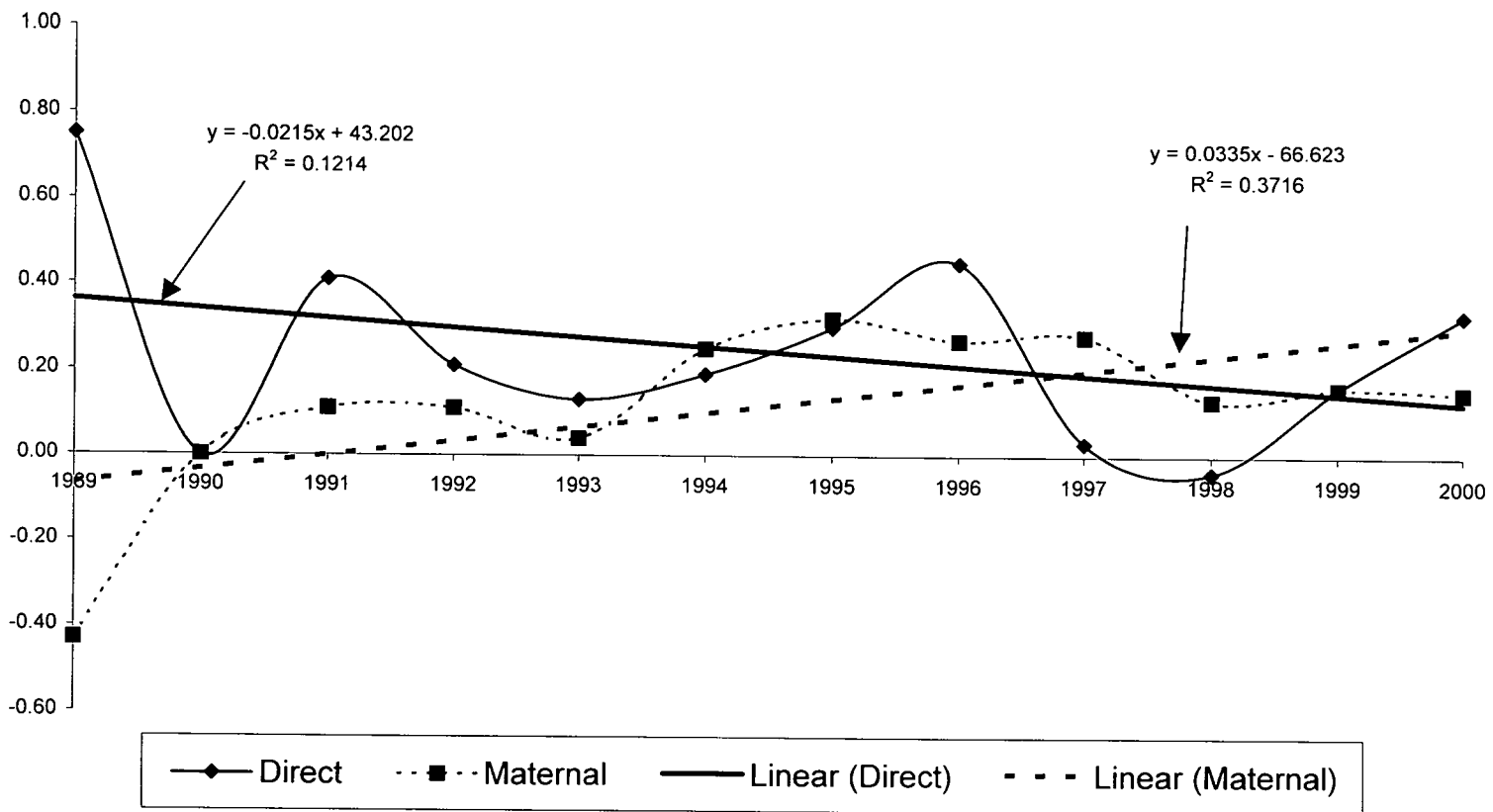


Figure 4.3 Genetic trends (direct and maternal) for gestation length of the data used in the present study

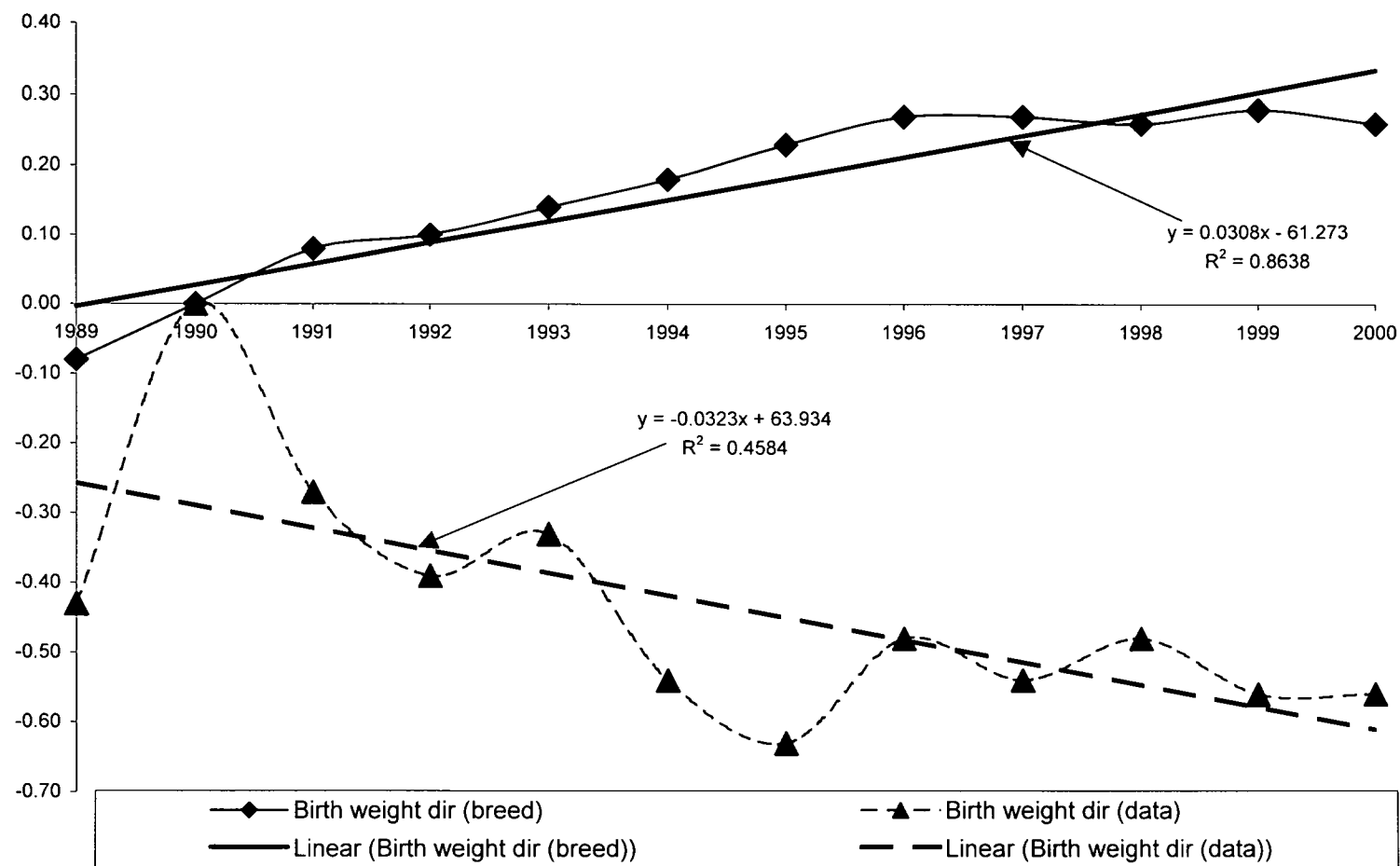


Figure 4.4 The direct genetic trends for birth weight of the Bonsmara breed and the data used in the present study

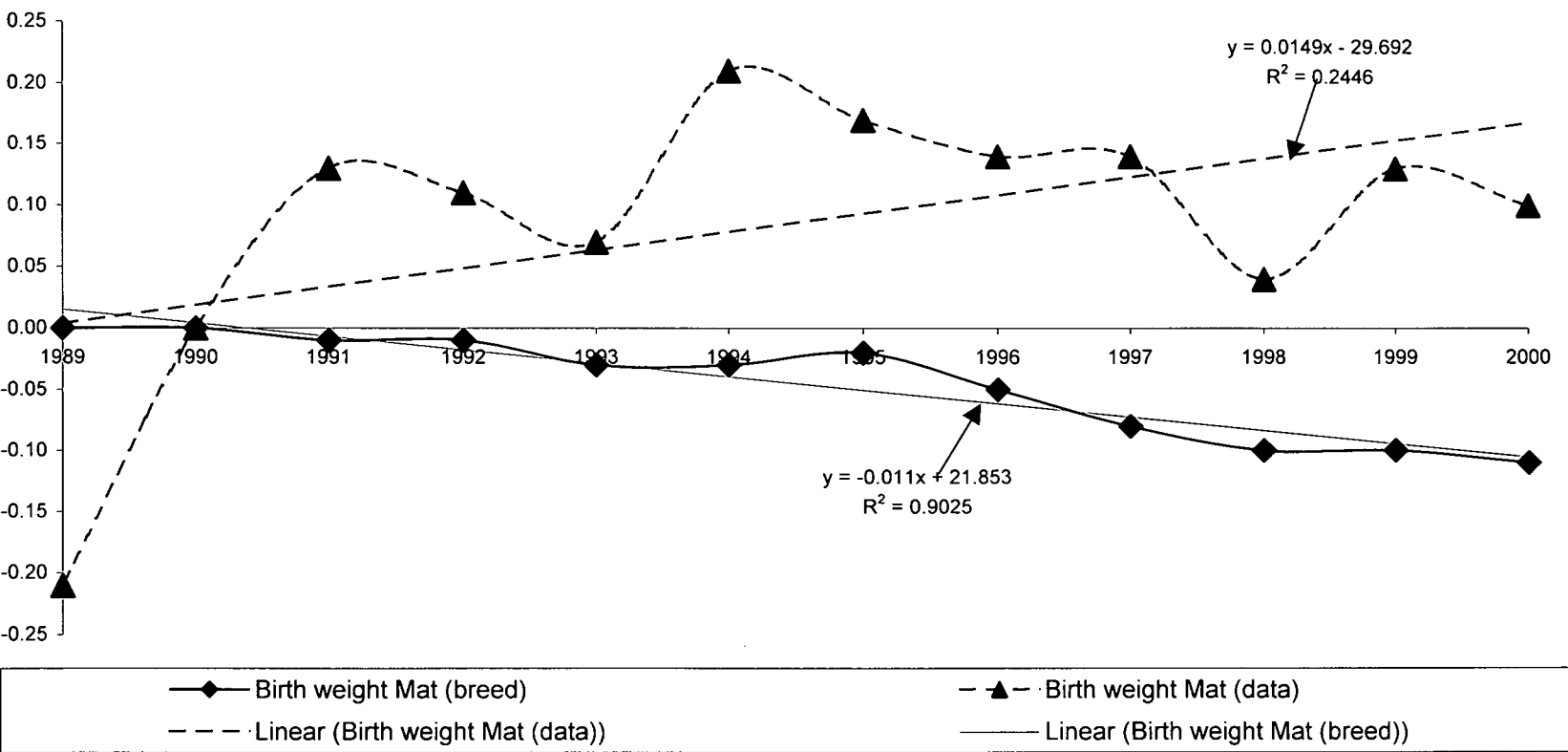


Figure 4.5 The maternal genetic trends for birth weight of the Bonsmara breed and the data used in the present study

## 4.4 Conclusion

The estimated breeding values for gestation length and birth weight show a large variation between the highest and lowest values (Appendix A and B). This is ideal for selection programmes that include these two traits. If, for example, the bull with the highest direct breeding value and the bull with the lowest direct breeding value, were mated with comparable sets of cows, the calves from the bull with the highest direct breeding (8.04) value would be born on average 18 days later than those from the bull with the lowest direct breeding value (-9.91) (Appendix A). The genetic trends for gestation length and birth weight showed that there was genetic progress for both traits over years.

## Chapter 5

### General conclusion

In recent years extensive research has been done on carcass traits, growth traits and reproduction. In the future more emphasis must be given to reproductive traits by researchers and breeders. Fertility is the most important factor in economical beef cattle farming. Female fertility can be influenced by gestation length. In this investigation gestation length and its relationship with birth weight was investigated.

The development of advanced statistical programmes for the animal breeder, such as VCE-REML of Groeneveld (1998) and SAS (SAS Institute Inc., 1996) made it possible to analyse large sets of field data. The computer capacity has also improved to such an extent that the most demanding datasets of the past can now easily be analysed. Univariate and multivariate mixed models were used to obtain genetic parameters for gestation length and birth weight.

Koots *et al.* (1994) reported that the heritabilities for reproductive traits were low (0.02-0.19). The heritabilities for gestation length in this investigation were in contrast, high (0.38). The results from the analyses where the traits were treated as traits of the calf indicated much higher accuracies, than when traits were treated as traits of the dam. Heritabilities were also lower, especially the maternal heritabilities which were in the range of 0.02. Prediction of estimated breeding values from data for gestation length analysed as when traits were treated as traits of the dam is dependent on two or more progeny. For these reasons all further analyses were done according to the first method mentioned above (traits treated as traits of the calf). This was also in agreement with the physiology of parturition.

The genetic correlation obtained in this investigation between gestation length and birth weight is moderate and positive (0.40), which is favourable. This

indicates that there will be a correlated response in gestation length when there is selection on birth weight or vice versa. The genetic trend for gestation length also showed that there was a response for shorter gestation length over the years through this correlation with birth weight.

The high heritability (0.38) of gestation length also indicates that direct selection for shorter gestation length is possible. There are advantages for the beef cattle breeder to select for shorter gestation length, which includes lower birth weights and the lengthening of the postpartum interval, allowing the dam more time to return to oestrus and increase the likelihood of becoming pregnant. Through gestation lengths' correlation with birth weight, calf size could be reduced, improving the ease of calving, which in return would increase the lifetime reproductive performance of cows. A longer gestation period could also prejudice an annual calving interval, which is a critical component in beef cattle production in South Africa.

In the light of the entire investigation the results suggest that gestation length can be recorded. By including the artificial insemination date where applied, as well as the calving date, in the National Beef Cattle Improvement Scheme. The practical implication of this suggestion is however not so easy, as beef cattle farming in South Africa is very extensive and artificial insemination is not commonly used.

The investigation that was done in the present study, and so all the other research works in animal breeding, was for genetic improvement. Van Vleck *et al.* (1987) suggested four guidelines in that respect:

- (i) Obtain accurate records;
- (ii) Define as accurately as possible the relative economic values of the economic traits;
- (iii) Make proper use of the records on the animal and its relatives;
- (iv) Use genetic evaluations.



## Abstract

The purpose of this study was to investigate the genetic and phenotypic parameters for gestation length and birth weight in Bonsmara cattle in South Africa. The genetic and phenotypic parameters were determined when the traits were firstly treated as traits of the calf and secondly as traits of the dam.

A total of 26962 gestation length and birth weight records were used for this investigation. The data was collected from 1989 to 2000. The phenotypic correlation between gestation length and birth weight was moderate and positive (0.22). The sources of non - genetic variation for gestation length and birth weight were sex, herd x year x season (HYS) and age of dam (linear and quadratic). When the traits were treated as traits of the calf all the sources of non-genetic variance were highly significant ( $P < 0.001$ ). Age of dam quadratic was not significant for birth weight when the trait was treated as a trait of the dam.

The traits were analysed through univariate and bivariate analyses. Five basic models were used for the univariate analysis. The five models took the direct genetic, maternal genetic, and/or permanent maternal environmental genetic effects into account. The appropriate random effects were also included in, or excluded from the models. The model that fitted the data best was then used for a bivariate analysis. The direct heritability through the bivariate analysis was 0.38 for gestation length and 0.23 for birth weight. Maternal heritability was lower, 0.09 for gestation length and 0.11 for birth weight. The direct genetic correlation (0.40) and the maternal genetic correlation (0.57) between gestation length and birth weight were positive. In the above results the traits were treated as traits of the calf. The direct heritabilities for gestation length and birth weight, when the traits were treated as traits of the dam, were 0.15 and 0.16 respectively through bivariate analysis. The maternal heritabilities for gestation length and birth weight

were very low to negligible (0.02 and 0.003). The direct genetic correlation (0.41) between gestation length and birth weight was positive, but the maternal genetic correlation (-0.83) was negative.

Estimated breeding values (EBVs) for gestation length and birth weight were calculated for each animal in the data. The genetic trends for gestation length and birth weight were also determined. The trend for gestation length showed that there was a correlated response for shorter gestation length through the possible direct selection for lower birth weight. The trend for birth weight showed that there was selection for lower birth weight.

## Opsomming

Die doel van die studie was om die genetiese en fenotipiese parameters van dragtigheidslengte en geboortegewig in Bonsmara beeste te ondersoek. Eerstens is die genetiese en fenotipiese parameters bereken wanneer die eienskappe as 'n meting van die kalf hanteer is. Tweedens is die eienskappe as 'n meting van die moeder hanteer.

'n Totaal van 26962 dragtigheidslengte en geboortegewig rekords is vir die ontledings gebruik. Die data het oor die tydperk 1989 tot 2000 gestrek. Die fenotipiese korrelasie was positief (0.22). Die bronne van nie-genetiese variasie was geslag, kudde x jaar x seisoen (HYS) en ouderdom van moeder (lineêr en kwadratiese). Al die bronne van nie-genetiese variasie het 'n betekenisvolle ( $p < 0.001$ ) invloed op die berekeninge gehad. Bogenoemde het gegeld ten opsigte van die hantering van die eienskappe as 'n meting van die kalf. Waar die eienskappe as 'n meting van die moeder hanteer is, was die effek van ouderdom van moeder (kwadratiese) vir geboortegewig nie betekenisvol ( $P < 0.001$ ) nie.

Die eienskappe is ontleed deur enkelkenmerk- en multikenmerk ontledings. Vyf basiese modelle is gebruik vir die enkelkenmerk ontleding. Hierdie modelle het die direk genetiese, maternaal genetiese en permanente maternale omgewing genetiese effekte in berekening gebring. Die toevallige effekte is ook in- of uitgesluit in die ontledings. Die model wat die data die beste verklaar het is gebruik vir die multikenmerk ontleding. Die direkte oorerflikheid is 0.38 vir dragtigheidslengte en 0.23 vir geboortegewig. Maternale oorerflikhede was laer, 0.09 vir dragtigheidslengte en 0.11 vir geboortegewig. Bogenoemde resultate is verkry toe die eienskappe hanteer is as 'n meting van die kalf. Die genetiese korrelasies (direk en maternaal) tussen dragtigheidslengte en geboortegewig was positief (0.40 en 0.57). In die geval waar die eienskappe as 'n meting van die moeder hanteer is, is heelwat laer oorerflikhede verkry. Die direkte oorerflikheid vir dragtigheidslengte en geboortegewig was 0.15 en 0.16.

Maternale oorerflikhede vir dragtigheidslengte en geboortegewig in die geval was 0.02 en 0.003. Die direkte genetiese korrelasie tussen dragtigheidslengte en geboortegewig is in die geval positief (0.41) maar die maternale genetiese korrelasie is negatief (-0.83).

Teelwaardes vir dragtigheidslengte en geboortegewig is bereken vir al die individuele diere in die data. Die genetiese tendense is ook bereken vir dragtigheidslengte en geboortegewig. Die genetiese tendens vir dragtigheidslengte toon aan dat dit korter geword het oor die jare as gevolg van die gekorreleerde respons op seleksie vir laer geboortegewigte. Die genetiese tendens van geboortegewig toon aan dat daar geselekteer is vir laer geboortegewigte.

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## Appendix A

*Estimated breeding values for gestation length (AI bulls)*

Computer number	Estimated breeding value (days)	Accuracy
<b>Maternal (lowest)</b>		
13657507	-2.32	48
14251474	-2.04	61
14547236	-1.99	78
3473253	-1.74	72
6666572	-1.70	55
<b>Direct (lowest)</b>		
36159754	-9.91	91
15064462	-9.30	94
16748147	-9.22	99
5975040	-6.97	78
16712135	-6.52	89
<b>Maternal (highest)</b>		
6323034	2.63	78
23039241	2.20	36
3473154	2.16	84
6665178	2.09	76
19974021	2.04	79
<b>Direct (highest)</b>		
6298012	8.04	96
14251474	7.13	90
26285171	7.05	88
5231626	6.91	82
23884968	6.39	77

## Appendix B

*Estimated breeding values for gestation length (all the animals)*

Computer number	Sex	Estimated breeding value (days)	Accuracy
<b>Maternal (lowest)</b>			
38808341	1	-2.13	44
33563487	1	-2.11	56
34172981	1	-2.09	50
31895097	2	-1.81	50
28143766	1	-1.80	69
<b>Direct (lowest)</b>			
26738468	1	-9.75	69
39113147	2	-9.74	73
38142204	2	-9.54	68
39492822	2	-9.24	73
42479675	2	-9.16	39
<b>Maternal (highest)</b>			
39402003	1	2.61	58
34777151	1	2.54	62
33278946	1	2.46	61
29532488	1	2.31	64
29536133	1	2.30	54
<b>Direct (highest)</b>			
41583568	1	9.36	72
41681388	1	9.04	69
41583550	2	9.02	70
28728301	1	8.58	69
44148351	1	8.54	66



## Appendix C

*Estimated breeding values for birth weight (AI bulls)*

Computer number	Estimated breeding value (kg)	Accuracy
<b>Maternal (lowest)</b>		
14251474	-1.49	65
6298012	-1.48	72
8323883	-1.46	55
29564077	-1.45	80
26285171	-1.34	73
<b>Direct (lowest)</b>		
36159754	-4.78	87
19482454	-4.10	91
11624319	-3.86	77
21851795	-3.73	82
6665178	-3.57	92
<b>Maternal (highest)</b>		
11153145	2.66	89
16712135	2.20	72
25297714	1.93	93
6323034	1.80	82
19875988	1.73	61
<b>Direct (highest)</b>		
16607418	3.68	92
29564077	3.34	96
11501319	3.24	95
22105852	3.21	92
16607640	2.86	87

## Appendix D

*Estimated breeding values for birth weight (all the animals)*

Computer number	Sex	Estimated breeding value (kg)	Accuracy
<b>Maternal (lowest)</b>			
28143766	1	-2.35	72
24902009	2	-2.05	46
39537022	2	-1.85	57
25566589	1	-1.81	71
28814044	1	-1.77	65
<b>Direct (lowest)</b>			
43855352	2	-4.59	64
33533423	1	-4.23	61
38396271	2	-4.21	64
42479709	2	-4.21	64
3644591	2	-4.18	68
<b>Maternal (highest)</b>			
34777151	1	2.56	65
35605005	1	2.49	54
34279042	1	2.43	64
33278961	1	2.41	66
32892580	1	2.33	68
<b>Direct (highest)</b>			
29353588	1	4.01	76
26490292	1	3.84	69
28031151	1	3.46	63
35655695	1	3.44	63
28031177	2	3.23	60

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