

**ESTIMATION OF GENETIC PARAMETERS FOR GROWTH  
TRAITS IN SOUTH AFRICAN BRAHMAN CATTLE**

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**ESTIMATION OF GENETIC PARAMETERS FOR GROWTH  
TRAITS IN SOUTH AFRICAN BRAHMAN CATTLE**

**by**

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## TABLE OF CONTENTS

	PAGE NO.
CHAPTER	
1 GENERAL INTRODUCTION	1
2 ORIGIN AND HISTORY OF THE BRAHMAN BREED	8
3 (CO) VARIANCE COMPONENTS AND GENETIC PARAMETERS FOR GROWTH TRAITS	11
3.1 Introduction	11
3.2 Materials and Methods	15
3.2.1 Data	15
3.2.2 Genetic analysis	18
3.3 Results and Discussion	21
3.3.1 Non-genetic factors	21
3.3.2 (Co) variance components and genetic parameters	22
3.3.2.1 Birth weight	22
3.3.2.2 Weaning weight	26
3.3.2.3 Yearling weight	29
3.3.2.4 Final weight	32
3.3.2.5 Correlation among traits	34
3.3.2.6 Direct and maternal genetic trends	41
3.3 Conclusion	45
4 INBREEDING IN THE SOUTH AFRICAN BRAHMAN BREED	46
4.1 Introduction	46
4.2 Materials and Methods	47
4.2.1 Data and statistical analysis	47
4.3 Results and Discussions	49
4.4 Conclusion	54

5 GENERAL CONCLUSIONS AND RECOMMENDATIONS	55
ABSTRACT	58
OPSOMMING	61
REFERENCES	64

# CHAPTER 1

## General Introduction

The Brahman is a tropically adapted *Bos indicus* breed developed from cattle of Indian origin (Sanders, 1980). It is one of the numerous cattle breeds in South Africa adapted to tropical and subtropical conditions (Campher *et al.*, 1998). The tropics can be a harsh and demanding environment in which to raise cattle. High temperatures, extreme humidity, poor-nutrient soils and threats of parasites are all factors limiting the production of beef cattle and making it a formidable and challenging place for the improvement of livestock. *Bos indicus* (Zebu) cattle are basically the only breeds that can thrive under these challenges (Magnabosco *et al.*, 2002). The Brahman breed, as it is classified under the genus and species *Bos indicus*, has its origin in these harsh climates and is well adapted to the rigors of tropical agriculture (Peacock *et al.*, 1999; Magnabosco *et al.*, 2002). This is supported by Mackinnon *et al.* (1991) who stated that growth rate in tropical environments depends on both the inherent ability of the animal to grow and the animal's resistance or adaptation to environmental stresses such as internal and external parasites as well as heat stress. According to Turner (1980) adaptation is a broad term used to describe the ability of animals to adjust to environmental conditions or to infer genetic modifications that make animals more suitable for existence under specific environmental conditions.

The characteristics of the Brahman breed, which distinguishes it from the others, are the hump over the shoulder, long legs, large pendulous ears, abundance of loose folds of skin under the neck and smooth hair coat (Peacock *et al.*, 1999). The main feature of the Brahman breed is its ability to withstand extreme tropical climates and to tolerate low quality feed during periods of food shortage in some areas as well as excelling in crossbreeding programmes (Cartwright, 1980). On the other hand, growth and physiological aspects of the *Bos indicus* are unique genetic attributes, which are different from those of the *Bos taurus* breeds (Turner, 1980). Cartwright (1980) also stressed that

the large difference exist in the anatomy and physiology of these animals compared to *Bos taurus* types, and therefore in production.

*Bos indicus* cattle are widely recongnised as adaptable to tropical and subtropical environments that are restrictive to *Bos taurus* cattle (Peacock *et al.*, 1999). Among the differences between *Bos indicus* and *Bos taurus* breeds are variation in heat and cold tolerance, reproduction, parturition and lactation, growth and maturation rates, temperament and complementarities (Cartwright, 1980; Turner, 1980). However, in most aspects, the animal and its productivity is the result of its genetic make-up or its genotype responding to the many non-genetic factors, which comprise of the environment in which it lives. In general, when comparing *Bos indicus* with *Bos taurus*, the *Bos indicus* cattle have slightly lower reproduction levels, are later maturing and have poorer beef quality. With reference to growth rate and maturation, Vargas *et al.* (1999) found that in Florida (USA) Brahmans heifers reach puberty at an average age of  $633 \pm 6.7$  days. Galiana & Arthur (1989) found that in general, *Bos indicus* heifers reached puberty at an older age than their *Bos taurus* heifer counterparts.

The Brahman breed has traits that are useful for a wide range of production systems, such as adaptability in harsh areas and combining ability with other breeds. Improvement of live performance traits is an increasingly important breeding goal in beef cattle and other livestock production systems (Peters *et al.*, 1998). Therefore, knowledge of the genetic parameters of traits in the selection programme is needed, to optimize breeding programmes and to predict genetic response to selection. Meyer (1992) and Ferreira *et al.* (1999) indicated that an animal model that includes individual performance and pedigree information would provide the beef industry with reliable estimates of genetic parameters and should result in improved genetic evaluation programmes. The manner in which this genetic improvement is to be achieved can be described using a selection objective (Van der Westhuizen & Matjuda, 1999).

Heritabilities and genetic correlations are essential population parameters required in livestock breeding researches as well as in the design and application of practical animal



breeding programmes. Genetic parameters are unique to the population in which they were estimated and they may change over time due to selection and management decisions (Koots *et al.*, 1994a; Lobo *et al.*, 2000). According to Liu *et al.* (1991) in practice it would be useful to know the empirical relationships (genetic, phenotypic and environmental correlations) of these measures of growth rate in the population. Therefore, genetic correlations simply describing the existing relationships among measured traits for a population are also needed. An example is high growth rates that are correlated with high birth weights (Roberson *et al.*, 1986; Simm, 1998).

Considerable research efforts have been directed towards estimating genetic parameters for various growth traits in beef cattle - in fact, much has already been achieved. Review articles by Mohiudin (1993), Koots *et al.* (1994a,b) and Lobo *et al.* (2000) describe many of the parameters estimates for several pre-weaning and post-weaning growth traits as well as reproduction traits in different beef cattle breeds from different countries. A breed such as the Brahman in South Africa has an important genetic base and increasingly been used (Kluyts, 1993), but there are still many issues to be investigated related to growth, reproduction and carcass traits. Despite improved genetic evaluation programmes, and the findings from diverse literature, the quest to predict new and more accurate genetic parameters for growth traits in South African Brahman cattle continues.

Performance testing around the world has been concentrating on measuring live weights at regular intervals, that is, birth weight (BWT), weaning weight (WWT), yearling weight (YWT), eighteen months weight or final weight (FWT) and mature weights (MWT) (Simm, 1998). The same author emphasizes that the current recording of live weights is a minimum requirement for beef breeding services, and more comprehensive recording (more traits and more animals) is needed for accurate evaluation. Records on the growth performance of the South African Brahman breed has been collected for many years, pedigree records traced back to 1955. Mostert *et al.* (1998) evaluated some performance records of Brahman cattle participating in the National Beef Cattle Improvement Scheme for the period of 1976 to 1996 using multivariate animal models. The present study

further evaluates the growth traits of South African Brahman cattle considering the total population.

Growth rate is an important trait in meat animals (Liu *et al.*, 1991). High growth rates and high weaning weights contribute to the efficiency of beef production. The reason for this is that efficiency depends on three basic elements, namely female production and maternal performance, reproduction as well the growth of the young after weaning (Dickerson, 1970; Meyer *et al.*, 1991; Schoeman & Jordaan, 1999; Van der Westhuizen & Matjuda, 1999). Even though high growth rate contributes to the efficiency, selection should not be based on growth traits only, as high weaning weights are associated with an increase in birth weights as well as high mature cow weights. Furthermore, high birth weights are often associated with dystocia, which can cause calf losses, reduced calf performance and reduced cow fertility. Roberson *et al.* (1986) stated that extreme birth weights could in turn cause production problems and economic losses for beef producers. High birth weights are also associated with high mature cow weights and this might lead to higher cow maintenance. In South Africa, Schoeman (1996) showed that body weight at any stage as well as weight gain are strongly related to breed mature size as estimated by the dam weight at weaning when characterizing beef cattle breeds by virtue of their performance in the National Beef Cattle Improvement Scheme.

Another factor to be considered when selecting for growth traits, is the relatively large negative genetic correlation between direct growth and maternal genetic effects. Other non-genetic factors are proposed to cause the negative correlation between maternal genetic effect and direct individual growth (Robinson, 1996b; Lee & Pollak, 1997; Meyer, 1997). According to Neser *et al.* (1996), Robinson (1996b) and Lee & Pollak (1997) ignoring the effect of sire x year or sire x herd-year-season interaction in the model causes the negative correlations between direct and maternal effects to be more pronounced. Likewise, Meyer (1997), who applied the “Falconer-Willham” model and additionally included sire x herd-year interaction, found that genetic correlations between direct and maternal to be considerably less negative compared to the ‘usual’ animal model.

Reproduction and growth are considered to be two primary traits in a breeding strategy, therefore the relationship between the two needed to be considered at all times in genetic evaluations (Archer *et al.*, 1998). Scholtz & Roux (1984) reported negative correlated responses on reproduction of cows selected for growth rate. However, new findings involving both experimental selection data (Mrode *et al.*, 1990; Morris *et al.*, 1992; Archer *et al.*, 1998) and field data (Meyer *et al.*, 1991; Mercandante *et al.*, 2003) disputed the negative association between the two, pointing out that selection of young animals based on body weights did not significantly affect the reproductive performance of cows.

In general, the reproductive performance of the Brahman has been reported to be low. However, Peacock *et al.* (1999) showed that Brahman cows compared favourably with the Angus and Charolais in terms of birth rate (89.9%), survival rate (90.8%) and weaning rate (81.6%). Vargas *et al.* (1999) also reported an average calving rate of 92.1%, 58%, and 83.9% in the first, second and third parity of Brahman cows in Florida (USA). The corresponding survival rates were 80.7%, 83.4% and 47.9%, whereas the weaning rate was 65.2%, 54.3% and 72% respectively. Based on these results, assumptions could be made that reproductive performance of the South African Brahman cattle is high. With this in mind, selection base on production traits could increase total herd efficiency in a selection programme. According to Miller *et al.* (1999) reproduction should be maximised but maternal aspects should be optimum. Furthermore, the fact that maintenance of reproductive efficiency in the herd is of particular concern cannot be disputed, however, increasing growth is important to increase output from production systems (Eler *et al.*, 1995).

Variance components are frequently estimated with records obtained through performance recording schemes from populations undergoing selection. Selection is known to increase inbreeding and relationship coefficients, which in turn contribute to the decrease in the ultimate rates of genetic gain after many generations (Colleau, 2002). Directional selection also decreases the additive genetic variance of a trait subject to selection and of correlated traits due to the covariance between animals, inbreeding and

gametic disequilibrium (Diaz *et al.*, 2002). Inbreeding (close breeding) as defined by Falconer & Mackay (1996) is the result of mating of individuals that are related to each other by common ancestors. Several studies discovered that selection using best linear unbiased predictors (BLUP) of breeding values leads to inbreeding due to the increase emphasis on family selection, particularly to traits with low heritability (Belonsky & Kennedy, 1988; Fernandez & Toro, 1999; Meszaros *et al.*, 1999; McDaniel, 2001). Even in the absence of BLUP selection, the rate of inbreeding is related to the age structure and an effective size of the breeding population (Meszaros *et al.*, 1999).

According to Meszaros *et al.* (1999) inbreeding is detrimental due to its effects on phenotype and thus profit on rate of genetic improvement. The basic genetic consequence of inbreeding is to promote what is technically known as homozygosity in a population (Burrow, 1993). One effect associated with inbreeding is so-called “inbreeding depression”, which is a decline in the average phenotypic performance due to inbreeding. However, inbreeding seems not to affect all traits with the same intensity (Fioretti *et al.*, 2002). Some characteristics (like meat quality) are hardly influenced by inbreeding; others (like reproductive efficiency) are greatly influenced by inbreeding (Burrow, 1998).

Inbreeding depression exists in some degree in all populations (Falconer & Mackay, 1996). This phenomenon is well documented in all major livestock, for example, effects in beef cattle have been reviewed by Burrow (1993). Diverse studies suggest that the level of inbreeding depression may vary amongst populations. Although inbreeding depression could compromise the immediate performance and survival of the population, it also exposes the recessive deleterious harmful genes to the action of selection (Analla *et al.*, 1999). In beef cattle, the effects of inbreeding were relatively minor at low levels of inbreeding, while animals that had inbreeding coefficients higher than 20% were more affected than those having milder levels of inbreeding (Burrow, 1993).

Taking the above into account, any genetic evaluation should consider the rate of inbreeding and its consequence on the mean phenotypic performances of the animals (Analla *et al.*, 1999). Pedigree analysis is an important tool to describe genetic variability

and its evolution across generations (Gutierrez *et al.*, 2003). According to Fernandez & Toro (1999) the need for controlling inbreeding refer not only to a better use of the genetic variability available and to reduce inbreeding depression in the selected trait, but also to reduced depression of fitness related traits, which might be the most serious drawback of inbreeding. Notter (1999) stated that in the past as well as in recent years considerable work has been done on the design of strategies to maintain genetic diversity in selection programmes. According to Fernandez & Toro (1999) these strategies are aimed at simultaneously optimising genetic gain and inbreeding, either by reducing the rate of inbreeding while keeping genetic gains at a predetermined level or by increasing selection response by restricting inbreeding. Different strategies can be classified according to the factor on which they act: (i) the selection criterion used (ii) the mating system imposed (iii) the number of selected individuals and their contribution to the next generation.

The main objectives of this study were:-

- (i) to evaluate growth traits in the South African Brahman cattle and
- (ii) to determine the inbreeding level.

## CHAPTER 2

### Origin and history of the Brahman breed

Modern cattle are divided into two species: *Bos taurus*, which originated in Europe and includes most modern breeds of dairy and beef cattle and *Bos indicus*, which originated in India and is characterised by a hump at the withers. The latter are now widespread in Africa and Asia, with lesser numbers imported to North America (primarily in the southern United States), Central America and Northern and Central South America. Zebu cattle are the humped cattle of the world and they are classified according to the location of the hump. Generally Zebu cattle are considered to be indigenous to parts of Asia and Africa. Zebu cattle are usually considered as *Bos indicus* and European cattle as the *Bos taurus* species. The size and the location of the thoracic humped (shoulder humped) and the cervico thoracic humped (neck humped) are quantitatively inherited, but the genetically cervico thoracic are intermediate between humped and non-humped in apparently all cases (Briggs, 1958; Sanders, 1980; Hetzel, 1988).

The Brahman breed was developed in the United State of America (USA) in the beginning of the 20<sup>th</sup> century; it was developed from an unknown mixture of Gir, Guzerat, Nelore and Indu-Brazil. There are over 30 strains of Zebu cattle in India, each of which originated in a province of India and for the most part are named after their native province. They can be classified into six major groups namely the Guzerat, the Nelore, the Gir, the Krishna Valley, the Indu-Brazil and the Sahiwal. The Guzerat, the Nelore and the Gir are the three principal strains that had an influence on the development of the American Brahman (Sanders, 1980).

According to Sanders (1980) the three principal strains brought to the United States differ slightly even though they are all Zebus. The Guzerat made the largest contribution to the development of the Brahman in comparison to the other two. At that stage the Guzerat were the most numerous breed in Northern India. They have long lyre-shaped horns;

short broad faces, long, broad, dropping ears that are open to front. Colour varied from light grey to black at maturity and was regarded as powerful draft animals as well as reasonable milk producers.

The second strain is the grey breed of Northern and Central India, called the Nelore. The Nelore is distinguished by a narrow head with short ears and horns. They are tall and lighter than the Guzerat, but heavily muscled Nelore cattle could also be found. They were also used for milk production and heavy draft work. It is believed that the modern American grey Brahman is probably between one-eighth and one-fourth Nelore (Sanders, 1980).

The third strain is the Gir. The native home of the Gir is the Gir Hills and Forest in the South of the Kathiawar Peninsula on the West coasts of India. This breed is distinctive in characteristics as compared to the Guzerat and the Nelore. It has long, pendulous ears, with the inside facing forward and the points turning inward so that the tips almost meet at the throat, especially in the calves. The forehead is narrow and prominent, with the horns emerging downward and backward from the outer edge. The colour can either be solid red or red and speckled (ranging from predominantly red to white). On most Gir cattle there is a well-defined patch of colour that is a different shade from the rest of the other breeds. Gir cows are good milk producers, but their teats are often too large for newborn calves to nurse without assistance. The sheath is also too large and pendulous (Sanders, 1980).

Zebu cattle entered the United States in the late 1800's in small numbers from India. Later in 1854 more different strains were introduced in large proportions. Mr J.W. Sartwelle of Houston, who was the first secretary of the association, formed the American Brahman Breeder's Association (ABBA) in 1924 and he proposed the name Brahman. In 1973 over 500,000 Brahman cattle had been registered by the ABBA. The Brahman is a distinctive breed in appearance with several features, which distinguishes it from other breeds. The other characteristics of this breed are their horns, which are usually curved upward and sometimes tilted to the rear. Currently, the American grey and

the red Brahmans are distinctively different types of cattle. The greys are developed by crossing the Guzerat and the Nelore, whereas the red Brahmans comes primarily from the Gir and Indu-Brazil with a little bit of Guzerat influence (Briggs, 1958; Sanders, 1980).

The first introduction of the Brahman into the Southern African occurred in 1954, when Mr. Jurgen Crantz of the former South-West Africa imported eight males and 10 females from Texas. Later in the same year (1954) more Brahmans were imported. Three years later a meeting of 13 people founded the Brahman Cattle Breeders' Society of South Africa. According to herd statistics in South Africa, Brahman cattle are amongst the most numerous breeds, following Bonsmara, Holstein and Jersey cattle (Campher *et al.*, 1998). The Brahman society developed a decentralised technical service, which was implemented by the Society in 1990; it has a linear type classification system based on subjective evaluation and objective measurements to support breed improvement.



## CHAPTER 3

### (Co) variance components and genetic parameters for growth traits

#### 3.1 Introduction

Growth rate remains the primary selection criterion for most beef cattle breeders around the world, thus the correct prediction of the genetic value of beef cattle is required for optimising genetic gain (Archer, 1998). Tosh *et al.* (1999) emphasised that values for genetic parameters are needed to implement breeding programmes and to assess breeding strategies. Furthermore, Ferreira *et al.* (1999) stated that growth traits in beef cattle are important in selection programmes. Consequently, the relative importance of direct and maternal genetic effects for growth should be considered when beef producers formulate breeding programmes. Knowledge of components of variance and genetic parameters are required in designing breeding programmes for genetic improvement (Eler *et al.*, 1995; Peters *et al.*, 1998).

A successful selection programme for improvement of performance traits in beef cattle depend on selection for a specific trait and understanding how selection for one trait may influence other production traits. The genetic relationship among growth traits has been studied by estimating genetic correlations between growth traits (Archer *et al.*, 1998). Methods to estimate (co)variance components and genetic parameters in beef cattle due to maternal effects have been presented by Meyer (1992; 1994; 1997) as well as several other authors.

Genetic evaluations are routinely done by breed associations to assess several important beef production traits. Best Linear unbiased prediction (BLUP) is the method of choice for genetic evaluation. BLUP makes maximal use of information from relatives. It is also the most effective method of separating genetic and environmental effects and permits across-herd and across year evaluations, provided that there are genetic links between herds or years (Crump *et al.*, 1997).

The prediction of the total genetic merit is complicated by the presence of a genetic antagonism between animal effects. It also varies widely among breeds (Robinson, 1996b). This is caused by the fact that birth weight and weaning weight are determined by the animal's own additive merit as well as maternal components (uterine capacity and milk production). The latter can be partitioned in an additive genetic and environmental component as shown by Meyer (1992) and Robinson (1996a). Increased computing power and software capabilities have facilitated the use of sophisticated statistical procedures to estimate variance components and predict breeding values. Estimates using a multitrait REML analyses on the South African Brahman cattle field data of animals participating in the National Beef Cattle Performance Testing Scheme (Mostert *et al.*, 1998) as well as other univariate estimates for *Bos indicus* breeds (Table 3.1) mostly showed negative estimates between the animal effects.

**Table 3.1** A summary of literature on genetic parameter estimates for growth traits in beef cattle

Source	Breed	Country	Model	$h^2_a$	$h^2_m$	$r_{am}$	$c^2$	$h^2_t$
<b>Birth weight</b>								
Meyer, 1992	Hereford	Australia	AMMP	0.41	0.08	0.04	0.05	0.46
Koots <i>et al.</i> , 1994a	Bt & Bi	Canada	AMMP	0.31	0.14	-0.27	-	-
Eler <i>et al.</i> , 1995	Nellore	Brazil	AMMP	0.22	0.12	-0.72	0.07	0.10
H-Mariam & K-Mersha, 1995	Boran	Ethiopia	AMMP	0.24	0.09	-0.55	0.00	0.17
Diop & Van Vleck, 1998	Gobra	Senegal	AMMP	0.07	0.04	-0.17	0.04	0.08
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.45	0.08	-0.35	-	-
Plasse <i>et al.</i> , 2002a	Brahman	Venezuela	AMMP	0.33	0.08	-0.37	0.03	0.28
Plasse <i>et al.</i> , 2002b	Brahman	Venezuela	AMMP	0.33	0.06	-0.02	0.08	0.30
<b>Weaning weight</b>								
Meyer, 1992	Hereford	Australia	AMMP	0.14	0.13	-0.58	0.23	0.09
Koots <i>et al.</i> , 1994a	Bt & Bi	Canada	AMMP	0.24	0.13	-0.30	-	-
Eler <i>et al.</i> , 1995	Nellore	Brazil	AMMP	0.13	0.13	-0.32	0.14	0.14
H-Mariam & K-Mersha, 1995	Boran	Ethiopia	AMMP	0.21	0.06	-0.57	0.14	0.21
Diop & Van Vleck, 1998	Gobra	Senegal	AMMP	0.20	0.21	-0.61	0.16	0.12
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.25	0.08	-0.33	-	-

Table 3.1 continues.....

Source	Breed	Country	Model	$h^2_a$	$h^2_m$	$r_{am}$	$c^2$	$h^2_t$
Plasse <i>et al.</i> , 2002a	Brahman	Venezuela	AMMP	0.07	0.14	-0.13	0.16	0.12
Plasse <i>et al.</i> , 2002b	Brahman	Venezuela	AMMP	0.08	0.13	0.11	0.13	0.16
<b>Yearling weight</b>								
Meyer, 1992	Hereford	Australia	AMMP	0.16	0.11	-0.48	0.05	0.12
Meyer, 1992	Zebu cross	Australia	AMMP	0.24	0.14	-0.38	0.025	0.21
Koots <i>et al.</i> , 1994a	Bt & Bi	Canada	AMMP	0.33	0.11 (unwght)	-	-	-
Eler <i>et al.</i> , 1995	Nellore	Brazil	AMMP	0.16	0.10	0.09	0.02	0.22
H-Mariam & K-Mersha, 1995	Boran	Ethiopia	AMMP	0.34	-0.05	0.68	0.05	0.24
Diop & Van Vleck, 1998	Gobra	Senegal	AMMP	0.24	0.21	-0.50	0.05	0.18
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.25	0.06	-0.21	-	-
<b>Final weight</b>								
Meyer, 1992	Hereford	Australia	AMMP	0.22	0.03	-0.20	0.09	0.21
Meyer, 1992	Zebu cross	Australia	AMMP	0.20	0.005	1.00	0.04	0.28
Diop & Van Vleck, 1998	Gobra	Senegal	AMMP	0.14	0.16	-0.28	0.04	0.15
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.22	0.03	-0.21	-	-
Plasse <i>et al.</i> , 2002a	Brahman	Venezuela	AMMP	0.13	0.08	0.49	0.01	0.26
Plasse <i>et al.</i> , 2002b	Brahman	Venezuela	AMMP	0.16	0.04	0.52	0.04	0.28

See **Table 3.4** for abbreviations, AMMP– Animal model with maternal effect and permanent maternal environmental effects, MAM– multitrait animal model, Bt & Bi- *Bos taurus* and *Bos indicus*, S.A.– South Africa, unwght- unweighted

The objectives of this study were to estimate (co)variance components for growth traits in the South African Brahman. Genetic correlations among the growth traits were also estimated to enable breeders to predict the consequences of selection for growth rate. Genetic trends were also derived to observe the genetic change that had taken place through the years.

## **3.2 Materials and methods**

### **3.2.1 Data**

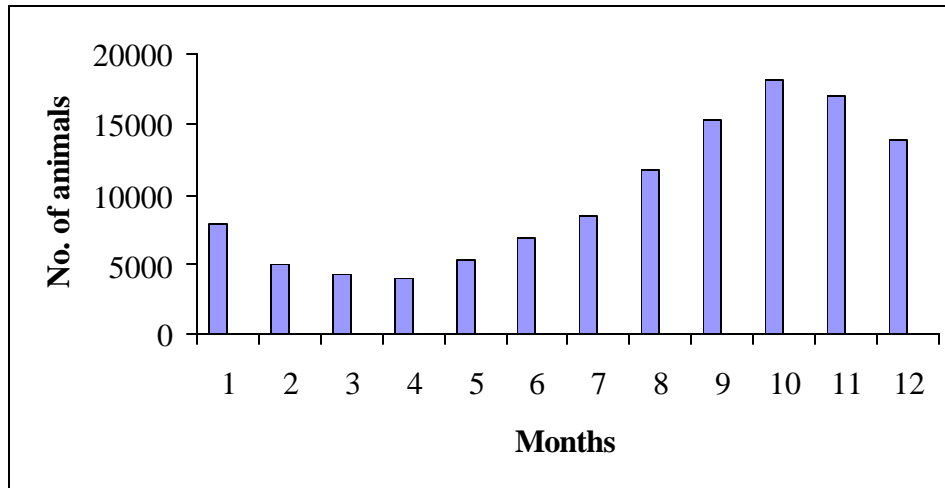
Data utilised in this study were obtained from the South African Brahman breeder's Society and consisted of 181 508 animals with pedigree information and 221 015 performance records ranging from birth to 18-months weight /final weight. The pedigree records had been collected since the introduction of the Brahman breed in South Africa in 1955 until 2002.

The classifications of weight classes were done following the Breedplan system (Anon., 2001) (Table 3.2). The age ranges for different traits were: weaning weight (80 – 300 days); yearling weight (301- 500 days) and final weight (501 – 900 days). Table 3.2 lists descriptive statistics of the performance records for the four traits evaluated in this study.

**Table 3.2** Description of data used for analyses

Traits	BWT	WWT	YWT	FWT
Number of animals before editing	67 336	62 159	41 313	32 602
Number of animals after editing	41 509	37 705	22 682	13 055
Number of sires after editing	1 410	1 252	871	555
Number of dams after editing	18 798	15 662	10 547	6 771
Dam age range (years)	3-13	3-13	3-13	3-13
Number of herds	131	95	72	48
Number of HYS	1 495	1 201	751	508
Management group	9	20	19	15
Average age (days)	-	210.06	379.59	558.39
Standard deviation (days)	-	30.36	39.46	36.18
Period	1987-2002	1985-2001	1985-2001	1985-2000

Edits consisted of checks for dates of birth; weighing-dates and age of the dam for each animal. All animals without a sire or a dam or without any weights were excluded from the analyses. Only dams which were three years and older were retained. Calving occurred throughout the year. However, most of the calving took place from September to November in all years. Seasons were then derived from the distribution of number of birth per month (Figure 3.1), comparison of performance means per month and testing the contrast between months using Tukey's studentised range tests with the probability of 5 %. Based on this analysis, the seasons of calving were finally classified as follows: January to July (1), and August to December (2). This was done because there were no distinct breeding seasons. Contemporary groups were obtained by grouping animals born in the same herd, year and season and of the same sex with a minimum of five animals per contemporary group.



**Figure 3.1** Distribution of number of birth records per month

Sires with at least five calves and herds with at least ten records were used for this analysis. All single-sire contemporary groups were eliminated and data of at least three years per herd were used. After editing, only data of 1985 – 2002 were considered in the analysis. The reason for using the data only from 1985 is that only a small number of records were recorded up to 1984.

In order to determine the fixed effects to be included in the model, a preliminary analysis was performed using the General Linear Models Procedure (PROC GLM) (SAS, 1999). Those fixed effects thought to be important enough to be included in the genetic analysis were sex, age of the dam at calving, herd-year-season, management group and age of the calf as a covariate for WWT, YWT and FWT. The following model was fitted for BWT, WWT, YWT and FWT: -

$$Y_{ijklmn} = \mu + s_j + hys_k + mgrp_l + ad_m + age_n + e_{ijklmn}$$

Where  $Y_{ijklm}$  = an observation of a trait on the  $i^{th}$  animal of the  $j^{th}$  sex of the  $k^{th}$  herd-year-season of the  $l^{th}$  management group of the  $m^{th}$  age of the dam and of the  $n^{th}$  age of the calf,

$\mu$  = Overall mean,

$s_j$  = fixed effects of the  $j^{th}$  sex ( $j = 1,2$ ),

$hys_k$  = fixed effects of  $k^{th}$  herd-year-season ( $k = 1,2,3,\dots,1495$ ),  
 $mgrp_l$  = fixed effects of  $l^{th}$  management group ( $l = 9,10,\dots,20$ ),  
 $adm_m$  = fixed effect of the  $m^{th}$  age of the dam in years ( $m = 3, 4,\dots,13$ ),  
 $age_n$  = fixed effects  $n^{th}$  age of the animal in days as a covariate ( $n = 80,81,\dots,900$ ) (was excluded in BWT) and  
 $e_{ijklmn}$  = residual error variance.

### 3.2.2 Genetic analysis

Variance components were estimated using the ASREML programme of Gilmour *et al.* (1999). The method involves maximising the likelihood function given the data. The most commonly used model is the animal model with only additive genetic variance (Goddard, 2001). The inclusion of herd-year-season x sire interaction in models for estimating variance components and for genetic evaluation in field data seems justifiable (Neser *et al.*, 1996; Meyer, 1997) as the Brahman in South Africa are bred in different ecological regions of the country, under very different management levels.

The single trait animal models for analyses as explained below in matrix notation are as follows: -

- Model 1       $Y = X\beta + Z_1a + e$   
 Model 2       $Y = X\beta + Z_1a + Z_3c + e$   
 Model 3       $Y = X\beta + Z_1a + Z_2m + e$  {without cov (a, m) = 0}  
 Model 4       $Y = X\beta + Z_1a + Z_2m + e$  {with cov (a, m) =  $As_{am}$ }  
 Model 5       $Y = X\beta + Z_1a + Z_2m + Z_3c + e$  {without cov (a, m) = 0}  
 Model 6       $Y = X\beta + Z_1a + Z_2m + Z_3c + e$  {with cov (a, m) =  $As_{am}$ }  
 Model 7       $Y = X\beta + Z_1a + Z_2m + Z_3c + Z_4cxs + e$  {without cov (a, m) = 0}  
 Model 8       $Y = X\beta + Z_1a + Z_2m + Z_3c + Z_4cxs + e$  {with cov (a, m) =  $As_{am}$ }  
 Model 9       $Y = X\beta + Z_1a + Z_2m + Z_4cxs + e$  {with cov (a, m) =  $As_{am}$ }



Where: -

$Y$  = vector of observation,

$\beta$  = vector of fixed effects influencing growth,

$a$  = vector of direct additive effects,

$c$  = vector of random permanent maternal environmental effects,

$m$  = vector of random maternal additive (dam) effects,

$cxs$  = vector of additional random effects of contemporary group by sire interaction \ herd-year-season x sire interaction,

$e$  = is vector of residuals and where

$X, Z_1, Z_2, Z_3$  and  $Z_4$  are incidence matrices relating observations to their respective fixed and random effects.

Based on the models presented above, the expectations of the random vectors  $a, m, c$  and  $e$  are all null vectors in a model without selection and the variance – covariance structure is:-

$$\text{Var} \begin{Bmatrix} a \\ m \\ c \\ cxs \\ e \end{Bmatrix} = \begin{Bmatrix} \mathbf{A}s_a^2 & \mathbf{A}s_{am} & 0 & 0 & 0 \\ \mathbf{A}s_{am} & \mathbf{A}s_m^2 & 0 & 0 & 0 \\ 0 & 0 & \mathbf{I}_{N_d}s_c^2 & 0 & 0 \\ 0 & 0 & & \mathbf{I}_{N_s}s_{cxs}^2 & 0 \\ 0 & 0 & 0 & 0 & \mathbf{I}_N s_e^2 \end{Bmatrix}$$

Where  $N_d$  is the number of dams;  $N_s$  is the number of herd-year-season x sire interaction;  $N$  is number of records;  $A$  is the numerator relationship matrix among animals in the pedigree file and  $I$  is an identity matrix of appropriate order. Furthermore,  $s_a^2, s_m^2, s_{am}^2, s_c^2, s_{cxs}^2$  and  $s_e^2$  are direct genetic variance, maternal genetic variance, direct genetic by maternal genetic covariance, permanent maternal environmental variance, sire by herd-year-season variance and residual error variance respectively and from which the phenotypic variance ( $s_p^2$ ) can be derived. The heritability estimates were obtained as  $h_a^2 = s_a^2/s_p^2$  (the direct heritability);  $h_m^2 = s_m^2/s_p^2$  (the maternal heritability) and where  $s_p^2 =$

phenotypic variance, which is the sum of all variance components to be estimated by the model of analysis. The total heritability was estimated as  $h^2_t = (s^2_a + 0.5s^2_m + 1.5s^2_{am}) / s^2_p$  according to Willham (1972).

Comparison of the different models was made using the likelihood ratio tests. Suitability of the model was considered when a significant ( $P < 0.05$ ) increase in the log likelihood occurred when adding an additional random effect. The differences between pairs of models were tested against the Chi-square distribution with degrees of freedom being the difference in number of variance or (co)variance components in the model. Based on that, Swalve (1993) suggested that a likelihood ratio test can be applied by multiplying the difference by -2 and comparing it to a Chi-square test statistics with one degree of freedom.

In the bivariate analyses, Models 9 and 7 were used to estimate the (co)variance structure of BWT with WWT and YWT whereas Model 9 was used for BWT and FWT. Similar Models were also used for WWT versus YWT and FWT, except YWT and FWT, where Models 9 and 4 were used. The bivariate or two-trait models include all components of the single trait model for the analyzed traits.

Annual genetic trends were also calculated for each trait by regressing mean breeding values of calves on birth year. All figures were plotted considering the animals born before 1985 as “base animals”, which means they were all joined in a unique group. That applies to figures about genetic and maternal trends. Genetic and maternal genetic trends were plotted as the average of the breeding values obtained from the solutions of the animal model equations against the year of birth.

### 3.3 Results and Discussion

#### 3.3.1 Non-genetic factors

The analysis of variance indicated that all fixed effects (sex, herd-year-season, age of the dam and age of the calf had a significant effect ( $p < 0.0001$ ) on all traits, except BWT for where age was excluded. Means, standard deviation (SD) and coefficient of variation (CV %) for different traits are presented in the Table 3.3. The weight increased as the number of days increased and male calves were heavier than females in all cases. Males were on average 1.77 kg heavier than females for BWT, 16.76 kg for WWT, 44.32 kg for YWT and 65.17 kg for FWT.

The coefficient of variation increased from birth weight to yearling weight and then decreases for final weight. Mostert *et al.* (1998) reported similar means for BWT ( $32.5 \pm 4.8$ ) and WWT ( $212.5 \pm 37.9$ ) while the means for YWT ( $270.0 \pm 50.6$ ) and FWT ( $353.1 \pm 67.7$ ) were slightly higher than the current study. Higher mean weights obtained in postweaning growth traits could be due to the age range classification used in this study.

Vargas *et al.* (1999) also reported similar means of  $32.3 \pm 0.39$  kg for BWT and 212, 192 as well as 211 kg for WWT in first, second and third parity for Brahman cattle in Florida, which indicates that the average performance of Brahman in South African could be similar to that of the breed in the United States. The weights of Brahman cattle presented in this study are slightly higher than those found in the literature. Plasse *et al.* (2002a) reported average weights of 28.2 kg, 157.5 kg and 292.4 kg for BWT, WWT and FWT respectively, in Brahman cattle in Venezuela. Magnabosco *et al.* (2002) found a comparatively low mean weight of 320.7 kg for Brahman cattle in Mexico at an average age of 17 months.

**Table 3.3** Descriptive statistics for BWT, WWT, YWT and FWT

Trait	Mean (kg)	SD (kg)	CV (%)	R <sup>2</sup> (%)	Min (kg)	Max (kg)
BWT	32.32	4.12	10.43	37.64	20	45
WWT	212.24	37.45	11.46	60.99	97	327
YWT	274.49	53.72	11.77	67.21	110	443
FWT	360.83	62.30	10.42	69.09	170	560

SD- Standard deviation, CV- Coefficient of variation, R<sup>2</sup>- Coefficient of determination, Min- Minimum and Max- maximum

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

The estimated (co)variance components and genetic parameters using univariate analysis for BWT, WWT, YWT and FWT are presented in Tables 3.4 - 3.7. Model nine fitted BWT best, while Model 7 was the best for WWT, YWT and FWT. A detailed discussion of the results of the variance components for BWT, WWT, YWT and FWT presented below as well as a summary of literature estimates (Table 3.1) above.

#### 3.3.2.1 Birth weight

Estimates of (co)variance components and genetic parameters for BWT of South African Brahman cattle are presented in Table 3.4, using nine different animal models (Model 1 to Model 9). Model 9, which included the covariance between direct and maternal effects resulted in a significantly better fit in comparison to the rest of the models when judged by the Log likelihood (Log L). The Model included a maternal genetic effect and a herd-year-season x sire interaction effect, while it excluded the permanent maternal environmental variance and the covariance between the animal effects. The inclusion of herd-year-season x sire interaction effect in the model affected all (co)variance components estimated, and also the correlation between animal effects. The inclusion of this component reduced both additive genetic variance and permanent maternal environmental variance.

Direct heritability estimated in Model 9 was 0.28, which is slightly higher than the estimates reported for Boran (*Bos indicus*) cattle in Ethiopia (0.24) (Haile-Mariam & Kassa-Mersha, 1995) and those reported for Nellore (*Bos indicus*) cattle in Brazil (0.22) (Eler *et al.*, 1995). The estimate of direct heritability in this study is below the weighted mean estimate (0.31) for several different beef breeds (Koots *et al.*, 1994a). It is also, less than the direct heritability (0.33) reported for *Bos taurus* and *Bos taurus* x *Bos indicus* crosses of (Meyer, 1992) and for Brahman cattle (0.33) in Venezuela (Plasse *et al.*, 2002a). Maternal heritability for birth weight was 0.11, this is slightly higher than the estimates of 0.08 and 0.07 obtained by Plasse *et al.* (2002a; 2002b) and the 0.09 obtained by Haile-Mariam & Kassa-Mersha (1995), but slightly below the estimates of 0.12 obtained by Eler *et al.* (1995). Diop & Van Vleck (1998) reported estimates of 0.04 for maternal heritability, which is far lower than estimates found in this study. The lower or higher direct heritability estimates of authors mentioned above is possibly due to the fact that they did not add sire x herd-year-season interaction effects to their models.

Generally, the maternal heritability is less than literature estimates of Meyer, (1992) and Koots *et al.* (1994a), which were 0.17 and 0.14 for mean estimates for *Bos taurus* and zebu crosses as well as the weighted means from different beef breeds, respectively. The correlation between direct and maternal genetic effects was -0.36. A similar estimate of -0.37 and -0.35 for Brahman cattle were obtained by Plasse *et al.* (2002a). This is also similar to the weighted mean obtained for several beef breeds by Koots *et al.* (1994a), but higher than the estimates of -0.55 for Boran (Haile-Mariam & Kassa-Mersha, 1995) and -0.72 for Nellore cattle (Eler *et al.*, 1995). It is, however, less than the estimate of -0.17 obtained for Gobra cattle by Diop & Van Vleck (1998). In contrast, Plasse *et al.* (2002b) found a positive estimate of 0.22 for the correlation between direct and maternal genetic effects for BWT.

The sire x herd-year-season interaction effect contributed 0.05 to the total phenotypic variance. Van Niekerk (2003) obtained the an estimate of 0.01 for BWT in Nguni cattle for sire x herd-year-season interaction as a proportion of the total variance. The total

heritability was 0.24. This is less than the estimates of 0.28 and 0.30 obtained by Plasse *et al.* (2002a; 2002b) in Brahman cattle. However, lower estimates of 0.10, 0.17 and 0.08 were found by the following authors: Eler *et al.* (1995) for Nellore, Haile-Mariam & Kassa-Mersha (1995) for Boran and Diop & Van Vleck (1998) for Gobra, respectively.

**Table 3.4** (Co) variance components and genetic parameters for BWT with the “best” model in bold

Item	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8	<b>Model 9</b>
$\sigma_a^2$	4.39	3.53	3.34	4.20	3.34	4.26	2.81	3.44	<b>3.37</b>
$\sigma_m^2$	-	-	0.64	1.52	0.35	1.05	0.35	0.796	<b>1.29</b>
$\sigma_c^2$	-	0.63	-	-	0.35	0.46	0.43	0.49	-
$\sigma_e^2$	7.56	7.64	7.79	7.34	7.72	7.24	7.66	7.35	<b>7.46</b>
$\sigma_{cxs}^2$	-	-	-	-	-	-	0.62	0.57	<b>0.57</b>
$\sigma_p^2$	11.95	11.79	11.78	11.88	11.77	11.88	11.88	11.94	<b>11.93</b>
SE	0.096	0.095	0.095	0.102	0.094	0.102	0.097	0.102	<b>0.102</b>
$\sigma_{am}$	-	-	-	-1.18	-	-1.12	-	-0.71	<b>-0.75</b>
$r_{am}$	-	-	-	-0.47	-	-0.53	-	-0.43	<b>-0.36</b>
SE	-	-	-	0.045	-	0.05	-	0.068	<b>0.06</b>
$h_a^2$	0.37	0.30	-	0.35	0.28	0.36	0.24	0.29	<b>0.28</b>
SE	0.013	0.014	-	0.22	0.02	0.022	0.016	0.022	<b>0.02</b>
$h_m^2$	-	-	0.05	0.13	0.03	0.088	0.03	0.07	<b>0.11</b>
SE	-	-	0.007	0.01	0.01	0.02	0.01	0.02	<b>0.014</b>
$c^2$	-	0.05	-	-	0.03	0.04	0.04	0.042	-
SE	-	0.0064	-	-	0.0098	0.0108	0.0099	0.0106	-
$\sigma_{cxs}^2 \setminus \sigma_p^2$	-	-	-	-	-	-	0.053	0.048	<b>0.05</b>
SE	-	-	-	-	-	-	0.00445	0.0045	<b>0.0045</b>
$h_t^2$	0.37	0.30	0.30	0.27	0.30	0.26	0.25	0.23	<b>0.24</b>
Log L	-72401.8	-72362.3	-72351.8	-72325.4	-72356.3	-72318.	-72249.2	-72238.1	<b>-72225.5</b>

$\sigma_a^2$ - direct additive genetic variance;  $\sigma_m^2$ - maternal additive genetic variance;  $\sigma_c^2$ - permanent environmental variance;  $\sigma_e^2$ - environmental variance/error variance;  $\sigma_{cxs}^2$ - contemporary group by sire variance;  $\sigma_p^2$ - phenotypic variance;  $\sigma_{am}$ - covariance between direct additive and maternal additive genetic effects;  $r_{am}$ - genetic correlation between direct additive and maternal additive effects;  $h_a^2$ - direct additive heritability;  $h_m^2$ - maternal additive heritability;  $c^2$ -  $\sigma_c^2 \setminus \sigma_p^2$ ;  $h_t^2$ - total heritability =  $[(\sigma_a^2 + 0.5\sigma_m^2 + 1.5\sigma_{am}) / \sigma_p^2]$ ; Log L- log likelihood

### 3.3.2.2 Weaning weight

In Table 3.5 the estimates of the (co)variance components and genetic parameters for WWT are presented. Unlike birth weight, Model 7 was the best model fitted for WWT. It is an animal model, which included direct genetic effect, maternal genetic effects, permanent maternal environmental effects and sire x herd-year-season interaction. The covariance between direct and maternal genetic effects was, however, excluded from the model. An additional random effect of herd-year-season x sire interaction effects in most cases greatly affects the estimates of all variance components under the model in question. The direct additive genetic variance is inflated when herd-year-season x sire interaction is not included in the model (Table 3.5). This is supported by Notter *et al.* (1992), Naser *et al.* (1996) and Meyer (1997) who stressed that fitting a sire x herd-year or season interaction have a consistent large and significant effect as an additional random factor. The same authors also shown that the fitting of a sire x herd-year-season interaction effect resulted in dramatic increases in the likelihood, accompanied by a reduction in the magnitude of the covariance between animal and maternal effects as well as direct and maternal heritability.

The direct heritability from the univariate analyses was 0.14. This is similarly to the results obtained by Eler *et al.* (1995) in Nellore cattle (Table 3.1). Plasse *et al.* (2002a; 2002b) found low direct heritability estimates of 0.07 and 0.08 for Brahman cattle, whereas Diop & Van Vleck (1998) found a higher estimate of 0.20 for Gobra (*Bos indicus*) cattle. The maternal heritability of 0.06, and was in agreement with the estimates of 0.05 and 0.06 reported for Gobra (Diop & Van Vleck, 1998) and Boran (*Bos indicus*) cattle in Ethiopia (Haile-Mariam & Kassa Mersha, 1995).

The weighted means for direct and maternal heritabilities in the review by Koots *et al.* (1994a) were 0.24 and 0.13, which is higher than the estimates found in this study. Mercadante & Lobo (1997) also found higher estimates of 0.29 and 0.13 for direct genetic and maternal genetic effects for Nellore heifers in Brazil. Estimates found by different authors (Table 3.1) are different from the estimates found in Table 3.5, possibly



because they excluded sire x herd-year-season interaction effect in their models. Nesor *et al.* (1996) obtained a value of 0.13 for direct heritability and 0.13 for maternal heritability in Bosmara cattle for models that included both permanent maternal and herd-year-season x sire interaction effect.

The calculated proportional permanent maternal environmental effect (0.07) was less than the results obtained by Meyer (1992) for Hereford cattle (0.23), as well as the value of 0.14 reported by both Eler *et al.* (1995) and Haile-Mariam & Kassa-Mersha (1995). Diop & Van Vleck (1998) obtained a value of 0.12 while a value of 0.16 and 0.14 was reported by Plasse *et al.* (2002a; 2002b) in two studies of different Brahman herds in Venezuela. Based on results in the present study, it appears that the permanent maternal environmental effects are not as important as the maternal genetic effects in the South African Brahman. This is in contrast to the results of Haile-Mariam & Kassa-Mersha (1995) in Boran cattle, Robinson (1996a) for Angus in Australia and Plasse *et al.* (2002a; 2002b) for Brahman cattle who found that the contribution of permanent maternal environmental effects and maternal genetic effects are equally important.

Sire x herd-year-season interaction as a proportion of the phenotypic variance equals 0.06. In comparison to the Bosmara cattle, Nesor *et al.* (1996) obtained a slightly high estimate of 0.084, whereas Nephawe *et al.* (1999) obtained the values ranging from 0.063 to 0.138 among the regions for WWT as a proportion of the total variance. Van Niekerk (2003) obtained an estimate of 0.086 in Nguni cattle for sire x herd-year-season interaction as proportion of the total variance. Estimates of 0.033 to 0.062 and 0.03 as proportion of the total variance was obtained by Notter *et al.* (1992) in Australian Angus and Lee & Pollak (1997) in American Simmental cattle respectively using models that included sire x year interaction effects for WWT.

The total heritability was 0.17, which is similar to the estimate of 0.16 and higher than estimate of 0.12 both found by Plasse *et al.* (2002a; 2002b). Eler *et al.* (1995) and Diop & Van Vleck (1998) also found low estimates of 0.14 and 0.12 respectively, whereas a higher estimate of 0.21 was obtained by Haile-Mariam & Kassa-Mersha (1995).

**Table 3.5** (Co) variance components and genetic parameters for WWT with the “best” model in bold

Item	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8	Model 9
$\sigma_a^2$	214.94	126.04	110.13	126.41	113.65	128.19	<b>84.86</b>	85.38	85.68
$\sigma_m^2$	-	-	67.64	91.57	29.96	47.53	<b>35.66</b>	36.22	78.01
$\sigma_c^2$	-	65.27	-	-	40.89	41.01	<b>39.92</b>	39.92	-
$\sigma_e^2$	414.69	421.97	436.09	426.87	427.80	419.99	<b>422.96</b>	422.69	436.24
$\sigma_{cxs}^2$	-	-	-	-	-	-	<b>35.34</b>	35.27	40.33
$\sigma_p^2$	629.6	613.3	613.9	615.2	612.3	613.6	<b>618.6</b>	618.7	635.1
SE	5.34	5.04	5.02	5.12	5.01	5.09	<b>5.16</b>	5.17	5.34
$\sigma_{am}$	-	-	-	-29.61	-	-23.16	-	-0.83	-5.14
$r_{am}$	-	-	-	-0.275	-	-0.297	-	-0.015	-0.063
SE	-	-	-	0.063	-	0.076	-	0.123	0.093
$h_a^2$	0.34	0.21	0.18	0.21	0.19	0.21	<b>0.14</b>	0.14	0.135
SE	0.013	0.014	0.014	0.017	0.014	0.017	<b>0.014</b>	0.016	0.016
$h_m^2$	-	-	0.11	0.15	0.05	0.08	<b>0.06</b>	0.06	0.123
SE	-	-	0.007	0.013	0.011	0.016	<b>0.011</b>	0.014	0.012
$c^2$	-	0.11	-	-	0.07	0.07	<b>0.06</b>	0.06	-
SE	-	0.007	-	-	0.011	0.011	<b>0.011</b>	0.011	-
$\sigma_{cxs}^2   \sigma_p^2$	-	-	-	-	-	-	<b>0.06</b>	0.060	0.064
SE	-	-	-	-	-	-	<b>0.005</b>	0.005	0.005
$h_t^2$	0.34	0.21	0.23	0.21	0.21	0.19	<b>0.17</b>	0.17	0.18
Log L	-140066	-139917	-139938	-139931	-139917	-139912	<b>-139794</b>	-139795	-140229

See **Table 3.4** for abbreviations.

### 3.3.2.3 Yearling weight

Estimates of (co)variance components and genetic parameters for YWT using nine different models are shown in Table 3.6. The same model (Model 7) fitted for WWT proved to be also the best model for YWT. Estimates of maternal heritability were smaller than direct heritabilities for all the models. Including sire x herd-year-season interaction effects in the model for YWT like BWT and WWT improved the fit of the model and affected the estimates of the variances (Table 3.6). A reduction in genetic and permanent maternal environmental variances were observed when fitting this component.

Direct heritability was 0.13, which is lower than estimates reported by (Eler *et al.*, 1995). However, higher estimates were reported by Haile-Mariam & Kassa-Mersha (1995) and Diop & Van Vleck (1998) (Table 3.1). Maternal genetic effects seem to be important even at this age, where the maternal heritability value was almost equal to that of WWT (Table 3.6). This is somewhat surprising, because the animals no longer depend on their dam and the weight at this age should reflect only direct effects of the genes for growth except for the carry over effects from WWT. However, maternal effects on post weaning growth traits of beef cattle have been found in some other breeds as well.

The maternal heritability for YWT was 0.05. A similar estimate was observed in Boran cattle (Haile-Mariam & Kassa-Mersha, 1995), whereas higher estimates were reported by Eler *et al.* (1995) and Diop & Van Vleck (1998). This might be explained by the fact that for animals raised on pasture with little or no supplementary feeding, the length of time between weaning and yearling may not be enough to buffer maternal effects existing at weaning (Eler *et al.*, 1995). This explanation is probably true for the situation where calves are weaned in the dry season and often lose weight before the next rainy season as observe in Gobra cattle (Diop & Van Vleck, 1998). The total heritability was 0.16. This is

below 0.22, 0.24 and 0.18 reported by Eler *et al.* (1995), Haile-Mariam & Kassa-Mersha (1995) and Diop & Van Vleck (1998), respectively.

The permanent maternal environmental effects amounted to 0.03 of the total phenotypic variance, which is slightly higher than the 0.02 reported for Nelore cattle by Eler *et al.* (1995), but similar to the 0.03 estimated for both the Australian Angus and zebu crosses (Meyer, 1992). Five percent was reported for Hereford cattle (Meyer, 1992), Boran cattle (Haile-Mariam & Kassa-Mersha, 1995) and Gobra cattle (Diop & Van Vleck, 1998). Estimate of the sire x herd-year-season interaction as proportion of the total variance amounted to 0.06. Similarly, Van Niekerk (2003) in Nguni cattle obtained an estimate of 0.0657 for sire x herd-year-season as a proportion of the total variance. However, Lee *et al.* (2000) obtained a slightly lower estimate of 0.05 for sire x region x year-season interaction as a proportion of the total variance in Korean Native cattle.

**Table 3.6** (Co) variance components and genetic parameters for YWT with the “best” model in bold

Item	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8	Model 9
$\sigma_a^2$	292.09	209.96	194.17	226.46	194.47	226.71	<b>144.23</b>	155.41	155.17
$\sigma_m^2$	-	-	76.39	136.36	50.08	106.78	<b>57.07</b>	76.57	107.54
$\sigma_c^2$	-	71.32	-	-	29.79	28.20	<b>31.24</b>	29.79	-
$\sigma_e^2$	777.00	774.62	785.89	769.66	781.06	763.47	<b>769.75</b>	764.59	769.05
$\sigma_{cxs}^2$	-	-	-	-	-	-	<b>67.12</b>	64.79	64.68
$\sigma_p^2$	1069	1056	1056	1059	1055	1058	<b>1069</b>	1069	1070
SE	11.18	10.83	1081	11.02	10.79	11.00	<b>11.29</b>	11.33	11.34
$\sigma_{am}$	-	-	-	-71.96	-	-67.57	-	-21.71	-26.032
$r_{am}$	-	-	-	-0.41	-	-0.43	-	-0.19	-0.20
SE	-	-	-	0.077	-	0.082	-	0.14	0.12
$h_a^2$	0.27	0.20	0.18	0.21	0.18	0.21	<b>0.13</b>	0.15	0.15
SE	0.016	0.017	0.017	0.021	0.017	0.021	<b>0.018</b>	0.021	0.021
$h_m^2$	-	-	0.072	0.129	0.048	0.10	<b>0.05</b>	0.072	0.101
SE	-	-	0.009	0.018	0.015	0.023	<b>0.014</b>	0.021	0.017
$c^2$	-	0.068	-	-	0.028	0.027	<b>0.029</b>	0.028	-
SE	-	0.009	-	-	0.014	0.015	<b>0.014</b>	0.014	-
$\sigma_{cxs}^2   \sigma_p^2$	-	-	-	-	-	-	<b>0.06</b>	0.06	0.06
SE	--	-	-	-	-	-	<b>0.007</b>	0.007	0.007
$h_t^2$	0.2732	0.20	0.22	0.18	0.21	0.17	<b>0.16</b>	0.15	0.16
Log L	-91185.1	-91151.5	-91147.5	-91139.0	-91132.4	-91137.4	<b>-91075.3</b>	-91074.5	91076.3

See **Table 3.4** for abbreviations.

#### 3.3.2.4 Final weight

Estimates of (co)variance and genetic parameters for FWT using nine models are presented in Table 3.7. Model 7, which was the best model for analyzing WWT and YWT, was also the best model for FWT. Surprisingly, maternal effects still exist for FWT. This was not expected as maternal effects are expected to fade out because animals no longer depend on their dams. The maternal heritability estimates was 0.03, a similar estimate of 0.028 was reported in Hereford cattle (Meyer, 1992). Plasse *et al.* (2002a; 2002b) reported the maternal heritabilities of 0.08 and 0.04 for 548 days weight in Brahman cattle. A very high estimate of maternal heritability of 0.16 was obtained in Gobra cattle (Diop & Van Vleck, 1998).

The direct heritability for FWT of South African Brahman cattle was 0.18. Diop & Van Vleck (1998) and Plasse *et al.* (2002a; 2002b) found a lower direct heritabilities of 0.15, 0.13 and 0.16 respectively. The total heritability was 0.20. The permanent maternal environmental as a proportion of the total variance was estimated to be 0.04, a similar estimate was observed by Diop & Van Vleck (1998) and a lower estimate of 0.01 was obtained by Plasse *et al.* (2002a). An estimate of 0.06 was obtained for sire x herd-year-season interaction as proportion of the total variance. Van Niekerk (2003) found an estimate of 0.05 for sire x herd-year-season interaction as a proportion of the total variance in the Nguni cattle, which is slightly below the estimate found in the present study. Contrary to these findings, Lee *et al.* (2000) found no contribution of this aspect to the total variance in Korean Native cattle.

**Table 3.7** (Co) variance components and genetic parameters for FWT with the “best” model in bold

Item	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8	Model 9
$\sigma_a^2$	448.18	349.42	333.24	360.27	335.41	362.81	<b>265.74</b>	265.36	262.71
$\sigma_m^2$	-	-	80.29	125.54	38.83	77.73	<b>46.68</b>	46.129	100.45
$\sigma_c^2$	-	79.69	-	-	46.92	48.13	<b>55.81</b>	55.82	-
$\sigma_e^2$	1009.03	1011.89	1026.90	1011.75	1018.51	1003.72	<b>1006.96</b>	1007.16	1016.77
$\sigma_{cxs}^2$	-	-	-	-	-	-	<b>80.46</b>	80.52	79.82
$\sigma_p^2$	1457	1441	1440	1443	1440	1442	<b>1456</b>	1456	1456
SE	20.38	19.90	19.87	20.19	19.86	20.19	<b>20.55</b>	20.59	20.58
$\sigma_{am}$	-	-	-	-54.78	-	-50.19	-	0.67	-3.69
$r_{am}$	-	-	-	-0.26	-	-0.30	-	0.006	-0.023
SE	-	-	-	0.13	-	0.15	-	0.30	0.21
$h_a^2$	0.31	0.24	0.23	0.25	0.230	0.25	<b>0.18</b>	0.18	0.18
SE	0.02	0.02	0.03	0.03	0.03	0.03	<b>0.03</b>	0.03	0.03
$h_m^2$	-	-	0.06	0.09	0.03	0.05	<b>0.03</b>	0.03	0.07
SE	-	-	0.013	0.025	0.022	0.031	<b>0.022</b>	0.029	0.024
$c^2$	-	0.05	-	-	0.033	0.033	<b>0.038</b>	0.038	-
SE	-	0.012	-	-	0.022	0.022	<b>0.03</b>	0.022	-
$\sigma_{cxs}^2   \sigma_p^2$	-	-	-	-	-	-	<b>0.06</b>	0.06	0.05
SE	-	-	-	-	-	-	<b>0.009</b>	0.009	0.009
$h_t^2$	0.31	0.24	0.36	0.24	0.25	0.23	<b>0.20</b>	0.20	0.21
Log L	-53792.5	-53782.0	-53782.3	-53781.1	-53781.2	-53780.1	<b>-53752.2</b>	53752.2	-53753.6

See **Table 3.4** for abbreviations.

### **3.3.2.5 Correlations among traits**

The estimates of the correlations from the bivariate analyses between the four growth traits in the South African Brahman cattle (i.e. BWT versus WWT, YWT, FWT and WWT versus YWT, FWT and YWT versus FWT) are given in Tables 3.8-3.9 as well as literature estimates in Table 3.10 below. The effect of the bivariate animal models in comparison to the univariate on the magnitude of the estimates of genetic parameters, and on the estimation of breeding values between traits is quite evident. As can be seen in Tables 3.8-3.9 heritabilities are higher in comparison to that of the univariate analysis (Tables 3.3 – 3.6). Genetic correlations between the traits studied were favourable, indicating that selection for one trait will improve others in a desired direction, helping the breeding process as a whole.



**Table 3.8** Estimates of (co) variance components from the bivariate analyses of BWT, WWT, YWT and FWT

TRAIT 1	BW	BW	BW	WW	WW	YW
TRAIT 2	WW	YW	FW	YW	FW	FW
(Co) variance's components						
$\sigma^2_{a1}$	3.2756	3.2576	3.1324	92.1260	93.4686	210.138
$\sigma^2_{a12}$	11.1297	8.5246	19.0427	105.973	145.114	223.634
$\sigma^2_{a2}$	97.5790	129.770	405.779	160.096	285.202	210.138
$\sigma^2_{m1}$	1.285	1.304	0.2753	56.2583	43.2871	67.1023
$\sigma^2_{m12}$	-	-	3.306	66.5062	59.9146	67.2328
$\sigma^2_{m2}$	43.92	81.65	58.3401	81.2705	77.4730	68.3611
$\sigma^2_{c1}$	-	-	-	15.4854	27.8514	-
$\sigma^2_{c12}$	20.185	8.5534	-	-	-	-
$\sigma^2_{c2}$	21.4404	2.8620	-	-	-	-
$\sigma^2_{e1}$	7.2026	7.2089	7.4921	389.837	-	718.456
$\sigma^2_{e12}$	5.331	8.7493	5.5436	265.407	270.498	457.44
$\sigma^2_{e2}$	373.376	682.544	885.279	710.291	934.141	892.141
$\sigma^2_{cxs1}$	0.4935	0.4958	-	25.9979	29.1235	5.8779
$\sigma^2_{cxs2}$	26.5264	0.4958	0.3376	41.6904	36.58	
$\sigma^2_{p1}$	7.140	9.330	10.90	538.2	552.6	995.7
$\sigma^2_{p12}$	19.09	21.17	27.89	437.9	475.5	748.3
$\sigma^2_{p2}$	502.1	889.1	1349	951.7	1333	1338
$\sigma^2_{am12}$	-2.468	-1.396	-	-	-	-
$\sigma^2_{am21}$	-0.4061	1.048	-	-	-	-

See **Table 3.4** and **Table 3.10** for other abbreviations

**Table 3.9** Genetic parameters and correlation between traits

TRAIT 1	BW	BW	BW	WW	WW	YW
TRAIT 2	WW	YW	FW	YW	FW	FW
$h^2_{a1}$	0.46	0.35	0.29	0.17	0.17	0.21
SE	0.1182	0.1126	0.0158	0.0155	0.0155	0.0187
$h^2_{m1}$	0.18	0.14	0.03	0.11	0.08	0.07
SE	0.0526	0.0486	0.0101	0.0097	0.0103	0.0121
$h^2_{a2}$	0.19	0.15	0.30	0.17	0.60	0.28
SE	0.0273	0.0351	0.0540	0.0184	0.0714	0.0277
$h^2_{m2}$	0.09	0.09	0.04	0.09	0.16	0.05
SE	0.0262	0.0336	0.0258	0.0092	0.0332	0.0127
$r_{a12}$	0.62	0.47	0.52	0.88	0.91	0.83
SE	0.08	0.11	0.09	0.04	0.04	0.03
$r_{m12}$	-	-	0.77	1.00	0.99	0.99
SE	-	-	0.36	0.04	0.08	0.0861
$r_{a1m2}$	-0.4204	-0.4241	0.05170	-	-	-
SE	0.0568	0.0567	0.0879	-	-	-
$r_{a2m1}$	-0.0147	0.0065	0.7682	-	-	-
SE	0.0203	0.0202	0.3633	-	-	-
$r_{p12}$	0.29	0.23	0.22	0.57	0.55	0.64
SE	0.04	0.05	0.02	0.005	0.007	0.006
$r_{e12}$	0.09	0.12	0.07	0.47	0.45	0.56
SE	-	0.02	0.03	0.009	0.001	0.01
$c^2_1$	-	-	-	0.03	0.05	-
SE	-	-	-	0.008	0.009	-
$c^2_2$	0.04	0.003	-	-	-	-
SE	0.02	0.03	-	-	-	-
$\sigma^2_{cxs1} \setminus \sigma^2_{p1}$	0.07	0.053	0.0310	0.05	0.053	0.006
SE	0.0176	0.0172	0.0104	0.005	0.0046	0.0098
$\sigma^2_{cxs2} \setminus \sigma^2_{p2}$	0.05	0.0826	-	0.044	0.077	-
SE	0.0091	0.0143	-	0.0056	0.0190	-
Log L	-121 286	-102 720	-88 631.8	-214 091	-181 704	-129 956

$r_{a12}$ - direct additive genetic correlation,  $r_{m12}$ - maternal additive genetic correlation;  $ra1m2$  and  $ra2m1$ - genetic correlation between direct effect of one trait and maternal effect of the other and vice versa,  $r_{p12}$ - phenotypic correlation;  $r_{e12}$  - residual correlation, See **Table 3.4** for other abbreviations

**Table 3.10** Summary of literature estimates of across trait correlations from bivariate and multivariate analysis of growth traits

Source	Breed	Country	Model	$r_a$	$r_m$	$r_c$	$r_e$	$r_p$
<b>Birth weight and weaning weight</b>								
Koots <i>et al.</i> , 1994a	Bt & Bi	Canada	BAM	0.50	-	-	-	-
Meyer, 1994	Angus	Australia	BAM	0.761	0.297	1.00	0.384	0.510
Meyer, 1994	Zebu cross	Australia	BAM	0.793	0.970	0.895	0.780	0.799
Eler <i>et al.</i> , 1995	Nellore	Brazil	MAM	0.23±0.13	0.21±0.15	0.27±0.21	0.14±0.03	0.15±0.05
H-Mariam & K-Mersha, 1995	Boran	Ethiopia	BAM	0.373	0.082	-	0.174	0.236
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.72	0.50	-	-	-
Plasse <i>et al.</i> , 2002a	Brahman	Venezuela	BAM	0.64	0.74	-0.04	0.28	0.33
Plasse <i>et al.</i> , 2002b	Brahman	Venezuela	BAM	-	-	-	-	-
<b>Birth weight and yearling weight</b>								
Koots <i>et al.</i> , 1994a	Bt & Bi	Canada	BAM	0.55	-	-	-	0.38
Meyer, 1994	Angus	Australia	BAM	0.700	-0.126	0.790	0.484	0.449
Meyer, 1994	Zebu cross	Australia	BAM	0.79	0.97	0.89	-	-
Eler <i>et al.</i> , 1995	Nellore	Brazil	MAM	0.16±0.06	0.18±0.10	0.45±0.25	0.12±0.03	0.14±0.04
H-Mariam & K-Mersha, 1995	Boran	Ethiopia	BAM	0.445	-0.033	-	0.069	0.188
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.52	0.32	-	-	-

Table 3.10 continues....

Source	Breed	Country	Model	$r_a$	$r_m$	$r_c$	$r_e$	$r_p$
<b>Birth weight and final weight</b>								
Meyer, 1994	Angus	Australia	BAM	0.589	-	-	0.327	0.486
Mostert <i>et al.</i> , 1998	Brahman	S.A	MAM	0.53	0.82	-	-	-
Plasse <i>et al.</i> , 2002a	Brahman	Venezuela	BAM	0.35	0.74	-0.59	0.28	0.33
<b>Weaning weight and yearling weight</b>								
Koots <i>et al.</i> , 1994b	Bt & Bi	Canada	BAM	0.79	-	-	-	0.65
Meyer, 1994	Angus	Australia	BAM	0.952	0.998	1.00	0.597	0.743
Meyer, 1994	Zebu cross	Australia	BAM	0.793	0.970	0.895	0.780	0.799
Eler <i>et al.</i> , 1995	Nellore	Brazil	MAM	0.74±0.05	0.84±0.07	0.80±0.17	0.64±0.01	0.70±0.01
H-Mariam & K-Mersha, 1995	Boran	Ethiopia	BAM	0.750	0.214	0.995	0.027	0.377
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.82	0.85	-	-	-
<b>Weaning weight and final weight</b>								
Meyer, 1994	Angus	Australia	BAM	0.863	-	0.653	0.712	-
Meyer, 1994	Zebu cross	Australia	BAM	0.690	0.988	0.910	0.629	0.656
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.79	0.77	-	-	-
Plasse <i>et al.</i> , 2002a	Brahman	Venezuela	BAMMP	0.64	0.96	1.00	0.72	0.74
Plasse <i>et al.</i> , 2002b	Brahman	Venezuela	BAM	0.66	0.70	1.00	0.57	0.64

Table 3.10 continues....

<b>Yearling weight and final weight</b>								
Meyer, 1994	Angus	Australia	BAM	0.986	-	-	0.753	0.867
Meyer, 1994	Zebu cross	Australia	BAM	0.926	0.966	1.00	0.689	0.767
Mostert <i>et al.</i> , 1998	Brahman	S. A.	MAM	0.90	0.69	-	-	-

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BAM - Bivariate animal models, Bt & Bi- *Bos taurus* and *Bos indicus*, MAM- Multitrait animal models, S.A. - South Africa

The genetic correlation between BWT and WWT estimate for additive direct effects was quite large (0.62). Plasse *et al.* (2002a) reported a similar genetic correlation of 0.64 and a high maternal genetic correlation of 0.74. The residual and phenotypic correlations between the BWT and WWT (Table 3.10) were less than the estimates (0.28 and 0.33) reported by Plasse *et al.* (2002a). Haile-Mariam & Kassa-Mersha (1995) found correlations of 0.37, 0.08, 0.17 and 0.23 for direct additive, maternal genetic, residual and phenotypic correlations, respectively, which are all below the estimate found in this study. In a multivariate analysis, Eler *et al.* (1995) estimated the correlations of 0.23, 0.21, 0.14 and 0.15 for the respective direct additive genetic, maternal genetic, residual and phenotypic correlations between BWT and WWT.

The additive genetic correlation between BWT and YWT (Table 3.9) was similar to the estimate of 0.45 reported for Boran cattle (Haile-Mariam & Kassa-Mersha, 1995), whereas the maternal genetic correlation (-0.033), residual correlation (0.07) and phenotypic correlation (0.19) were below the estimate found in this study. Eler *et al.* (1995) also found a lower direct genetic correlation (0.16) and high maternal genetic correlation (0.45) with almost equal residual (0.12) and low phenotypic correlation in a multivariate analysis between BWT and YWT. For BWT and FWT the direct genetic and maternal genetic correlations were 0.52 and 0.77, which is higher than estimates of 0.35 and 0.74 reported for Brahman cattle (Plasse *et al.*, 2002a). However, the residual correlation and phenotypic correlation (Table 39) were less than estimate of 0.28 and 0.33 (Plasse *et al.*, 2002a).

The direct additive genetic correlation (Table 3.9) between WWT and YWT was 0.88. This is slightly higher than the mean genetic correlation of 0.81 given in the review of Koots *et al.* (1994b) and the estimate of 0.75 obtained by Haile-Mariam & Kassa-Mersha (1995). The maternal genetic correlation was at unity between these two traits, whereas the residual (0.47) and phenotypic correlations (0.59) were higher than the estimates of -0.21, 0.027 and 0.38 for maternal, residual and phenotypic correlations reported in Boran (Haile-Mariam & Kassa-Mersha, 1995). The estimates of the correlations for WWT and FWT were close to unity (0.91), lower estimates of 0.64 and 0.66 were found by Plasse *et*

*al.* (2002a; 2002b). The value found in this study is again higher than the estimate of (0.69) reported for crossbred Australian zebu cattle by Meyer (1994). The maternal genetic correlation was also at unity. Similar observations have been made by other authors (Meyer, 1994; Plasse *et al.*, 2002a). Plasse *et al.* (2002b) reported an estimate of 0.70 for maternal genetic correlation between WWT and FWT in another Brahman herd in Venezuela. The estimate of the residual correlation was 0.44, which is less than the estimates of 0.72 and 0.57 reported by Plasse *et al.* (2002a; 2002b) also in Brahman cattle. The phenotypic correlation between WWT and FWT was 0.55, which is less than the estimates of 0.74 and 0.64 reported for Brahman cattle (Plasse *et al.*, 2002a; 2002b).

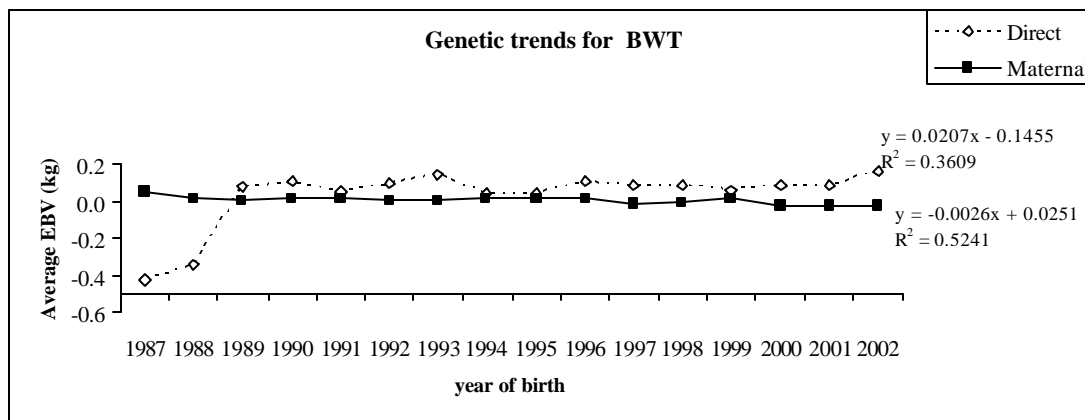
Results of the bivariate analyses for YWT and FWT are shown in Table 3.9. Estimates of the direct genetic correlations between these two weights were large (0.83). Similarly, Koots *et al.* (1994b) reported average estimates of direct additive correlation between yearling weight and post weaning weight gain to be 0.81. Estimates of the maternal genetic correlation between the two traits effects of dams for two-trait analyses was highly positive or at unity (0.99), but have little meaning because the permanent maternal environmental effect was not considered in the bivariate analysis, even though it was significant in univariate analysis. Another factor is that the effect of herd-year-season x sire was ignored for FWT between these two traits. Mostert *et al.* (1998) found a maternal genetic correlation of 0.69 between YWT and FWT whereas the direct genetic correlation was 0.90 in a multitrait analysis in South African Brahman cattle.

### **3.3.2.6 Direct and maternal genetic trends**

The direct and maternal genetic trends for 16 years (1985-2002) are presented in Figures 3.2 to 3.5. Only the results of the univariate analysis obtained under the best models for BWT, WWT, YWT and FWT were used for the estimation of the genetic trends. Genetic trends were all positive, except the maternal genetic trend for BWT, but the magnitudes varied considerably among the traits. The direct genetic changes for BWT calculated from the annual means of the estimated breeding values were not significant and were

close to zero. The genetic trend shows no increase over the years (Figure 3.2). A similar pattern for the maternal genetic trend was observed.

The direct genetic trends for BWT shows an average increase of 0.0207 kg per year, with an annual average decrease of 0.0026 kg for the maternal genetic trend and not different from zero ( $P>0.05$ ). The direct breeding value of BWT is important because it can have a major influence on calving ease. Plasse *et al.* (2002a; 2002b) obtained progress of 0.061 and 0.044 for direct and maternal genetic effects as well as 0.004 and 0.033 respectively, for BWT in the univariate analysis. Haile-Mariam & Philipson (1996), found a decrease in direct genetic effects of 0.002 while a progress in maternal genetic effects of 0.003 kg per annum for BWT in Boran cattle.



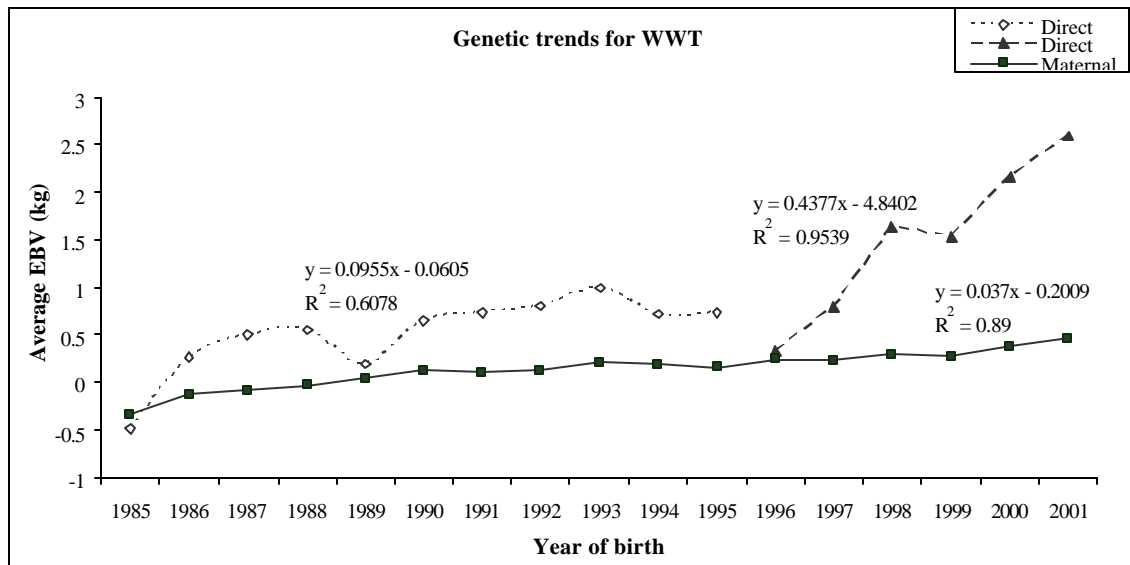
EBV - Estimated breeding value

**Figure 3.2** Annual direct and maternal genetic trends (kg) for BWT

Direct genetic progress for WWT was 0.1 kg per year from 1985 to 1995 and 0.4 kg per year from 1996 to 2001, whereas the maternal genetic progress was 0.04 kg per year (Figure 3.3). In 1998 a sharp increase in the direct genetic trend was observed without any effect on the maternal genetic trend. Progress obtained in the last 6 years could be mainly due to the implementation of the decentralised technical service in 1990, the Brahdex in 1991 and Elite Register Programme in 1992 (Champer *et al.*, 1998). The programmes were base on subjective evaluation and objective measurements as a supporting breed improvement services. A similar trend in direct and maternal genetic



effects for WWT was observed by Plasse *et al.* (2002a) in a Brahman herd. The annual direct and maternal genetic trends for 30 years were 0.126 kg and 0.044 kg respectively. Diop & Van Vleck (1998) did not observed any significant trend for direct and maternal genetic effects in Gobra cattle for WWT. Crump *et al.* (1997) obtained direct genetic trends in Simmental (0.84 kg), Limousin (0.59 kg), Charolais (0.84 kg), South Devon (0.57 kg) and Aberdeen (1.33 kg) in the United Kingdom (UK) for a period of 12 years.



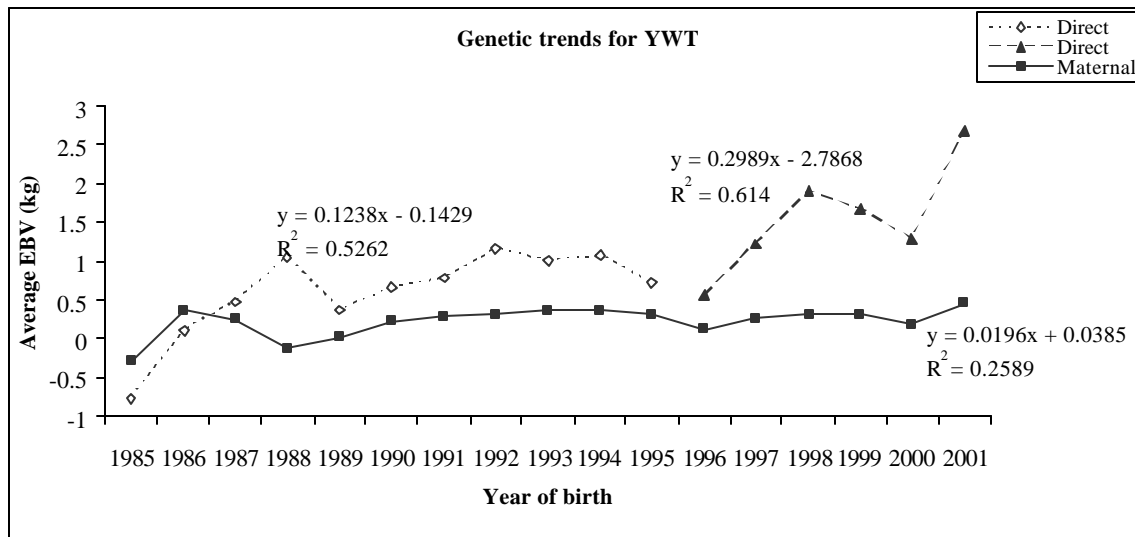
See Figure 3.2 for abbreviation

**Figure 3.3** Annual direct and maternal genetic trends (kg) for WWT

A similar pattern in WWT was also observed in YWT. However, there is a slight difference in the trends from 1996 - 2001. Despite, the differences in the genetic trends during the last 6 years for WWT, YWT and to a lesser extent in FWT (Figure 3.3 – Figure 3.5), the direct genetic progress have been much higher during this years in comparison to the progress obtained between 1985 and 1995. The progress is probably due to implementation of programmes (discussed above) or possibly selection methods or a change in management decisions.

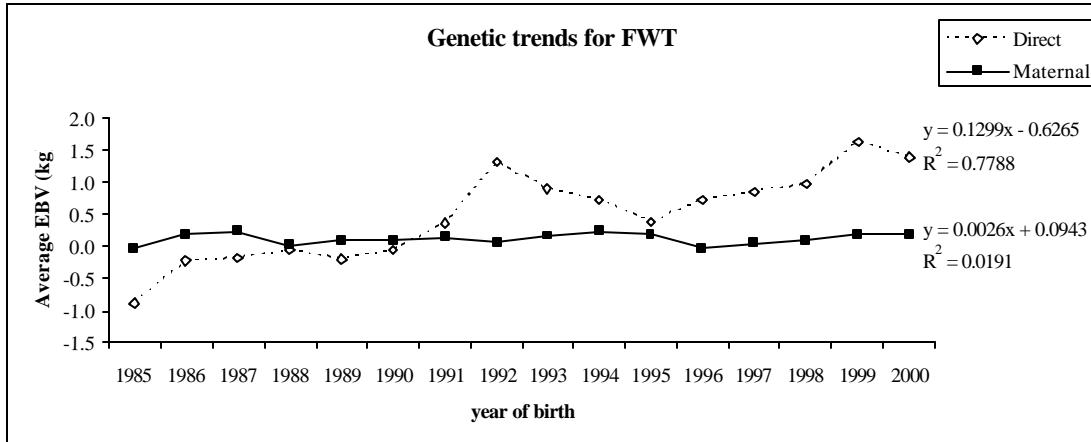
Progression in direct genetic effects for YWT (Figure 3.4) was 0.1 kg per year from 1985 – 1995 and 0.3 kg per year from 1996 – 2001. The genetic progress obtained from 1996 – 2001 for YWT was therefore mainly a correlated response, due to selection in WWT.

This is to be expected, as the direct genetic correlation between the two traits was 0.88. The maternal genetic progress for YWT was 0.008 kg per year and not significantly ( $P>0.05$ ) different from zero. Progress obtained in direct and maternal genetic effects (Figure 3.5) for FWT was 0.13 and 0.003 kg per year, respectively. Haile-Mariam & Philipson (1996) found a progress of 0.22 kg for direct genetic effects and a decrease in maternal genetic effects of 0.005 kg per year for YWT in Boran cattle. Plasse *et al.* (2002a; 2002b) found progress of direct and maternal genetic effects of 0.486 kg and 0.251 kg as well as 0.263 kg and 0.251 kg per year for FWT in Brahman cattle. In UK, Crump *et al.* (1997) calculated the direct genetic progress in YWT to be 1.527, 1.042, 1.586, 1.192 and 2.493 kg for Simmental, Limousin, Charolais, South Devon and Aberdeen Angus respectively. Diop & Van Vleck (1998) also did not observed any significant trend in YWT and FWT in Gobra cattle for direct and maternal genetic effects.



See Figure 3.2 for abbreviation

**Figure 3.4** Annual direct and maternal genetic trends (kg) for YWT



See Figure 3.2 for abbreviation

**Figure 3 5** Annual direct and maternal genetic trends (kg) for FWT

### 3.3 Conclusions

The results presented in this study identify not only the models of choice to be used in analyses of growth traits but also showed the influence of permanent maternal environment and maternal effects on the estimation of (co)variance components in the South African Brahman breed. Low to intermediate estimates of heritability indicate that genetic changes in animal weight can be accomplished by selection. Results indicate no antagonistic relationships among animal effects at weaning, yearling and final weights. Negative genetic (co)variances between direct and maternal effects for birth weight indicate a genetic antagonism between these sources and should be considered in selection procedures, as they can influence long term genetic trends.

Estimates of phenotypic and genetic correlation between growth traits were moderate to high. Selection would be effective for either weight and would produce important correlated responses for all measurements of growth. Genetic trends were positive but very low for all traits, except the maternal genetic trend for birth weight, which was negative.

## Chapter 4

### Inbreeding in the South African Brahman breed

#### 4.1 Introduction

Accurate selection of genetically superior animals for the next generation is of the utmost importance for genetic improvement (Fernandez & Toro, 1999). According to Weigel (2001), recent advances in genetic selection programmes have greatly increased the annual response to selection, but rates of inbreeding have likewise increased substantially. The response to short term selection depends on the intensity and accuracy of selection (Tseveenjav *et al.*, 2001). In the short term, breeding companies requires a sufficiently high rate of gain to either maintain or strengthen their competitive position (Bijma *et al.*, 2001). On the other hand, in the long-term selection depends on how much variability is maintained and how much inbreeding depression occurs over generations and therefore on the effective population size (Bijma *et al.*, 2001; Tseveenjav *et al.*, 2001). According to Burrow (1998), Fernandez & Toro (1999), Bijma *et al.* (2001) and Tseveenjav *et al.* (2001) the avoidance of inbreeding depression either in short or long-term selection programmes is important and requires restriction of the rate of inbreeding.

Maintaining genetic variation within a breed is important for its commercial future as stipulated by Tseveenjav *et al.* (2001). It has been evident in several studies that the loss of variation within a breed can cause inbreeding depression, hence a decline in the performance of the traits of economic importance (Burrow, 1993; Pariacote *et al.*, 1998; Lutaaya *et al.*, 1999; Weigel, 2001; Tseveenjav *et al.*, 2001). In order to understand the impact that inbreeding is having on populations, several studies have been focused on the current levels of inbreeding in various populations (Nomura *et al.*, 2001) in Japanese Black cattle and (Weigel, 2001) in dairy cattle to mention a few. The exclusion of closely related mating reduces the average coefficients of inbreeding throughout, but it does not affect the rate at which inbreeding accumulates (Falconer & Mackay, 1996).

Inbreeding does not affect all species or traits with the same intensity. Generally, inbreeding affects reproductive traits and survival more than traits with higher heritabilities such as growth (Burrow, 1993; 1998; McDaniel, 2001; Fioretti *et al.*, 2002). In addition, inbreeding level in livestock populations, despite intensive selection on closely related animals is usually not too high (Burrow, 1993; 1998; McDaniel, 2001; Szwaczkowski *et al.*, 2004). In the South African Brahman cattle the question might arise as to what level inbreeding has accumulated. Pedigree information dated back to animals born in the late 1955s were kept by the South African Brahman Cattle Breeders' Society. Therefore, inbreeding relative to as far as 1955 can be estimated. The current study is a continuation of investigation conducted by Kluyts (1993), who studied the inbreeding effects of the same breed, but emphasising only on two particular years (1967 and 1982). The main objective of the study was to obtain insight in the current status of inbreeding in the South African Brahman cattle breed.

## **4.2 Materials and Methods**

### **4.2.1 Data and statistical analysis**

Data utilised in this study consists of 181 508 edited pedigree records of animals born between 1955 and 2002. Edits included checking for (i) individuals that appear before parents, (ii) individuals that appeared as both a sire and a dam, (iii) individuals that were parents of themselves and (iv) duplicate records. Individuals that appear before parents were re-numbered to give them a new identity, the re-numbering was done considering the date of birth of the animals and the digits of new identity not to exceed its offspring as parent. The individuals that appear as both a sire and a dam were also re-number and given a new identity. Duplicate records and individuals that were parents of themselves were deleted. There were animals without a sire or dam or both in the total pedigree records.

Inbreeding coefficients for individual animals were calculated by inverting the diagonal of the inverse relationship matrix,  $\mathbf{A}^{-1}$  using the MTFNRM programme of the

MTDFREML package (Boldman *et al.*, 1995). The pedigree records (181 508) were used to calculate inbreeding coefficients, which yielded 189 706 records (Table 4.1).

Inbreeding coefficients for individual animals were extracted from the additive relationship matrix to estimate inbreeding depression in each trait. The available edited records for growth traits used to estimate inbreeding depression were 41 509, 37 705, 22 682 and 13 055 for birth weight (BWT), weaning weight (WWT), yearling weight (YWT) and final weight (FWT) respectively as shown previously in Chapter 3 (Table 3.2). Inbreeding depression was estimated as the regression of performance on individual and dam inbreeding coefficients using an animal model. In the model, individual and dam inbreeding coefficients were fitted as covariates. The univariate animal model was applied using the ASREML software programme of Gilmour *et al.* (1999) assuming the model

$$Y = X\beta + Z_1a + Z_2m + Z_4hyss + e;$$

where  $Y$  = vector of observations

$\beta$  = vector of fixed effects influencing the trait,

$a$  = vector of direct additive effects,

$m$  = vector of random maternal genetic effects,

$hyss$  = vector of additional random effects of herd-year-season x sire interaction,

$X$ ,  $Z_1$ ,  $Z_2$ ,  $Z_3$  and  $Z_4$  are incidence matrices relating observations to their respective fixed and random effects and  $e$  = is a vector of residuals.

The covariance between direct and maternal genetic effects was included in the covariance matrix for the random effects ( $a$  and  $m$ ). The vector of fixed effects included sex, herd-year-season, management group, age of the calf, age of the dam and direct and maternal inbreeding by first considering linear effects and secondly, linear and quadratic effects in the same model. The effects of permanent maternal environment were excluded from the final model due to singularities. A singularity is reported in ASREML when there is either a linear dependence in the design matrix and therefore no information left to estimate the corresponding effect or no data for that fixed effects, because ASREML handles singularities by setting them to zero and ignoring equations detected as aliases.

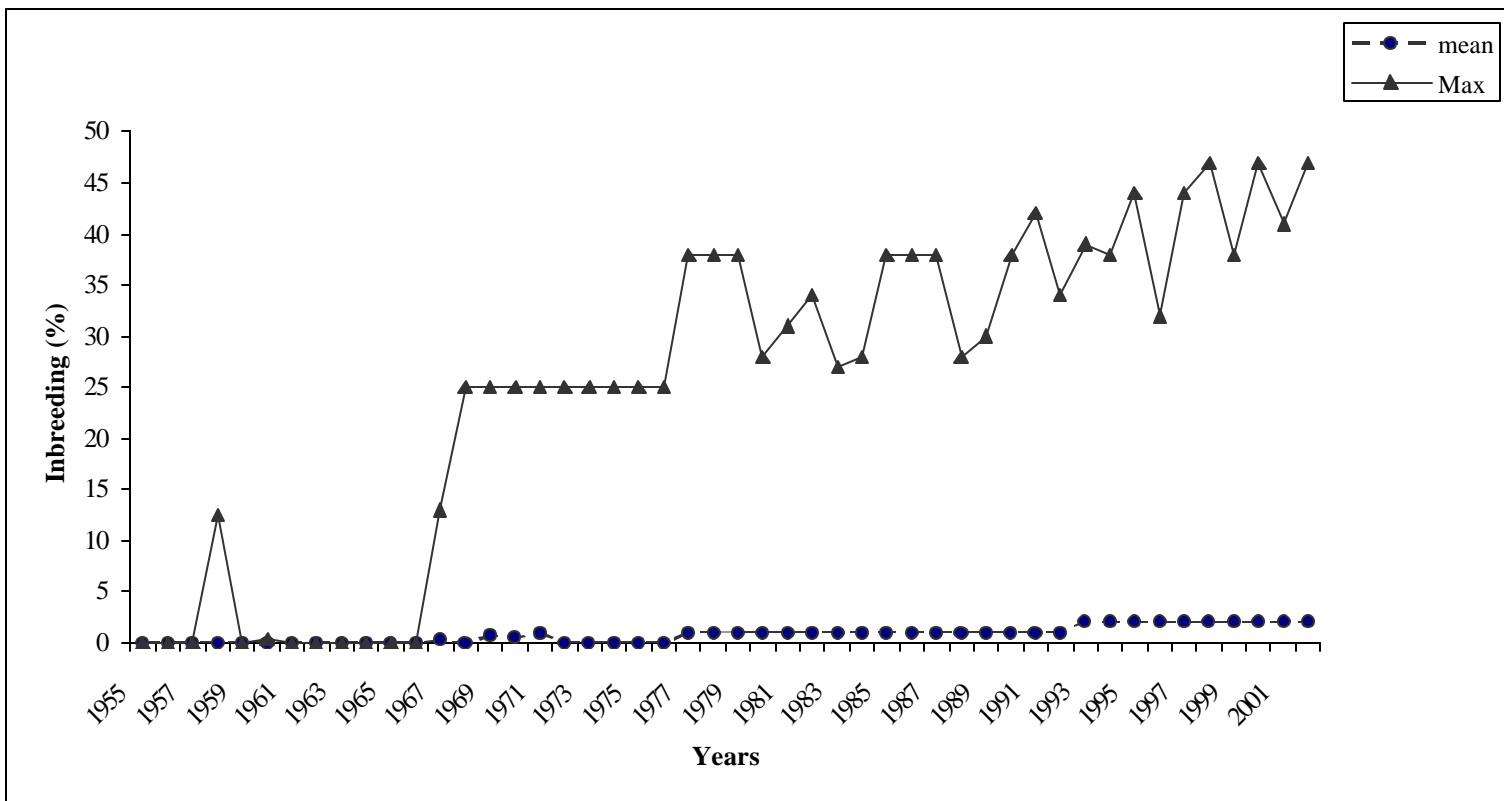
### 4.3 Results and Discussion

Table 4.1 shows the number of animals and average inbreeding coefficients of South African Brahman cattle from 1955 to 2002. Figure 4.1 illustrates the annual mean and maximum level of inbreeding. The annual mean inbreeding coefficients were found to range from 0 to 2% over years. The minimum level of inbreeding was zero over the years and not shown in the trend, whereas the maximum level of inbreeding per year fluctuates between 0% and 47%. The fluctuation is caused by some individuals that are highly inbred within the herds. However, the average inbreeding with the herds in all years was also low and almost equal to the population average. All most 60% of the animals were non inbred, whereas at least 40% of animals were inbred with an average inbreeding coefficient of 1%. The level of inbreeding for the inbred animals was 3% with a maximum inbreeding coefficient of 47%. Kluyts (1993) obtained inbreeding coefficients of 2.2 and 1.28% for 1967 and 1982 respectively in the two sample years in the South African Brahman cattle.

**Table 4.1** Description of the population

	N	Decimals
Total number of animals including base animals	189 706	
Pedigree	181 508	
Non inbred	112 398	0.593 (Of the total)
Inbred animals	77 308	0.408 (Of the total)
Average <b>F</b> of		
all animals		0.01
inbred animals		0.03
Maximum <b>F</b>		0.47

N? number of animals, F? inbreeding coefficients



**Figure 4.1** Annual mean and maximum individual level of inbreeding (%)



Regression coefficients of BWT, WWT, YWT and FWT on inbreeding of individual and dam for a change of 1% in inbreeding are shown in Table 4.2. The results suggest that a 1% increase in inbreeding of the individual does not significantly ( $P>0.05$ ) decrease BWT and WWT. On the other hand, the maternal inbreeding suggests that a 1% increase in inbreeding of the dam will increase BWT with 0.004 kg and decrease WWT with 0.241 kg.

The observed significant and positive effect of dam inbreeding on BWT is in contrast to some literature estimates (see Table 4.3). However, a positive significant effect of dam inbreeding is in agreement to the results found in the literature review of Burrow (1993) using regression techniques. Haile-Mariam & Philpson (1996) suggest that if the estimated inbreeding level of dams is less than 1%, its effect on performance is probably low. The authors also found that if the inbreeding of the individual and its dam are correlated, the inclusion of both might cancel each other. Similarly, Pariocote *et al.* (1998) stated that the inconsistency of the effect of dam inbreeding on BWT might be associated with an interaction between levels of dam inbreeding and individual inbreeding. This is probably true for the present study as the average inbreeding levels of the population is 1%.

Considering YWT and FWT linearly, the increase of inbreeding correspond to a decrease in performance, except maternal performance in FWT which showed a significant ( $P<0.001$ ) increase (Table 4.2). The results obtained are consistent with the literature estimates in Table 4.3 for YWT ranging from a decrease of 0.35 kg to 1.068 kg per 1% change in inbreeding of the individual among the breeds. On the other hand, the range for FWT was from 1.068 kg to 1.493 kg decrease per 1% change in inbreeding of the individual. The effect of dam inbreeding, however, ranged from a decrease of 0.0129 kg to 0.21 kg and an increase of 1.03 kg for YWT and FWT respectively.

**Table 4.2** Regression coefficients of the traits on inbreeding of an individual and dam for a change of 1% increase in inbreeding

Trait	No.	Regression coefficients			
		Linear			
		Individual		Dam	
BWT (kg)	41 509	-0.016*		0.004***	
WWT (kg)	37 705	-0.418*		-0.241***	
YWT (kg)	22 682	-0.689**		-0.120***	
FWT (kg)	13 055	-0.957***		0.011***	
		Linear	Quadratic	Linear	Quadratic
BWT (kg)	41 509	-0.001***	-0.081***	0.028***	-0.130***
WWT (kg)	37 705	-0.461***	0.254***	-0.483***	1.490***
YWT (kg)	22 682	-0.851***	0.973***	-0.179***	0.364***
FWT (kg)	13 055	-1.361***	2.449***	0.236***	-1.368***

No. – Number, \*\*\*<sup>3</sup>P<0.0001, \*\*<sup>2</sup>P<0.01, \*<sup>1</sup>P>0.01

**Table 4.3** Summary of published estimates of inbreeding depression (linear) on growth traits in various beef cattle breeds

Trait	No.	Mean F	Breed	Individual	Significance	Dam	Significance	Source
BWT (kg)	6 137	0.144	Several beef breeds	-0.07	P<0.05	0.02	P<0.05	Burrow, 1993
	2 592	0.035	Tropical beef breeds	-0.038 ± 0.039	N.S	-	-	Burrow, 1998
	8 065	0.098	Hereford	-5.80 ± 1.14	P<0.05	-4.67 ± 1.31	P<0.05	Pariacote <i>et al.</i> , 1998
WWT (kg)	11 764	0.163	Several beef breeds	-0.34	P<0.05	-0.30	P<0.05	Burrow, 1993
	4 082	0.010	Boran	0.34 ± 0.11	P<0.05	-	-	Haile-Mariam & Philipson, 1996
	2 592	0.035	Tropical beef breeds	-0.720 ± 0.171	P<0.001	-	-	Burrow, 1998
	27 406	0.098	Hereford	-44.52 ± 6.59	P<0.05	-56.10 ± 8.41	P<0.05	Pariacote <i>et al.</i> , 1998
	57 172	0.016	Grey cattle	34.503, 85 <sup>MS</sup>	P<0.01	24,15 <sup>MS</sup>	N.S	Quiroz <i>et al.</i> , 2000
			Piedmontese cattle	-0.116	P<0.05	-0.0059	P<0.05	Fioretti <i>et al.</i> , 2002
YWT (kg)	1 812	0.131	Several beef breeds	-0.53	P<0.05	-0.21	P<0.01	Burrow, 1993
	2 417	0.010	Boran	-0.56 ± 0.14	P<0.05	-	-	Haile-Mariam & Philipson, 1996
	2 580	0.035	Tropical beef breeds	-1.068 ± 0.187	P<0.001	-	-	Burrow, 1998
	14 317		Grey cattle	3607942 <sup>MS</sup>	P<0.01	92695 <sup>MS</sup>	N.S	Quiroz <i>et al.</i> , 2000
	18 949 <sup>M</sup>	0.020	Piedmontese cattle	-0.874	P<0.05	-0.0286	P<0.05	Fioretti <i>et al.</i> , 2002
	36 184 <sup>F</sup>	0.017	Piedmontese cattle	-0.350	P<0.05	-0.0129	P<0.05	Fioretti <i>et al.</i> , 2002
FWT (kg)	1532	0.285	Several beef breeds	-1.30	P<0.05	1.03	P<0.05	Burrow, 1993
	2 557	0.035	Tropical beef breeds	-1.493 ± 0.237	P<0.001	-	-	Burrow, 1998

MS - Mean Square, N.S - Not significant, F - Female, M- Male,

Inbreeding effects estimated on the basis of two approaches (linear and quadratic) are listed in Table 4.2. In case of inbreeding depression (estimated *via* quadratic regression) were slightly higher in comparison to linear regression or linear regression together with quadratic (Table 4.2), however some estimates were positive. Similarly, Haile-Mariam & Philipson (1996) obtained a positive significant value (see Table 4.3) for WWT, which is similar to the observation found in this study. The effect of dam inbreeding was significant ( $P < 0.001$ ) for all traits. However, BWT and FWT were positive (estimated *via* linear regression), whereas negative quadratically. On the other hand, the estimates found in WWT and YWT (considering linear and quadratic simultaneously) were negative linearly and positive quadratically. Similarly, Quiroz *et al.* (2002) obtained a significant effect on individual inbreeding for WWT and YWT, but a non significant ( $P > 0.01$ ) effect on dam inbreeding also considering both linear and quadratic effects simultaneously.

#### **4.4 Conclusions**

The main conclusion to be drawn from the present study is that both the level and rate of inbreeding per year were low in the Brahman breed, and hence the effects of inbreeding on performance traits were relatively low, although significant. Nicholas (1989) suggested that inbreeding rates of up to 0.5% per year should be acceptable in animal breeding programmes. It appears that rates of inbreeding in the breed are well below the critical levels suggested by the author and consideration of additional methods to avoid inbreeding is not necessary at the present time. However, unless care is taken to restrict the accumulation of inbreeding in future generations, the level of inbreeding could be increased due to selection based on animal model BLUP of breeding values which is currently being practiced by Brahman breeders in South Africa (Anon, 2001).

## Chapter 5

### General conclusions and recommendations

The main objective of animal breeding is to obtain genetic improvement in economically important traits mainly by selection. Thus, the major objective of breeders of beef cattle seedstock has been to maximize the rate of genetic change. The same applies to animal breeding scientists, who have used the principle of maximising genetic change to predict the genetic value of individual animals or groups of animals (e.g. genetic trends) as well as to predict the consequences of natural selection and evolution. Developments in the areas of statistics and computing continue to enable more realistic modeling and analyses of traits.

Maximising the rate of genetic change can indeed be valuable, but only when selection objectives are valid. The genetic improvement of body weights (growth traits) should not be overemphasized in future studies. Though it is not part of the study, the emphasis should rather be on the genetic and environmental improvement of total cow efficiency under extensive conditions for sustainable production systems. Selection emphasis should also be given to adaptability and functional efficiency. These will include fertility, fleshing ability, calving ease, survivability and temperament. Although selection for growth traits will continue, it will not be growth rate as known in the past, it will be growth rate in relation to other economic important traits in the herd. However, selection will be difficult because most of the fitness, adaptability and functional efficiency traits are hard to measure and low in heritability.

Taking the above into account, conclusions can be drawn that selection for growth traits is not easy as it can be envisaged. These leads to the cautiousness about balanced selection programmes that must be developed and implemented in respect of the genetic variation in adaptive capacity of animals, as expressed in their resistance to disease, their reproductive rates and welfare. In order to define the desired genotype, knowledge on relevant genetic and biological relationships within the animal, the relationship between

the animal and the farm environment and constraints on the production system is needed. The availability of genetic parameters for South African Brahman cattle breeders will allow conducting a genetic evaluation of its herd. Application of BLUP methodology in these genetic evaluations will help accelerate genetic changes and further promote the economic important traits within the breed.

The results from univariate analyses have shown that the contribution of maternal and permanent maternal environment for WWT, YWT and FWT are small, indicating that these traits are more under direct gene control. BWT had a higher maternal heritability than all other traits studied. Furthermore, direct and maternal genetic effects for BWT were unfavourably correlated and they should be included in the genetic evaluation of BWT and WWT. Genetic trends for WWT, YWT, and FWT showed more or less the same tendencies.

There is no definitive agreement in the literature on the age at which maternal effects become important in beef cattle. Genetic parameters for South African Brahman cattle showed the importance of maternal effects at yearling weight even at 18 months of age (Final weight). Future selection plans need to consider maternal effects even for postweaning traits in order to optimize expected total response over the long term. Genetic correlations among traits were, in general, high and positive; indicating that selection for or against one trait would result in concomitant genetic change in the other traits.

Genetic improvements in cattle originate in seedstock herds. Inbreeding affects the rate of genetic improvement and hence a loss of genetic variation. The loss of variation will ultimately result in a decline in the genetic progress. The most important concept to remember about inbreeding is that practicing high level of inbreeding may result in a decline in average phenotypic merit for various economic important traits, more importantly to reproductive traits. Although the performance of inbred animals has been slightly decreased, the results obtained showed that inbreeding at present, is not a serious problem in the South African Brahman breed. Unless care is taken to restrict the

accumulation of inbreeding in future, the level of inbreeding could be increased due to selection based on animal model BLUP of breeding values which is currently being practiced by Brahman breeders in South Africa.

## Abstract

The present study was carried out to estimate genetic, phenotypic and environmental parameters for growth traits, genetic trends as well as the level of inbreeding in the South African Brahman breed. The data used were obtained from the South African Brahman Breeders' Society and consisted of pedigree information of 181 508 animals and 221 015 performance records, ranging from birth to 18-months weight /final weight collected between 1955 and 2002. Performance records available before editing as classified according to age ranges were birth weight (BWT) = 67 336, weaning weight (WWT) (80–300 days) = 62 159, yearling weight (YWT) (301-500 days) = 41 313 and final weight (FWT) (501-900 days) = 32 602. The linear animal model used included the fixed effects of contemporary group (herd-year-season), sex, management group, age of the calf, age of the dam. Direct genetic, maternal genetic and permanent maternal environmental as random effects as well as sire x herd-year-season interaction as an additional random effect. Preliminary analyses showed that all fixed effects had a significant ( $P < 0.0001$ ) effect on all traits studied.

Genetic parameters for growth traits were estimated using ASREML software by fitting univariate and bivariate animal models. Production traits considered after editing were BWT = 41 509, WWT = 37 705, YWT = 22 682 and FWT = 13 055 records collected between 1985 and 2002. The reason for using the data only from 1985 is that only a small number of records were recorded up to 1984. The direct heritability estimates of BWT, WWT, YWT and FWT were 0.28, 0.14, 0.14 and 0.18 respectively. The corresponding maternal heritability estimates were 0.11, 0.06, 0.05 and 0.03 respectively. The maternal



permanent environmental component due to the dam contributed 3 - 7 % of the total phenotypic variance of the traits under consideration. The corresponding contribution of sire x herd-year-season interaction ranges from 5 - 6%. The genetic correlation between animal effects was -0.36 for BWT, other traits studied did not show an antagonism between animal effects. The prospects of improvements of these traits by selection seem possible and the contributions of permanent maternal environmental effect are not equally important as maternal effects though the effects are small.

Estimates of phenotypic correlations were low to moderate (0.22 to 0.64), whereas genetic correlations were moderate to high (0.47 to 0.91). Genetic correlations between BWT and WWT, YWT and FWT were 0.62, 0.47, and 0.52 respectively. The corresponding genetic correlations between direct and maternal effects of the same trait ( $r_{am}$ ,  $r_{ma}$ ) were (-0.4204, -0.014), (-0.4241, 0.0567) and (0.05170, 0.0879) respectively. Genetic correlations between WWT and postweaning weights were 0.88 and 0.91 for YWT and FWT respectively. The corresponding maternal correlation was at unity. Lastly, the genetic and maternal correlation between YWT and FWT were 0.83 and unity, respectively.

Positive genetic trends were observed for all traits except for the maternal genetic trend for BWT, which had a slightly negative slope. Direct genetic progress for BWT was 0.0207 kg/year (1987-2002), whereas progress for WWT was 0.1kg/year (1985-1995) and 0.4 kg /year (1996-2001). Progression in direct genetic effect for YWT was 0.1kg/year (1985- 1995) and 0.3 kg/year (1996-2001) whereas progress for FWT was 0.13 kg/year (1985-2001). The maternal genetic trends were -0.003, 0.04, 0.008 and

0.003 kg/year for BWT, WWT, YWT and FWT, respectively. Genetic progress was in general low over the years for all traits. Therefore, estimation based on BLUP of breeding values may be more important in the future and should be considered to maximise opportunities for genetic change.

Inbreeding level and its possible influence on growth traits of the South African Brahman cattle were investigated. Inbreeding coefficients were calculated by inverting the diagonal of the inverse relationship matrix using the MTDFNRM program of the MTDFREML package. Inbreeding depression was estimated as the regression of performance on individual and dam inbreeding coefficients using an animal model. The mean inbreeding of the population was very low (0.01) with an average of (0.03) for inbred animals. Although regression coefficients of BWT, WWT, YWT and FWT on inbreeding of animal and dam were significant for all traits, the results showed that inbreeding at present is not a serious problem in the South African Brahman breed.

**Keywords:** Brahman, growth traits, genetic and phenotypic parameters, inbreeding, genetic trends

## Opsomming

Die doel van hierdie studie was om genetiese, fenotipiese en omgewingsparameters vir groei-eienskappe vir die Suid-Afrikaanse Brahmanras te beraam, asook genetiese tendense en die vlak van inteling by dié ras. Data met stamboominligting van 181 508 diere en 221 015 prestasie-rekords wat wissel van geboorte- tot 18-maandegewig / finale gewig, versamel tussen 1955 en 2002, is van die Suid-Afrikaanse Brahmaantelersvereniging verkry. Onverwerkte prestasie data wat beskikbaar is, word geklassifiseer volgens die verskillende ouderdoms groepe. Hierdie prestasie data is as volg: geboortegewig (BWT) = 67 336, speengewig (WWT) (80-300 dae) = 62 159, jaar-oudgewig (YWT) (301-500 dae) = 41 313 en finale gewig (FWT) = 32 602. Die lineêre dieremodel wat gebruik is het die volgend vaste effekte ingesluit, kontemporêre groep (kudde-jaar-seisoen), asook geslag, bestuursgroep, ouderdom van die kalf, ouderdom van die moeder. Direkte genetiese, maternale genetiese en permanent maternale omgewing as toevallige effekte, so wel as vaar x kudde-jaar-seisoen interaksie as 'n addisionele toevallige effek. Voorlopige ontledings het getoon dat alle vaste effekte 'n hoogs betekenisvolle ( $P < 0.0001$ ) effek op alle eienskappe wat bestudeer is gehad het.

Genetiese parameters vir groei-eienskappe is beraam deur gebruik te maak van die ASREML- sagteware deur enkel- en twee-eienskapdieremodelle te pas. Na verwerking was die volgende aantal rekords beskikbaar, BWT = 41 509, WWT = 37 705, YWT = 22 682 en FWT = 13 055. Hierdie rekords is tussen 1985 en 2002 ingesamel is. Die rede waarom dat slegs vanaf 1985 af gebruik word is, dat daar min record was tot en met 1984. Die direkte oorerflikheidsberamings van BWT, WWT, YWT en FWT was 0.28, 0.14, 0.14 en 0.18, onderskeidelik. Die maternale permanente omgewingskomponent te wyte aan die moeder het 3 – 7 % van die totale fenotipiese variansie van die eienskappe wat oorweeg is, bygedra. Die ooreenstemmende bydrae van vaar x kudde-jaar-seisoen interaksie wissel van 5 – 6 %. Die genetiese korrelasie tussen diere-effekte was  $-0.36$  vir BWT, terwyl ander eienskappe wat bestudeer is nie 'n antagonisme tussen diere-effekte getoon het nie. Die verbetering van hierdie eienskappe deur seleksie blyk moontlik te

wees en die bydrae van permanente maternale omgewingseffek is nie van gelykstaande belang as maternale effekte nie, alhoewel die effekte klein is.

Beramings van fenotipiese korrelasies was laag tot middelmatig (0.22 tot 0.64), terwyl genetiese korrelasie middelmatig tot hoog was (0.47 tot 0.91). Genetiese korrelasies tussen BWT, WWT, YWT en FWT was 0.62, 0.47 en 0.52, onderskeidelik. Die ooreenstemmende genetiese korrelasie tussen direkte en maternale effekte van dieselfde eienskap ( $r_{am}$ ,  $r_{ma}$ ) was (-0.4204, -0.014), (-0.4241, 0.0567) en (0.05170, 0.0879), onderskeidelik. Genetiese korrelasies tussen WWT en na-speengewigte was 0.88 en 0.91 vir YWT en FWT, onderskeidelik. Die ooreenstemmende maternale korrelasie was een. Ten laaste was die genetiese en maternale korrelasie tussen YWT en FWT 0.83 en een, onderskeidelik.

Positiewe genetiese tendense is waargeneem vir alle eienskappe, behalwe vir die maternale genetiese tendens vir BWT, wat 'n effense negatiewe helling gehad het. Direkte genetiese vordering vir BWT was 0.0207 kg/jaar vir die jare 1987-2002, terwyl die vordering vir WWT vir die jare 1985-1995 was 0.1 kg/jaar en 0.4 kg/jaar vir die jare tussen 1996-2001. Vordering in direkte genetiese effekte vir YWT vir die jare 1985-1995 was 0.1 kg/jaar en 0.3 kg/jaar vir die jare tussen 1996-2001, terwyl die vordering vir FWT was 0.13 kg/jaar vir die jare tussen 1985-2001. Die maternale genetiese tendense was -0.003, 0.04, 0.008 en 0.003 kg/jaar vir BWT, WWT, YWT en FWT, onderskeidelik. Genetiese vordering oor die jare was oor die algemeen laag vir alle eienskappe. Daarom mag beraming gebaseer op BLUP van teelwaardes belangriker in die toekoms word en behoort dit oorweeg te word om geleenthede vir genetiese verandering te maksimeer.

Die intelingsvlak en die moontlike invloed daarvan op groei-eienskappe van die Suid-Afrikaanse Brahmanbeeste is ondersoek. Intelingskoëffisiënte is bereken deur die diagonaal van die inverse verhoudingsmatriks om te keer deur gebruik van die MTDENRM-program van die MTDREML-pakket. Inteeltverval was beraam as die regressie van prestasie op individuele en moeder-intelingkoëffisiënte deur gebruik van 'n

dieremodel. Die gemiddelde inteelt van die populasie was baie laag (0.01), met 'n gemiddelde van (0.03) vir ingeteelde diere. Alhoewel regressie-koëffisiënte van BWT, WWT, YWT en FWT op inteling van dier en moeder betekenisvol vir alle eienskappe was, het die resultate getoon dat inteling op hierdie stadium nie 'n ernstige probleem in die Suid-Afrikaanse Brahmanras is nie.

**Sleutelwoorde:** Brahman, groei-eienskappe, genetiese en fenotipiese parameters, inteling, genetiese tendense.

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