A GENETIC ANALYSIS OF BIOLOGICAL AND ECONOMIC EFFICIENCY OF POST-WEANING FEEDLOT PERFORMANCE IN BEEF CATTLE

BY

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"Declaration

I, the undersigned, hereby declare that the work contained in this thesis is my own original work and that I have not previously in its entirety or in part submitted it at any university for a degree.

ABSTRACT

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It is generally accepted that feed intake and growth (gain) are the most important economic components when calculating profitability in a growth test or feedlot. Feeding cost of animals is a major determinant of profitability in livestock production enterprises. Genetic selection to improve feed efficiency aims to reduce the cost of feeding in beef cattle production and thereby improve profitability.

The objective of this study was to define a clear selection objective to enable South African beef breeders and especially the feedlot industry to select for post-weaning growth or feedlot performance and to identify factors influencing profitability in a feedlot environment.

Because of the recording of individual feed intake and weight gain values in the South African Agricultural Research Councils' centralized growth tests, it was also possible to calculate a phenotypic value for feedlot profitability (R-value) for each bull tested in a centralized growth test. (Co)variances, using multitrait as well as random regression models, for and between feedlot profitability, weaning weight and other production, reproduction and efficiency traits were estimated. Residual feed intake (RFI) and feed conversion ratio (FCR) as efficiency traits were also compared to growth (average daily gain (ADG), weaning weight (WW) and shoulder height (SHD)), reproductive (scrotum circumference (SCR)) and profitability (feedlot profitability) traits measured in growth tests of young Bonsmara bulls.

Consequently, a single post-weaning growth selection index value based on the economic and breeding values of different selection criteria related to feedlot profitability was composed. (Co)variance components, heritabilities and genetic correlations for and between initial weight (IW), final weight (FW), total feed intake (FI) and shoulder height (SHD) were estimated through the use of multitrait restricted maximum likelihood (REML) procedures. These breeding values (EBVs) were then used in a selection index to calculate a single economical value for each animal.

This economical value is an indication of the gross profitability value or gross test value (GTV) of the animal in a post-weaning growth test.

The heritability estimate of 0.36 for R-value, obtained from the multitrait analysis, shows that this trait is genetically inherited and that it can be selected for. The heritability for R-value obtained from the single trait random regression model varied between 0.57 and 0.62. The genetic correlations between the R-value and the other traits, obtained from the multitrait analysis, varied from negligible to high. The heritability estimated for FCR was 0.34 and for RFI 0.31 with a genetic correlation estimate of 0.75 between the traits. The estimated genetic correlation between profitability (R-value) and FCR and RFI were –0.92 and –0.59, respectively. The genetic correlation estimate of –0.92 between FCR and R-value is largely due to the part-whole relationship between these two traits. This is also shown in their genetic trends. The genetic correlations and expected correlated responses between RFI and FCR with R-value suggest that indirect selection for R-value through the direct selection for FCR and/or RFI will result in slower genetic progress in R-value than direct selection for R-value. However, where the R-value cannot be calculated and/or where direct selection for R-value is not possible, it would be better to select indirectly for R-value through the use of FCR rather than RFI. Consequently, a regression equation was developed (with an R^2 of 0.82) to estimate a feed intake value for all performance-tested Bonsmara bulls which were group fed and whose feed intakes were unknown. These predicted feed intake values made it possible to calculate a feedlot or post-weaning growth profitability value (R-value) for all tested bulls even where individual feed intakes were unknown. Subsequently, an R-value for each bull was calculated in a favourable economic environment (FEE), an average economic environment (AEE) and in an unfavourable economic environment (UEE). The high Pearson and Spearman correlations between the EBVs based on AEE and the other two environments suggested that the average economic environment could be used to calculate EBVs for R-value or feedlot growth profitability. It is therefore not necessary to change the carcass, weaner or feed price on a regular basis to account for possible re-rankings based on R-value EBVs.

Heritabilities for IW, FW, FI and SHD were 0.41, 0.40, 0.33 and 0.51, respectively. The highest genetic correlations between these traits were the 0.78 (between IW and FW) and 0.70 (between FI and FW). GTV values varied between –R192.17 and R231.38, with an average of R9.31. The Pearson correlations between EBVs (for production and efficiency traits) and GTV range from -0.51 to 0.68. The lowest correlation (closest to zero) was 0.26 between the Kleiber ratio (KLB) and GTV. Correlations of 0.68 and –0.51 were estimated between average daily gain (ADG) and GTV and feed conversion ratio (FCR) and GTV, respectively. The heritabilities of the different traits included in the selection index suggest that it is possible to select for a GTV. The selection index

can benefit feedlotting in selecting offspring of bulls with high GTV values to maximize profitability.

The Pearson and Spearman correlations between the R-value EBVs and the index values (GTV) were very high (0.97). This high correlation of 97% indicates that it is not important which method is used to calculate a genetic post-weaning growth of feedlot profitability value. The selection index value is, however, more simplified than the feedlot profitability with less assumption. Therefore, it is recommended that the post-weaning selection index value be used as a selection objective in breeding programmes to improve post-weaning growth profitability rather than the more complex feedlot profitability value.

OPSOMMING

'N GENETIESE ANALIESE VAN DIE BIOLOGIESE EN EKONOMIESE DOELTREFFENTHEID VAN NASPEENSE GROEI IN VLEISBEESTE IN DIE VOERKRAAL

deur

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Dit word algemeen aanvaar dat voerinname en groei die twee ekonomies mees belangrike komponente in die berekening van 'n naspeense groei- of voerkraalwinsgewindheidswaarde is. Voerkostes is 'n bepalende faktor van winsgewindheid in enige lewendehawe boerderypraktyk. Seleksie om voerdoeltreffendheid te verbeter, verminder dus die voerkostes in vleisbeesproduksie en gevolglik 'n verhoging in die winsgewindheid.

Die doelwit van die studie was om faktore te identifiseer wat 'n invloed op winsgewindheid in die voerkraalomgewing het asook om 'n duidelike seleksiedoelwit te formuleer wat die Suid-Afrikaanse vleisbeestelers en veral die voerkraalbedryf instaat sal kan stel om vir naspeense groei-doeltreffendheid of voerkraalwinsgewindheid te selekteer.

As gevolg van die aantekening en rekordhouding van weeklikse individuele voerinnames en gewigstoenames van alle prestasiegetoetsde bulle, in 'n gesentraliseerde groeitoets deur die Suid-Afrikaanse Landbou Navorsingsraad getoets, was dit moontlik om vir elk van hierdie bulle 'n fenotipiese voerkraalwinsgewindheidswaarde (R-waarde) te kon bereken.

(Ko)variansies is vir en tussen voerkraalwinsgewindheid, speengewig en ander produksie-, reproduksie- en doeltreffendheidseienskappe bereken deur van meereienskap en ewekansige regressie modelle gebruik te maak. Twee doeltreffendheidseienskappe naamlik residuele voerinname (RFI) en voeromsetverhouding (FCR) is ook met groei (gemiddelde daaglikse toename (ADG), speengewig (WW) en skouerhoogte (SHD)), reproduksie (skrotumomvang (SCR)) en winsgewindheidseienskappe (voerkraalwinsgewindheid (R-waarde)) vergelyk, om sodoende te bepaal watter een die mees geskikte eienskap is om indirek vir voerkraalwinsgewindheid of winsgewindheid in naspeensegroei te selekteer. Gevolglik is 'n enkele seleksie-indeks vir naspeense

groei, gebaseer op teeltwaardes en ekonomiese waardes vir die verskillende eienskappe, wat 'n invloed op naspeense groei winsgewindheid het, gestruktueer.

(Ko)variansiekomponente, oorerflikhede en genetiese korrelasies vir en tussen begingewig (IW), eindgewig (FW), voerinname (FI) en skouerhoogte (SHD) is bereken deur van 'n meereienskap (REML) ontleding gebruik te maak. Hierdie teelwaardes (EBVs) is vervolgens in 'n seleksie-indeks gebruik om 'n enkele ekonomies of voerkraal-winsgewindheids seleksie-indekswaarde (GTV) vir elke dier te bereken. Hierdie ekonomiese waarde is 'n aanduiding van die bruto winsgewindheidswaarde of bruto toetswaarde (GTV) van die dier in 'n naspeentoets.

Die oorerflikheid, vanuit die meereienskapontleding vir R-waarde beraam, was 0.36. Hierdie oorerflikheid dui daarop dat die eienskap oorerflik is en dat dit wel moontlik is om daarvoor te selekteer. Die ooreflikhede van R-waarde, voorspel vanuit die enkeleienskap ewekansige regressie-ontleding varieer tussen 0.57 en 0.62. Die genetiese korrelasie tussen R-waarde en ander eienskappe, vanuit die meereienskap ontleding beraam, varieer tussen weglaatbaar klein tot hoog. Die oorerflikheid van FCR was 0.34 en van RFI 0.31 met 'n genetiese korrelasie van 0.75 tussen die twee eienskappe. Die genetiese korrelasie tussen R-waarde en FCR, en R-waarde en RFI was onderskeidelik -0.92 en -0.59. Die rede vir die hoë negatiewe genetiese korrelasie tussen R-waarde en FCR van -0.92 is omdat dieselfde komponente in die berekening van die twee eienskappe gebruik is. Dit word ook in die genetiese tendense weerspeël. Die genetiese korrelasies en verwagte gekorreleerde responsies tussen R-waarde en FCR, en tussen R-waarde en RFI dui daarop dat stadiger genetiese vordering verkry sal word in R-waarde deur direkte seleksie vir beide FCR en RFI as wat verkry sal word deur die direkte seleksie vir R-waarde. Wanneer 'n R-waarde egter nie bereken kan word nie of waar dit nie moontlik is om direk vir R-waarde te selekteer nie, sal vinniger genetiese vordering in R-waarde gemaak word deur die direkte seleksie vir FCR as vir RFI.'n Regressievergelyking is geformuleer (met 'n R^2 van 0.82) om vir alle prestasiegetoetsde bulle, waar bulle in 'n groep gevoer is en individuele voerinnames onbekend is, 'n voerinnamewaarde te voorspel. Hierdie voorspelde voerinnames maak dit moontlik om vir elke prestasiegetoetsde bul ,'n naspeengroei- of voerkraalwinswaarde (R-waarde) te bereken, al is hulle individuele voerinnames onbekend. Vervolgens is drie verskillende R-waarde vir vleisproduksie vir elke bul bereken naamlik, in 'n gunstige ekonomiese omgewing (FEE), 'n gemiddelde ekonomiese omgewing (AEE) en 'n ongunstige ekonomiese omgewing (UEE). Die hoë Pearson en Spearman korrelasies tussen die EBVs vir R-waarde, bereken in die AEE en die EBVs in die ander twee ekonomiese omgewings, dui daarop dat die AEE gebruik kan word om EBVs vir naspeense groei- of voerkraalwins te bereken. Dit is dus nie nodig om op 'n gereelde grondslag die karkasprys, lewendige speenkalfprys of die voerprys te verander nie.

Oorerflikhede, vanuit die meereienskap ontledings vir IW, FW, FI en SHD verkry, was onderskeidelik 0.41, 0.40, 0.33 en 0.51. Die hoogste genetiese korrelasies tussen die eienskappe was 0.78 tussen IW en FW en 0.70 tussen FI en FW. GTV indekswaardes varieer tussen –R192.17 en R231.38 met 'n gemiddelde waarde van R9.31. Die Pearson korrelasies tussen die EBVs van produksie- en doeltreffenheidseienskappe en GTV het tussen –0.51 en 0.68 gevarieer. Die korrelasie naaste aan zero, van 0.26, was die korrelasie tussen GTV en die Kleiber-verhouding. Die korrelasies tussen GTV en ADG, en GTV en FCR was onderskeidelik 0.68 en –0.51. Die oorerflikhede van die verskillende eienskappe wat in die seleksie-indeks ingesluit is, dui daarop dat die indekswaarde wel oorerflik is en dat seleksie hiervoor wel moontlik is. Hierdie indekswaarde kan deur die voerkraalindustrie gebruik word om nageslag van diere met hoë GTV waardes te selekteer om sodoende maksimum wins uit die voerkraal te genereer.

Die Pearson en Spearman korrelasies tussen R-waarde EBVs en die indekswaardes (GTV) was besonder hoog (0.97). Hierdie hoë korrelasie dui daarop dat dit geen verskil sal maak watter een van die twee metodes gebruik word in die berekeninge van 'n naspeense groei- of voerkraalwinswaarde nie. Die seleksie-indeks metode is egter minder gekompliseerd met minder aannames as in die geval van die rekeningkundige fenotipiese benadering (R-waarde). As gevolg hiervan, word die naspeense seleksie-indeks waardes (GTV) aanbeveel om te gebruik as 'n teeldoelwit in telingsprogramme om naspeense groei- of voerkraalwins geneties te verbeter, eerder as die meer gekompliseerde fenotipiese voerkraalwins (R-waardes) metode.

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CHAPTER 1

GENERAL INTRODUCTION

Beef producers are faced with constantly decreasing real returns due to the fact that input prices increase. The increasing input prices for beef production enterprises are a direct consequence of higher feed prices. The primary component of a balanced growth or feedlot diet and the most expensive component for beef cattle in South Africa is maize. The high maize prices are due to the fact that South Africa has a semi-arid climate and that returns per hectare of maize produced are lower than countries with more favourable conditions. This results in an increase in production costs and ultimately higher maize prices. To aggravate this situation the South African government does not subsidize input cost associated with agricultural enterprises. This has resulted in a negative growth rate in terms of the real price of beef over the last few decades. To ensure the same level of return on investment, greater levels of efficiency are thus required.

The National Beef Cattle Performance Testing Scheme of South Africa (NBCPTS) was started on the 4th of December 1959. The primary aim of the NBCPTS being to supply the beef industry with objective performance information in order to improve the biological and economic efficiency of beef production through genetic improvement and improved management practices.

The Animal Improvement Institute of the Agricultural Research Council manages the NBCPTS and is responsible for the technical control and supervision of the scheme. The NBCPTS can be subdivided into five different phases, namely Phases A, B, C, D and E. In Phase A all cows and their progeny are evaluated. This is done by recording cow weights, birth weights, weaning weights, and reproduction rate as well as cow efficiency. Post-weaning, calves can enter a Phase B, C or D post-weaning growth test. Heifers, bulls and oxen can all enter a Phase B test. In the Phase B test animals are evaluated through measuring post-weaning growth under farm conditions. Yearling weights, 18-month weights and body measurements are traits measured in the Phase B test.

In South Africa, young bulls with the potential to be used for stud purposes can enter either a Phase C or D growth test. In a Phase C test the post-weaning performance of young bulls is evaluated. This is undertaken at a central testing centre under standardized intensive feeding conditions for a period of 84 days, which follows an adaptation period of 28 days. Traits measured in the Phase C growth test or centralized growth test are weight gain, individual feed intake, scrotum

circumference and body length and height. On completion of the centralized (Phase C) growth test average daily gain (ADG), feed conversion ratio (FCR) and Kleiber ratio (where the Kleiber ratio estimate is the ADG divided by the bull's metabolic weight ($ADG/weight^{0.75}$)) are calculated for each bull tested.

Costs involved in a Phase C growth test are high and breeders cannot afford to send all of their potential stud bulls to be tested. For this reason, breeders only send their superior young bulls. The remaining young bulls, potentially to be used for stud purposes, will participate in an on-farm growth test (Phase D growth test). Ten or more bulls of the same breed from one or more breeders are tested on the farm of a breeder for post-weaning growth and efficiency. Test lengths of the on-farm or Phase D growth tests can vary between 84 and 270 days depending on the growth rate of the bulls. The same traits are measured in the Phase D and C growth tests with the exception of feed intake and FCR, which are only measured in the Phase C test.

The Phase E test is a progeny carcass evaluation test in which the qualitative and quantitative traits of a progeny group (at least 8 progeny of the same sex) of a sire are evaluated on completion of a growth test. Traits measured and evaluated in Phase E are carcass weight, dressing percentage, percentage fat, muscle and bone in the carcass, meat tenderness and marbling.

The Animal Improvement Institute's Animal Breeding Division calculates breeding values on an annual basis for traits measured in the various phases of the Scheme, provided sufficient measurements have been recorded for a genetic evaluation to take place.

One important question still remains. What is the economic value of these traits and which traits contribute significantly to profitability in a beef production enterprise, especially in the feedlot industry? No livestock production enterprise is sustainable without a favourable return on investment (profit).

Dickerson (1969) defined biological objectives as "the relative economic importance of the major components of performance in terms of the approximate direct effect of each on cost per unit of production". Because changes in production systems can change biological objectives, Dickerson (1970) stressed that genetic decisions should be made with an eye to the future of animal production. Due to the implications of genotype × environment interactions, Dickerson (1978)

recommended that each biological type should be evaluated under the production system for which it is best suited.

Biological inputs (e.g., feed intake) are only worth consideration if they are associated with an expense. Water is a major "biological" input in an animal production system, yet seldom considered in efficiency studies due to its relatively low cost.

Dickerson (1976; 1978) recognized that non-feeding costs represented major sources of expense in livestock production and were not always directly related to animal performance. Production systems make use of different inputs, each with potentially different prices, and yielding different types of products, each with potentially different market values. Relative economic values of inputs and outputs need to be considered explicitly.

Dickerson (1976) also defined biological objectives in terms of efficiency (e.g. cost per unit of value produced) rather than profit (e.g. income minus expense). He stated that efficiency is more realistic than profit because sale prices tend to fluctuate around a narrow margin above production costs, so that lower costs benefit consumers more than producers.

The cost of feed is an important variable affecting the profitability of beef production. The perspective should, however, always be that the efficiency of the cow, as the basis of beef production, cannot be compromised as she consumes between 70% and 94% of the energy required up to weaning. Even when the TDN (total digestible nutrients) consumed is traced to marketing age, after feedlotting of the calf, the cow still consumes between 56% and 70% thereof (Ferrell & Jenkens, 1984; Urich et al., 1984; van Oijen et al., 1992; Johnston, 2002). Slaughter stock, however, usually consume expensive feed, particularly those finished on high concentrate feedlot diets. Manipulation of the environment and cattle management can be used to reduce feed costs and it has also been known for several decades that feed intake and measures of feed efficiency are heritable in beef cattle (Johnston, 2002).

In South Africa more than 70% of all beef consumed is the result of intensively fed feedlot cattle. Because of the general consensus that feed intake and growth are the most important economic components when calculating profitability (biological efficiency) in a growth test or feedlot, inclusion of feed intake and growth information in selection decisions would facilitate genetic improvement of efficiency and profitability in beef cattle production systems. In order to include

efficiency of feed intake and growth in selection decisions, appropriate measurements of these traits are required.

Horton (1998) stated that the cattle that invariably make the most money in feedlots are those that gain the most weight, in the shortest period of time, on the least amount of feed. Horton (1998) also found that carcass characteristics do not have as much of an influence on profitability as feed conversion because there has not been as much variation in carcass value found as in gain and feed conversion ratio. Horton (1998) found that a 20% change in feed conversion ratio, average daily gain and quality grade affected profit per head by $62, $10 and $7, respectively. These results highlight the importance of feed conversion ratio in any livestock enterprise.

The collection of large numbers of individual feed intake records in South Africa by the NBCPTS enabled researchers to investigate the genetics of feed efficiency traits such as feed intake, feed conversion ratio, daily feed intake, residual feed intake and Kleiber ratio. Johnston (2002) stated that although initially it may seem logical, selection for reduced feed intake alone inevitably results in a correlated reduction in mature weight. Therefore various functions of output of beef per unit of feed are used as measures of feed efficiency. The most common index of efficiency is gross efficiency defined as the ratio of output (e.g. gain) over feed inputs (e.g. kg feed eaten). Feed conversion ratio (FCR) is the inverse of gross efficiency. Many researchers have shown FCR to be strongly negatively correlated with growth rate. It is therefore argued that selection for faster growth rates will achieve improvements in feed efficiency mainly through a reduction in maintenance costs due to fewer days on feed to attain the same weight endpoint. Whilst selection for growth rate may negate the need to measure feed intake, it is likely to lead to higher mature weights, which may be undesirable in the cow-herd. Conversely, the trait net feed intake or residual feed intake (RFI) is computed in such a way as to be phenotypically independent of weight and gain (Johnston, 2002). RFI was first proposed by Koch *et al.* (1963) and is the difference between actual feed intake and the expected feed intake requirements for maintenance of body weight and production (e.g. gain). Kennedy *et al.* (1993) showed that although RFI is phenotypically independent of production it is not necessarily genetically independent. Many other measures and definitions of efficiency exist (e.g. cow/calf efficiency, maintenance efficiency) and several are discussed in detail in the review of Archer *et al.* (1999).

Individual feed intake values for individual bulls are recorded by the NBCPTS. Data used in this study was obtained from the NBCPTS' national database. Only performance testing data of

Bonsmara bulls was used in this study. Bulls are sent to one of the Agricultural Research Council (ARC) central testing stations where live weight and individual feed intake are recorded on a weekly basis.

On arrival, bulls enter a four-week adaptation period so as to gradually adapt to the feed ration as well as their new environment. The adaptation period was also implemented to eradicate the effect of compensatory growth, where animals entering the same growth test originate from different farms with different feeding regimes and climates. It thus eliminates pre-test environmental differences between calves. The centralized or Phase C tests were originally 20 weeks long (140 days). In 1990 it was shortened to a 16-week test period (116 days) and in 1999 to a 12-week test period (84 days) as recommended by Archer & Bergh (2000).

Although a clear definition of a trait is important in a genetic evaluation programme, the key trait that should be measured is feed intake. Selection index methodology can be used to ensure the correct trait emphasis in a multitrait selection framework (Johnston, 2002). Barwick (2002) discussed the effect of trait definition and the presence of other measures on the derivation of economic values and index weightings for costing feed. The choice of which trait to include in a genetic evaluation programme will depend on the data being recorded, the model used to compute breeding value predictions and the method used to construct indices.

Neither management nor nutrition can alter an animal's genetic composition to be more profitable and more efficient. The effect of management and nutrition will also not be transmitted to the progeny. Therefore, the only way in which to improve a population's efficiency genetically is through selection. Selection is the process by which a herd (or population) is changed genetically through utilizing visual appraisal (appearance) or objective measurements (metric traits) (Scholtz *et al.*, 1999). These traits all have a genetic basis and will respond to selection. Selection is a critical decision because the effects of today's decisions will remain in the herd for many years. A breeder must therefore carefully consider his breeding objectives and selection decisions to ensure his beef production enterprise obtains its objectives.

Van der Westhuizen & Matjuda (1999) stated that the beef breeder in South Africa will have to revise breeding objectives constantly to maintain a sustainable supply of superior genetic material and to provide quality products to clients down the production line. The ultimate aim for seed stock and beef producers alike is to produce quality products at a profit to enable them to retain the edge on the competition.

The initial definition of a breeding objective is a crucial step in establishing a breeding programme. If the objective is poorly defined, or not defined at all, the implementation of an effective system of evaluation can result in genetic changes in an undesirable direction.

Presently in South Africa, no clear objective exists to select directly for post-weaning growth or feedlot profitability. Advanced breeders have selected indirectly for profitability through the selection of growth rate or feed conversion ratio. The question that needs to be answered is whether it is better to select directly for the objective, which in this study is a post-weaning growth or feedlot profitability value, than to select for individual criteria or traits that are related to the objective (e.g. growth rate, feed conversion ratio or residual feed intake) or a selection index value based on a number of related selection criteria or traits.

As mentioned, the most crucial step in any breeding programme is a clearly defined breeding or selection objective. The aim of this study is to define a clear selection objective to enable the South African beef breeders, and especially the feedlot industry, to select for post-weaning growth or feedlot profitability. Also, to investigate the genetic correlations between the objective and other exiting selection criteria that are related to the objective (these traits or selection criteria include feed conversion ratio (FCR), average daily gain (ADG) and residual feed intake (RFI)), to determine whether it is better to select directly for the objective (post-weaning growth or feedlot profitability value) than to select for the exiting efficiency criteria related to the objective or to select for a selection index value based on related criteria.

CHAPTER 2

DEFINING A CLEAR SELECTION OBJECTIVE TO SELECT FOR POST-WEANING OR FEEDLOT PROFITABILITY IN BEEF CATTLE

2.1 Introduction

Growth and feed intake are the two most economical important traits that should be considered in the calculations when a post-weaning growth or feedlot profitability value is calculated. Various reproductive, productive and efficiency traits in beef cattle are currently measured in South Africa's Agricultural Research Council's (ARC) Beef Cattle Improvement Scheme. Young bulls are measured for growth, efficiency and body measurements in centralized or in an on-farm growth tests. In the centralized growth tests individual feed intakes and weight gains are recorded on a weekly basis. A post-weaning growth or feedlot profitability value (or economical efficiency value) can be calculated for each bull tested in a centralized growth test.

Economical important traits such as body weight, feed intake, feed conversion ratio, feedlot profitability, etc., change with time in growing animals (Henderson, 1982). Measurements can thus be taken at any time in an animal's life, which is why these traits are called "infinite dimensional traits" (Kirkpatrick & Heckman, 1989). Different genes turn on and off during an animals' development stages causing changes in the physiology and consequently in the performance of an animal over its life time. Therefore, as is the case with phenotypes, the expression of genotypes changes over time as well.

Serial or repeated measurements are usually modelled using two approaches. The first approach is where every measurement is treated as a different trait. This approach thus leads to a multiple trait analysis. The multitrait analysis does consider the genetic correlations among traits; however, it does not use the information concerning the time lag between measurements. The second approach is a so called two-step procedure or a fixed regression procedure (Lewis *et al.*, 2002). The fixed regression approach, however, allows the population mean to be modelled over time, e.g. lactation curves in dairy cattle and growth curves in growing steers. The fixed regression parameters for the growth curve of individual animals are estimated in the first step, and genetic evaluation of estimated curve parameters using mixed model methodology is performed later. However, this may not be the most appropriate procedure. The estimated curve parameters are highly correlated, and

fitting the curves to individual animals may become problematic due to the exclusion of the environmental effects (Lewis *et al.*, 2002) and also due to the fact that only one breeding value is predicted for the entire curve or interval.

Repeated or consecutive measurements can be modelled more accurate by applying random-regression methodology, where the regression parameters and genetic values for animals are estimated jointly. Genetic values and other random effects are treated as a function of time. Variances also change continuously over time. Kirkpatrick *et al.*, (1990) showed that phenotypic as well as genetic variances can be modelled as a function of time by applying covariance functions. Through the use of random-regression covariance functions it is now possible to estimate heritabilities and breeding values on any given time period on the trajectory or curve.

Random-regressions have already been applied in routine genetic evaluations in dairy cattle (Schaeffer *et al.*, 2000), growth in pigs (Huisman *et al.*, 2002), cow weights (Meyer, 1998a; 1999; 2000a), growth in beef cattle (Meyer, 2000b) and weight gain in beef bulls tested in testing stations (Schenkel *et al.*, 2002).

The next question that arises is whether this economical objective must be treated in terms of efficiency or as a profit value and to what extent price fluctuations influence this objective. The economic environment changes over time because feed and carcass prices change on a regular basis and can show extreme fluctuations. This must be taken into consideration with the estimation of a economical feedlot or post-weaning growth profit value because, when the feed price decreases and the carcass price stays the same or even increases, animals that consumes feed above average feed intake, with a lower feed conversion ratio (FCR), could become more profitable, while an animal with a good FCR but consuming less feed could become less profitable. It could be expected that the ranking of the animals, based on their profitability breeding values (EBVs), could change.

The aim of this study was to calculate a profitability value for each performance tested bull, tested either in a centralized or an on-farm growth test (through the use of a regression equation), and to estimate genetic parameters (heritabilities and genetic correlations) for and between feedlot profitability, other efficiency and productive traits using multitrait as well as random-regression methodology. Secondly, to conduct a study to estimate the effect of fluctuation in weaner price as well as carcass and feed prices and their effect on the ranking of the animals based on profitability EBVs.

2.2 Materials and Methods

The data analysed in this study was collected from the centralized growth test stations of the Agricultural Research Council (ARC). Bulls are sent to one of the ARC central testing stations where live weights and individual feed intake are recorded weekly.

On arrival, bulls enter a four-week adaptation period to gradually adapt to the feed diet. These growth tests were originally 20 weeks long (140 days). In 1990 it was shortened to a 16-week test period (116 days) and in 1999 to a 12-week test period (64 days) as was recommended by Archer & Bergh (2000).

Table 2.1 Composition of diet

	Min.	Max.
Metabolic Energy	11 MJ/kg	
Crude-protein	135 g/kg	150 g/kg
Non-degradable protein	45 g/kg	
Urea		7 g/kg
Protein from NPN (% RP)		20%
Crude-fibre	125 g/kg	
Roughage	200 g/kg	
Fat	30 g/kg	70 g/kg
Calcium	6 g/kg	10 g/kg
Phosphorus	3 g/kg	5 g/kg
Ca : P ratio	1.5 : 1	2.5 : 1
Sulphur	1.5 g/kg	3 g/kg
N : S ratio	8 : 1	12 : 1
Potassium	5 g/kg	13 g/kg
Magnesium	2.5 g/kg	
Vitamin A	4 500 000 IE/ton	
Vitamin D3	250 000 IE/ton	
Vitamin E	5 000 IE/ton	
Vitamin B1	3 000 IE/ton	
Niacin	100 000 IE/ton	
Copper	15 mg/kg	
Manganese	40 mg/kg	
Zinc	54 mg/kg	
Cobalt	0.5 mg/kg	
Iodine	2 mg/kg	
Iron	50 mg/kg	
Selenium	0.15 mg/kg	
Monensin	290 g/t	
Zinc Bacitracin	250 g/t	

Table 2.1 present the balanced feed diet currently being fed during the 12-week centralized growth test. Figure 2.1 presents the phenotypic weekly feed intakes for 11 839 Bonsmara bulls tested in centralized growth tests tested between 1970 and 2001. One should, however, keep in mind that different test lengths were used over this time period. As a result of the variation in test length, weeks 1 to 12 represent data of 11 839 Bonsmara bulls, weeks 13 to 16, 8 830 bulls and weeks 17 to 20, 3 934 bulls. On average a bull participating in a 140 days test consumed 1 442 kg of feed (10.3 kg daily intake) over the entire test period. Likewise the average bull participating in a 116 days test consumed 1 192kg of feed (10.3 kg daily intake). The average bull participating in an 84 days test consumed an average of 851 kg of feed (average daily intake of 10.1 kg). These average daily feed intakes of 10 kg per day correspond to the average daily feed intakes obtained by Archer *et al.* (1998) and Herd & Bishop (2000).
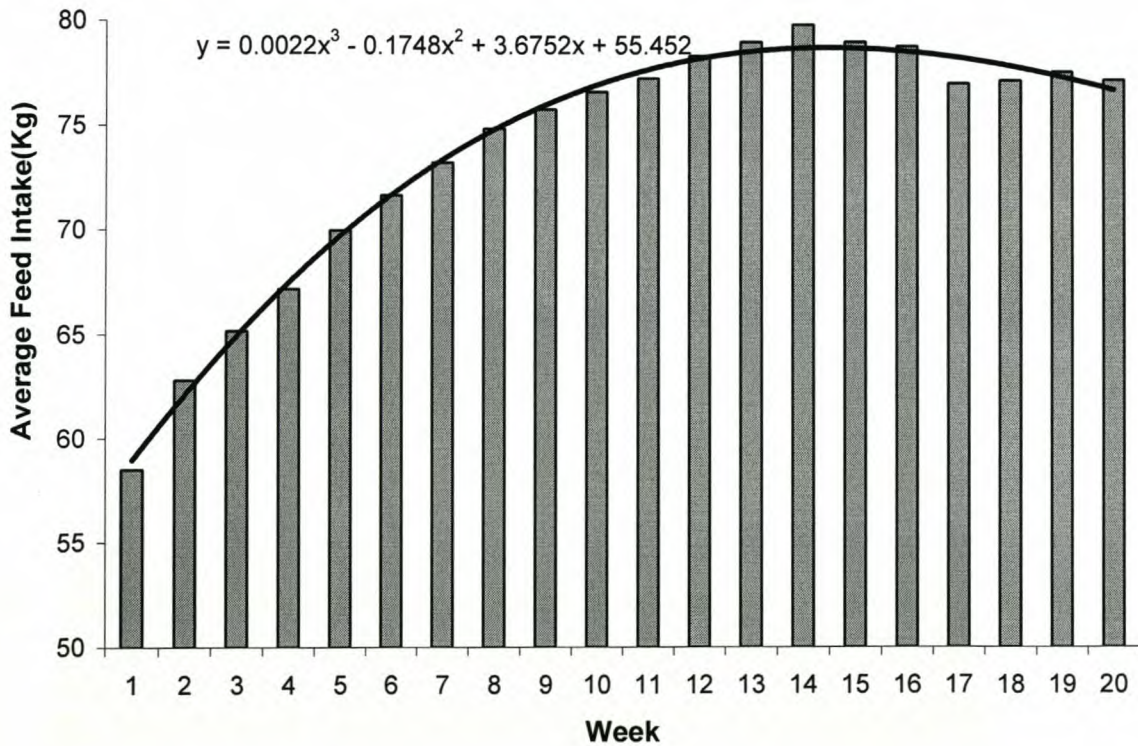

The curve is described by $y = 0.0022x^3 - 0.1748x^2 + 3.6752x + 55.452$

Figure 2.1 Average Weekly Feed Intake (kg)

The average feed intake gradually increased from week one (58.5 kg/week) up to and including week 14 (79.8 kg/week), where after it declined slightly and stabilised over weeks 18, 19 and 20 (77.19 kg/week). The sudden drop in feed intake after week 16 is the result of differences in the diet formulations used in the different test lengths. In the 20-week growth test the diet contained 357.5

g/kg roughage whereas the 16-week and 12-week growth tests diets contained only 200 g/kg roughage. Figure 2.2 presents the average weekly feed intakes for the three different test lengths, respectively. The average weekly feed intake of the 116-day test was higher then either the 84 or 140 days test periods, and is the reason for the increase in the average weekly feed intake from week 12 to week 13 in Figure 2.1. The sudden drop in the average weekly feed intake in Figure 2.1 after week 16 is the result of the much lower average weekly feed intakes of the 140 days test period compared to those of the 84 or 116 days test periods (Figure 2.2).
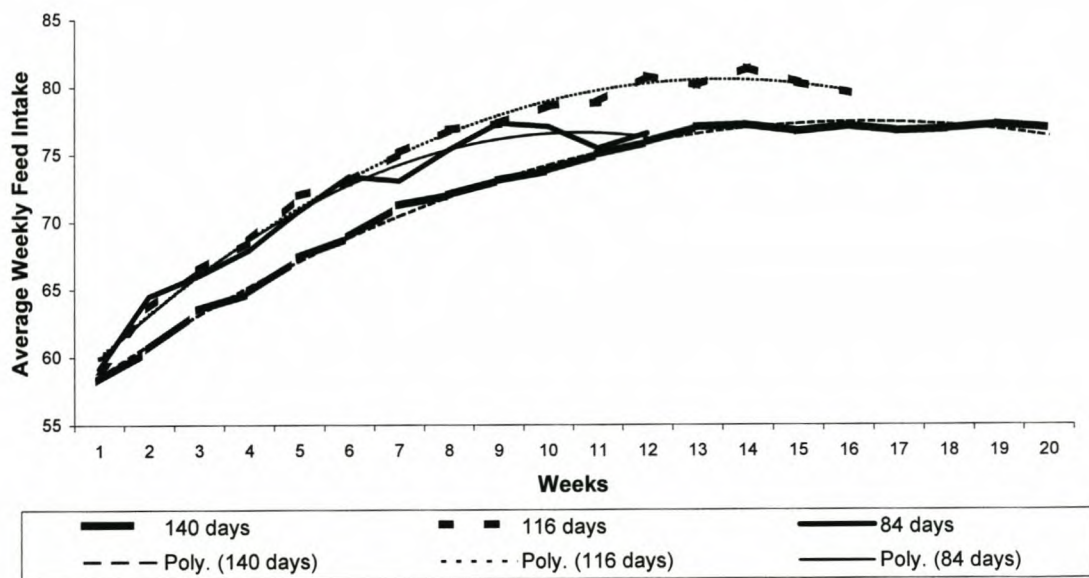

Figure 2.2 Average weekly feed intake (kg) for different test lengths

Figure 2.3 is a presentation of the average body weight from week one up to and including week 20 for all bulls tested in a centralized growth test. From the figure it is apparent that the bulls' body weights increased linearly over time, at an average of 11.0 kg per week. The scale used is in fairly large increments, therefore smaller differences will not be as apparent.
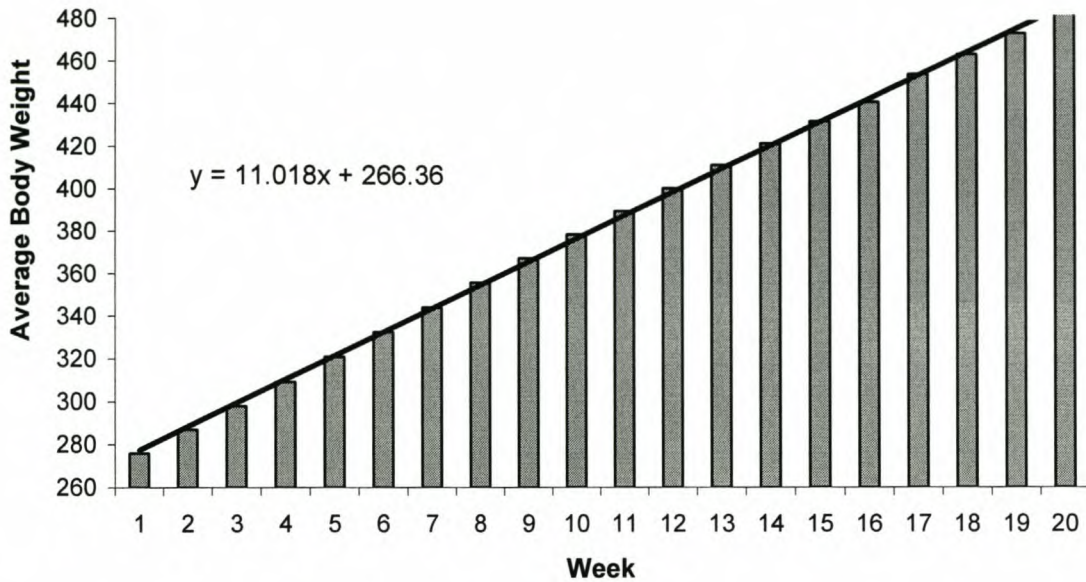
$$y = 11.018x + 266.36$$

Figure 2.3 Average weekly body weight of centralized tested bulls (kg)

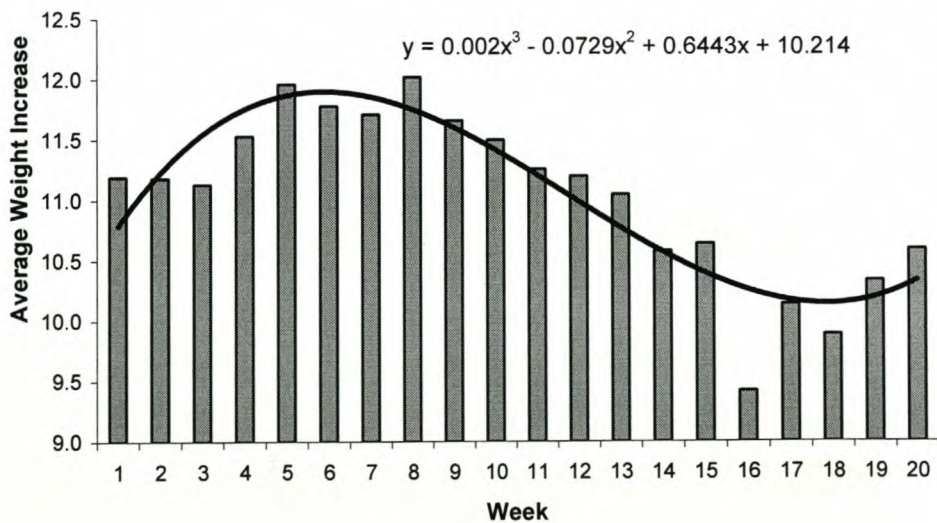$$y = 0.002x^3 - 0.0729x^2 + 0.6443x + 10.214$$

Figure 2.4 Average weekly weight gain (kg)

Figure 2.4 indicates the average weekly gain. From Figure 2.4 it is apparent that the average weekly gain increased from week 1 to week 8 with an average of 12.02 kg per week, where after it decreased with a sudden drop at week 16 and increased again from weeks 17 to 20. This decline in weekly gain up to week 16 is the result of differences in diet compositions used in the different test

periods over years. In the 20-week growth test the diet contained 357.5 g roughage per kg of feed, whereas the 16-week and 12-week growth tests diets contained only 200g of roughage per kg of feed. The average weekly feed intake of the 16 week test was also higher then either the 12 or 20 week test periods and is the reason for the increase in the average weekly gain. Therefore, the average feed conversion ratio (Figure 2.5) showed a gradual increase from week one (6.3kg feed/kg body weight increase) up to and including week 16 (9.4kg feed/kg body weight increase) where after it improved slightly. Once again this pattern is the result of different feed diets used in the different test periods used over years, especially, the differences in the percentage roughage. The average poor FCR of 9.4 kg feed per kg body weight increase at week 16 is also the result of the higher percentage roughage in the diet because different diets resulted in different growth patterns which explains unexpected patterns in the graphs. Furthermore, animals may have also changed genetically over time.
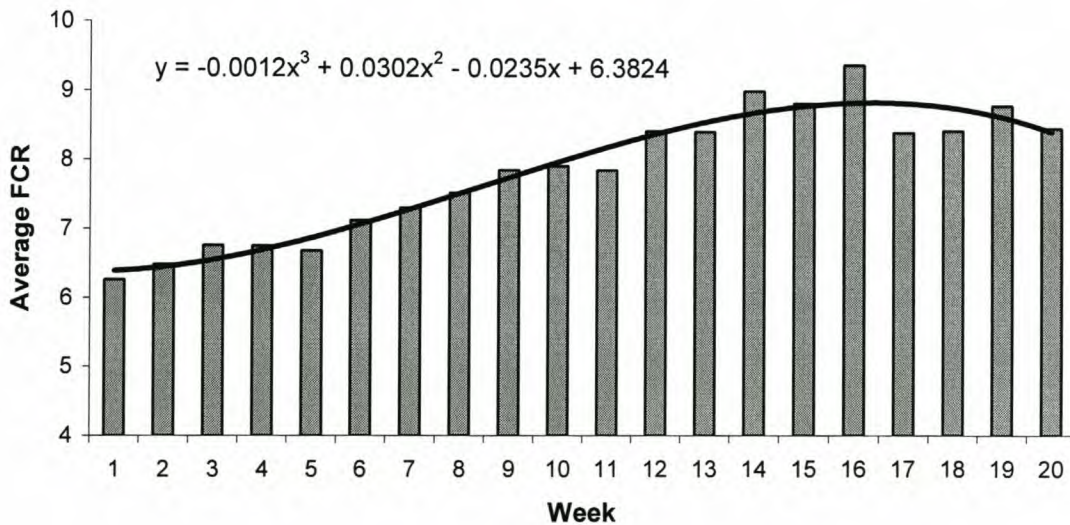
$$y = -0.0012x^3 + 0.0302x^2 - 0.0235x + 6.3824$$

Figure 2.5 Average weekly feed conversion ratio (FCR)

In the prediction of a feedlot or post-weaning growth profitability value, feed intake is required in the calculation. Young weaner bull calves are sent to one of the ARC central testing stations where individual feed intake and weights are recorded on a weekly basis. Body measurements are also measured at the onset and completion of the test. In South Africa, however, the majority of bulls tested in a post-weaning growth test are tested in an on-farm growth test where bulls are group fed and individual feed intakes are unknown. Of the 82 778 Bonsmara bulls that were performance tested only 11 835 (14%) were tested in a centralized growth test of the South African Agricultural Research Council (ARC), while the majority (70 943 or 86%) were tested in an on-farm growth test

where individual feed intakes are unknown. Therefore, two datasets were used in this Chapter. The first data set only includes bulls tested in the centralized tests while the second data set includes bulls tested in an on-farm growth test. The first data set consists of the individual feed intake and weights of 10 318 bulls taken on a weekly basis. After appropriate editing the data set for the estimation of variance components were reduced to 6 738 recorded bulls.

Efficiency and productive traits measured in the centralized growth tests are feed intake (FI) and body weight (BW) on a weekly basis as well as shoulder height (SHD), scrotum circumference (SCR) and body length (BDL) at the end of the testing period. An average daily gain (ADG) value is then calculated for each bull at the end of the testing period by means of a regression, taking all weekly measurements during the duration of the testing period in account. Individual feed conversion ratios were derived for each bull as the total FI divided by the weight gain during the testing period. Therefore, FCR is the amount of feed consumed by the animal in order to gain a kilogram in body weight. Weaning weights (WW) for these bulls were obtained from the ARC pre-weaning recording programme.

Subsequently, by using all the available recorded information, a feedlot profitability value or post-weaning growth value in Rand (South African currency) (R-value) for each bull was calculated as if the tested bull was fed under feedlot conditions and sold to an abattoir. The following equation was used to calculate this value for each centralized growth tested bull:

$$R\text{-value} = [\text{Uwt} \times \text{CPr/kg}] - [(\text{BWt} \times \text{BWtPr/kg}) + (\text{FI} \times \text{FPr/kg}) + ((\text{BWt} \times \text{BWtPr/kg}) \times ((\text{Br}/365) \times \text{Tl}) + (\text{VC})] \quad\quad\quad (2.1)$$

where :
Uwt	=	Slaughter weight (55% of final weight);
CPr/kg	=	Price per kilogram carcass weight;
BWt	=	Body weight on commencement of the test;
BWtPr/kg	=	Live weight price per kilogram for weaners;
FI	=	Feed intake;
FPr/kg	=	Feed price per kilogram;
Br	=	Interest rate;
Tl	=	Test length;
VC	=	Veterinary costs.

The following assumptions were made in order to simulate a profit value and to create a comparable basis for a statistical analysis:

- Live weight weaner calf price at R8.25 per kilogram (The initial weight at onset of the growth test is used).
- A3 Carcass price of R12.35 per kilogram (It is assumed that all bulls are classified as A3 carcass grade).
- Feed cost set at R0.90 per kilogram.
- Interest rate on an overdraft account at 14%.
- It is assumed that all slaughter costs are covered by the fifth quarter (skin, intestines and head).
- Dressing percentage of 55%. (55% of the weight of the bull on completion of growth test).
- Veterinary costs of R3.50 per week (approximately R60 for a 4 week adaptation period and 12 week test).

The importance of non-genetic sources of variation on the traits was determined by the PROC GLM procedure of SAS (2000). Only effects which were statistical significant (P < 0.001) were subsequently included in the final models fitted. Non-genetic sources that were included in the models for weaning weight (WW) were the linear and quadratic regression of the age of the dam, the linear and quadratic regression of the age of the animal at weaning and the contemporary group for weaning weights (herd, weaning date, treatment code and sex) as a fixed effect (1 246 levels). For ADG, only the linear regression of the age of the dam and the contemporary group fixed effect for the growth test (test centre, test year, test phase and test number) were included in the model (514 levels). For SHD the linear and quadratic regressions of the age of the animal at the end of the growth test, the linear regression of the age of the dam and the contemporary group fixed effect for the growth test were included as non-genetic sources. For FCR and R-value the linear regression of the age of the animal at the end of the growth test and age of dam were included with the contemporary group effect as a fixed effect. All of the above mentioned non-genetic sources were significant (P < 0.001) and were therefore included in both models. Table 2.2 gives a summary of the different models fitted.

Table 2.2 Summary for the different models fitted in genetic evaluation for different traits

Factor	Effect	Levels	WW	ADG	SHD	FCR	R-Value
Age	C				X	X	X
Age^2	C				X		
Dam age	C		X	X	X	X	X
Dam age^2	C		X				
Weaning age	C		X				
Weaning age^2	C		X				
Growth test contemporary group	F	514		X	X	X	X
Weaning contemporary group	F	1 246	X				

WW = Weaning weight, ADG = Average daily gain, SHD = Shoulder height, FCR = Feed conversion ratio, R-Value = feedlot profitability, Age$^{(2)}$ = Linear and quadratic regression of the age of the animal at the end of the growth test, Dam age$^{(2)}$ = Linear and quadratic regression of the age of the dam at end of test, Wean age$^{(2)}$ = Linear and quadratic regression of the age of the animal at weaning, C = Covariate, F = Fixed effect, Growth test contemporary group (test centre, test year and test number), Weaning contemporary group (herd, wean date and treatment).

Variance components, heritabilities and genetic correlations for and between WW, ADG, SHD, FCR and R-value were estimated by using a multitrait restricted maximum likelihood (REML) procedure, using the VCE package developed by Groeneveld (1994).

The following model equation was used for analysis:

$$y = Xb + Za + e, \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (2.2)$$

where :

y = vector of the observations for the ith trait,

b = vector of fixed effects for the ith trait,

a = vector of random animal effects for the ith trait,

e = vector of random residual effects for the ith trait,

X and Z = incidence matrixes relating records of the ith trait to fixed and random animal effects, respectively.

Subsequent to the estimation of variance components, breeding values for each animal in the pedigree file were predicted for the different traits under investigation. The genetic trend for R-value and FCR were obtained through the use of these predicted breeding values obtained above.

For the random-regression models, two weekly feed intake and growth measurements were used to calculate a feedlot profitability value for each centralized growth tested animal on a two weekly basis from onset of the testing period up to the end of week 12 of the centralized growth testing period. The dataset used for the covariance function random-regression animal model analysis consist out of 42 690 repeated measurements of 6 738 tested bulls. These bulls are the progeny of 1 294 sires and 5 468 dams. The average age of these tested bulls on onset of the growth test was 323 days. The youngest and oldest animal entered the growth test in the final data set was 191 and 381 days of age, respectively.

The dependencies of weight gain, feed intake and profitability on age of the animal (in days) were modelled using orthogonal (Legendre) polynomials to the first order (linear). The orthogonal (Legendre) polynomials on age were used to pattern covariance matrices using REML procedure. A preliminary study for an appropriate fixed part of the model was done using the SAS statistical package (SAS, 2000). Only effects that were statistically significant ($P < 0.001$) were subsequently included in the final models fitted. The model included the fixed effect of the contemporary group (as was discussed previously) as well as the linear and quadratic regression of dam age (the age of the dam at the end of the growth test) as a covariate. The fixed regression part of the model included the age of the animal in days while the random parts of the model were the random-regression animal model coefficients for the additive and permanent environmental effects.

Following the notation of Kirkpatrick *et al.* (1990, 1994), the random-regression model for records over time (including additive genetic and permanent environmental random effects) could be represented as follows:

$$y_{ij} = F + \sum_{m=0}^{n-1} b_m \phi_m(t_{ij}) + \sum_{m=0}^{n_G-1} \alpha_{im} \phi_m(t_{ij}) + \sum_{m=0}^{n_P-1} \gamma_{im} \phi_m(t_{ij}) + \varepsilon_{ij}$$

$$y = Xb + Za + Z^*p + e$$

where :

y_{ij} represent the observations; F are the fixed effects in the model; $\phi_m(t_{ij})$ are the covariates as a function of age with t_{ij}, the jth age of animal i standardized to range -1 to $+1$, and with ϕ_m, the mth orthogonal Legendre polynomial for n the order of fit (with ϕ_m evaluated for t_{ij}, there will be n coefficients for each age); b_m is the mth fixed regression coefficient; α_m and γ_m are the mth additive genetic and permanent environmental random-regression coefficients for cow i; n_G and n_P are orders of fit for additive genetic and permanent environmental effects; and ε_{ij} is the temporary environmental effect or measurement error.

Kirkpatrick *et al*. (1990, 1994) further indicated that random-regression is an extension to regular linear mixed model, but with incidence matrices (**X** and **Z**) containing coefficients other than zeros and ones. Coefficients of 1 are replaced by functions of ages at which the records are taken (i.e., $\phi_m(t_{ij})$). The "design" matrix of covariates (standardized ages, incorporating orthogonal polynomial coefficients) is **Z** for all animals, whereas **Z*** is the part of **Z** corresponding to only those animals with records. The model's first and second moments are:

$$E(y) = Xb$$

$$V(y) = Z(K_G \otimes A)Z' + Z^*(K_p \otimes I)Z^{*'} + R$$

where :

A and **I** are the numerator relationship matrix and an identity matrix, respectively; K_G and K_P are the matrices of genetic and permanent environmental (co)variances (coefficients of the covariance functions, CF), with dimensions equals to order of fit of the CF in the analysis; **R** is the variance of the temporary environmental effects (error term), which is a diagonal matrix allowing for different variances by age t.

The DFREML-DXMRR programmes (Meyer, 1998b) were used for the random-regression genetic evaluation. The DXMRR software of random-regression models (Meyer, 1998b) fits coefficients of Legendre polynomials as a default, allowing for reduced order of fit and reduced rank. The software permits for up to two sets of random-regression coefficients, modelling additive genetic and

permanent environmental effects. Corresponding covariance functions for the additive genetic and permanent environmental effects are then estimated; from them, corresponding (co)variances matrices can be recreated for either all ages represented in the data or for selected ages. Heterogeneity of temporary environment variances, corresponding, for example, to ages represented in the data, can also be accommodated.

As mentioned previously, the majority (86%) of performance tested Bonsmara bulls were group fed in an on-farm growth test. Traits measured in the on-farm growth tests were initial weight (weight of the bull at the beginning of the testing period), final weight (the weight of the bull at the end of the growth test period), and SHD. Once again an ADG value as well as a Kleiber ratio estimate (KLB), where the Kleiber ratio estimate is the ADG divided by the bull's metabolic weight taken at the end of the growth test were calculated for each bull at the end of the testing period.

In order to predict a feed intake value for on-farm tested bulls of (which individual feed intakes are unknown), a step-wise regression, using the PROC REG procedure of SAS (2000), was performed on centralized growth test data, where individual feed intakes were known. All traits measured in an on-farm and centralized growth tests were initially included in the step-wise regression. With the help of these predicted feed intake values, a feedlot or post-weaning profitability value (R-value) could be calculated for each bull, tested in an on-farm growth test (equation 2.1).

Genetic variance components estimated fitting the model (equation 2.2) for bulls tested in the centralized growth test were used to estimate an R-value breeding value for each bull tested in an on-farm growth test, using the multitrait animal model as was discussed.

To address the problem of the fluctuation in weaner live weight, carcass and feed prices and the effect they have on the R-value, the monthly average weaner, A3 (according to the South African classification system) carcass and feed prices were obtained from The South African Feedlot Association (SAFA), South African Meat Industry Company's (SAMIC) web pages and from the central testing station of the ARC-Irene from January 1998 to June 2002, respectively. These prices were then used to calculate a ratio between meat and feed prices over years to identify the most profitable, as well as the least profitable environments in which to produce beef from the feedlot.

The PROC REG procedure of SAS (2000) was used to calculate three regression equations to predict post-weaning growth profitability (R-value) breeding values for an unfavourable economic

environment (UEE), an average economical environment (AEE) and for a favourable environment (FEE) for beef production. The PROC CORR procedure of SAS (2000) was then used to obtain Pearson and Spearman correlations between R-values and estimated breeding values calculated in the three different economic environment situations.

2.3 Results and Discussion

Figure 2.6 shows the average profit per week. Profit increased linearly from week one (from a loss of R141.51) to week ten (with a profit on R105.81) where after it decreased sharply to week twenty showing a loss of R555.47. From Figure 2.6 it is clear that average profit reached a maximum at week ten. At the end of week ten the bulls have been fed for 98 days (28 days adaptation and 70 days in the test). This is in agreement with the average feeding period of 100 days used by the feedlots, as well as the optimum test length of 70-84 days recommended by Archer & Bergh (2000) (after a 4 week adaptation period).
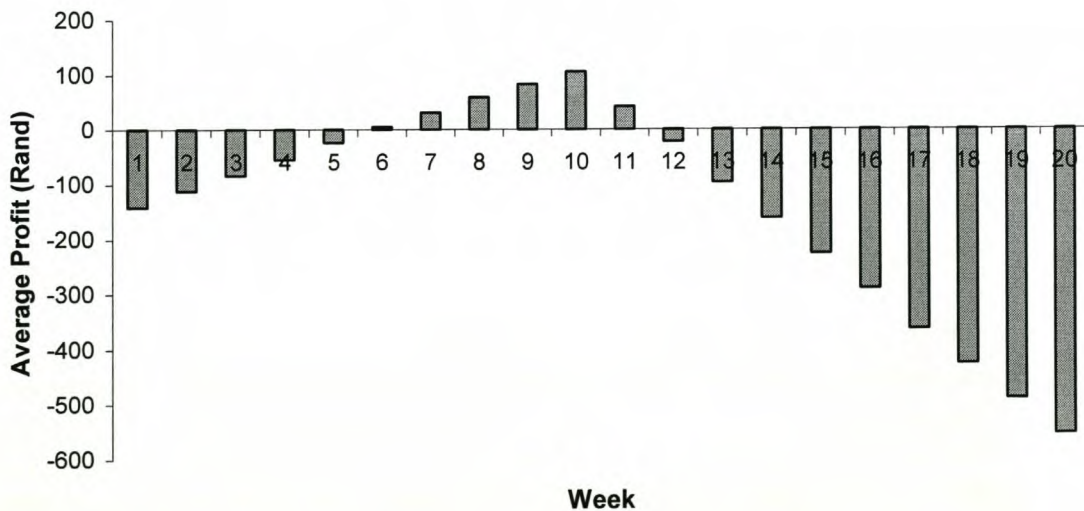

Figure 2.6 Average weekly profit (R-Value)

Table 2.3 presents the general statistics for the different traits and covariates, included in the different models.

Table 2.3 General statistics for the different traits and covariates in models

Trait/Covariates	Min.	Max.	Avg.	Std. Dev.
WW (kg)	125	375	234	30.67
ADG (g)	857	2680	1654	237.60
SHD (mm)	1060	1580	1195	35.13
FCR (kg/kg)	3.7	9.7	6.4	0.81
R-Value (R)	-825	494	-224	141.28
Age (days)	272	410	358	26.61
Dam age (days)	669	6032	2195	1008.14
Weaning Age (days)	150	269	205	23.30

The average age of the animals at weaning was 205 (± 23.3) days with an average weaning weight (WW) of 234kg (± 30.7kg). This is 20kg heavier then the average 205 days adjusted weaning weight of the Bonsmara breed (males and females) for the birth years 1993 to 1998 (Anonymous, 1999). The average age of the animals at the end of the growth test was 358 (±25.6) days, reflecting the age limits set on young bulls participating in centralized growth tests. The age of the dams varied from 1 year and 10 months (669 days) to 16 years, with an average of 6 years of age. The mean of FCR (6.4±0.81) corresponds with the mean FCR of 6.5±0.9 obtained by Arthur *et al.* (2001). The less profitable animal in the growth tests resulted in a loss of R824.78 while the most profitable animal showed a profit of R494.36 under the assumptions mentioned earlier. The average R-value was a loss of R223.93 (± R141.28). This is the result of many animals being fed for a period longer than the optimal. It also indicates that a feedlot has to select the most profitable animals to be able to make a profit under these circumstances.

Table 2.4 presents the heritability and genetic correlation estimates (with standard errors) for and between the different traits under investigation obtained from the multitrait analysis.

Table 2.4 Heritability (on diagonal) and genetic correlation estimates (above diagonal) for and between traits using multitrait analysis

Trait	WW	ADG	SHD	FCR	R-Value
WW	**0.30 ± 0.02**	0.29 ± 0.04	0.54 ± 0.03	-0.04 ± 0.05	-0.22 ± 0.05
ADG		**0.36 ± 0.01**	0.48 ± 0.02	-0.69 ± 0.01	0.65 ± 0.01
SHD			**0.51 ± 0.02**	-0.23 ± 0.02	0.10 ± 0.02
FCR				**0.34 ± 0.01**	-0.92 ± 0.01
R-Value					**0.36 ± 0.01**

The heritability for and genetic correlation estimates between WW, ADG, SHD and FCR are in the same order as those mentioned by Koots *et al*. (1994a; b) and Anonymous (1999).

The heritability estimate of 0.36 for R-value shows that this trait is genetically inherited and that it can be selected for. The genetic correlations between the R-value and the other traits varied from negligible to high. The genetic correlation of 0.10 between SHD and R-value indicates that SHD is of no real value in selecting for feedlot profitability.

The high genetic correlations of ADG and FCR with R-value were expected, as these two traits are the main contributors to the variance in R-value. The correlation of –0.92 between FCR and R-value is a result of this part-whole relationship. This was expected because for each kg less feed an animal consumes in order to gain a kg in body weight, the more profitable the animal becomes. Therefore, one can select indirectly for profit through the use of FCR as selection criterion, though with a smaller correlated response. The relative correlated response (Falconer & Mackay, 1996) in R-value where FCR been the selection criterion was 0.87. This indicates that only 87% of the possible genetic improvement will be made in profitability (R-value) if selection for FCR takes place in comparison to direct selection for R-value.

Figure 2.7 and 2.8 represent the genetic trends for FCR and R-value for the Bonsmara growth tested animals, respectively. From these figures, it is clear that there was an improvement in feedlot profitability and FCR since 1986.
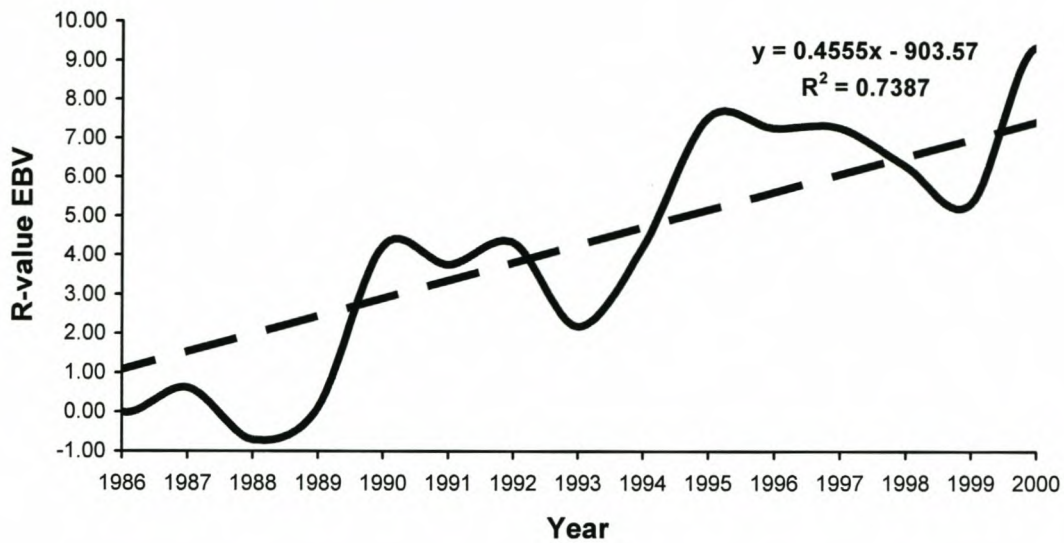
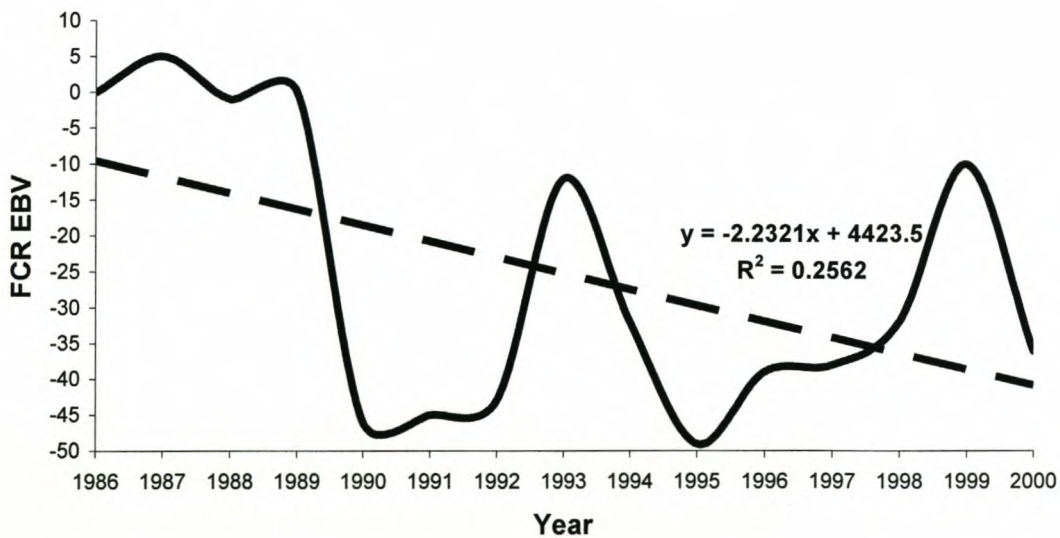**Figure 2.7** Genetic trend of R-value in the Bonsmara Phase C animals

Figure 2.8 Genetic trend of FCR in the Bonsmara Phase C animals

Figure 2.9 present the heritability estimates for weight of the trajectory of age in days obtained from the random-regression analysis. From Figure 2.9 it is apparent that the heritability of 0.59 decreases slightly to 0.56 as age increase. The heritabilities obtained from the random-regression are, as would be expected, higher then the heritability of 0.30 obtained for weaning weight from the multitrait analysis. Malovrh (2003) obtained heritabilities for growth (weights) in Brown Swiss

bulls, using random-regression methodology, between 0.19 and 0.52. Malovrh (2003) also found a slight decrease in heritability with an increase in age.
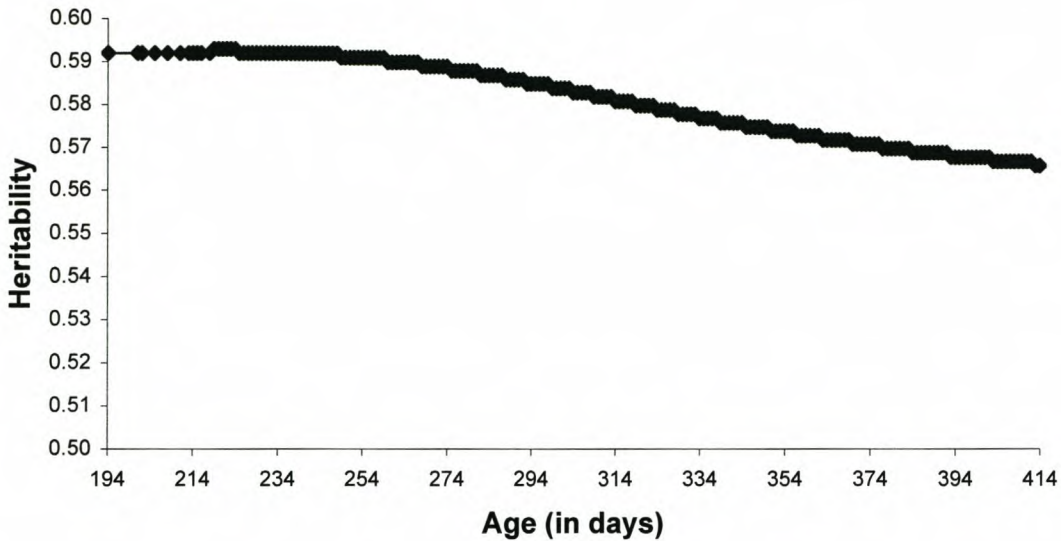

Figure 2.9 Heritabilities estimates for weight obtained from the random-regression model

Figures 2.10 and 2.11 represent the heritabilities for feed intake and feedlot profitability on the trajectory obtained from the respective unitrait random-regression analyses.

The heritability estimates for feed intake decrease from 0.45 (at 194 days of age) to 0.28 at 314 days of age where after the heritability increase again to 0.44 at the age of 414 days (Figure 2.10). The heritability for feedlot profitability obtained from the random-regression varied between 0.62 and 0.57, which are both higher than the heritability of 0.36 obtained from the multitrait analysis. As shown by Figure 2.11, the heritability for feedlot profit decreases slightly to 0.57 at 326 days of age where after the heritability stabilized around 0.58.
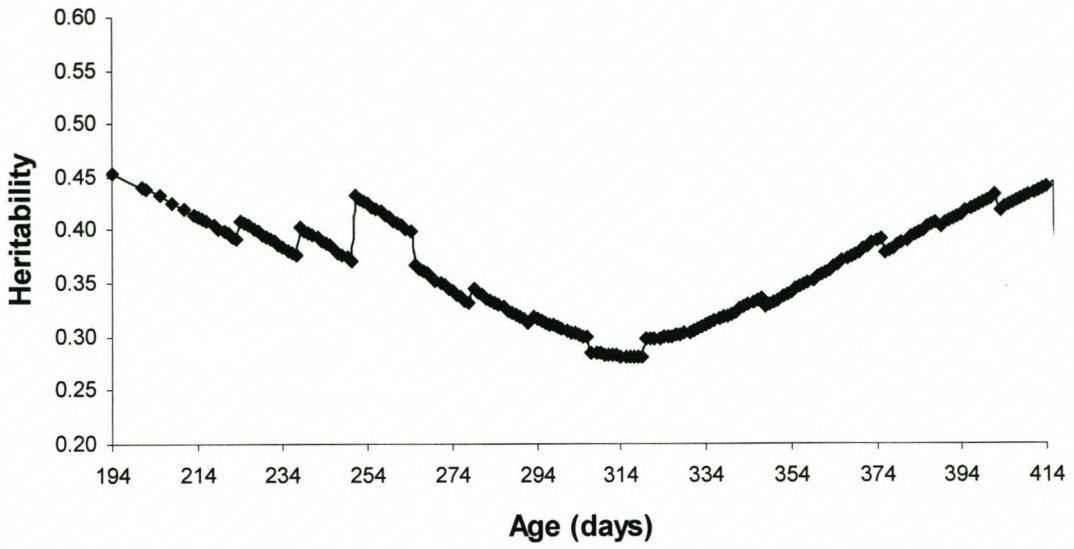
25

Figure 2.10 Heritabilities estimates for feed intake obtained from the random-regression model
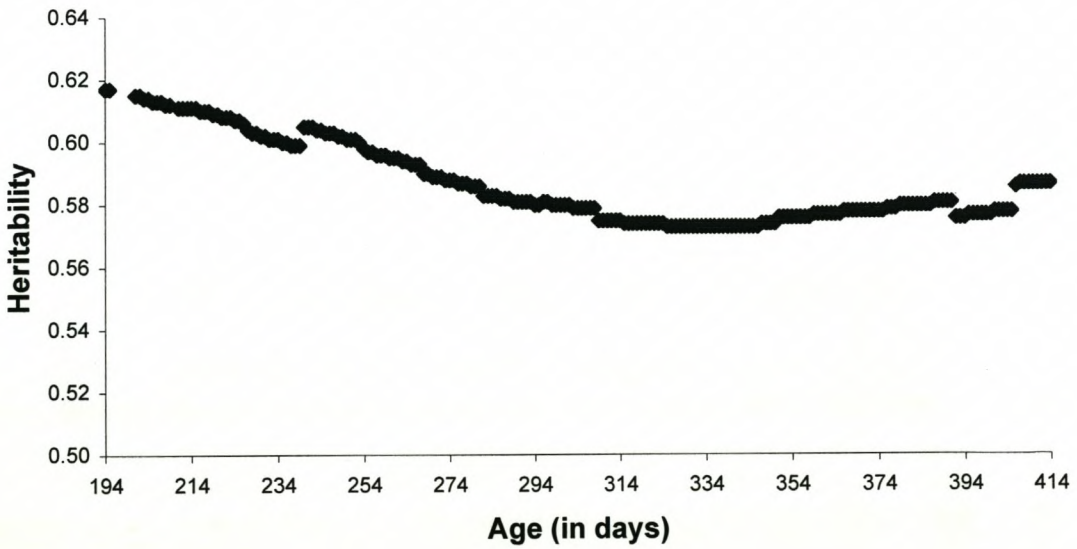

Figure 2.11 Heritabilities estimates for feedlot profitability obtained from the random-regression model

Table 2.5 presents the final multiple stepwise regression model used to predict feed intakes of centralized tested animals.

Table 2.5 Final multiple stepwise regression model to predict feed intake values on centralized tested animals

	R-square = 0.8242		C(p) = 403.3563		
Source	**DF**	**Sum of Squares**	**Mean Squares**	**F**	**Prob>F**
Model	3	628047213	209349071	18323.2	<.0001
Error	11723	133939745	11425		
Total	11726	761986957			
Variable	**Parameter Estimate**	**Standard Error**	**Type II Sum of Squares**	**F**	**Prob>F**
INTERCEPT	-453.535	9.622	25386770	2221.96	<.0001
Initial weight	-1.87188	0.056	12738115	1114.90	<.0001
Length of test	5.98811	0.067	92292882	8077.88	<.0001
Final weight	3.28156	0.039	78959021	6910.84	<.0001

		Summary of Stepwise Procedure for Dependent Variables: R-value				
Step	**Variable Entered**	**Partial R-Square**	**Model R-Square**	**C(p)**	**F Value**	**Pr > F**
1	Length of test	0.6691	0.6691	11097.40	23708.60	<.0001
2	Final weight	0.1384	0.8075	1554.23	8429.79	<.0001
3	Initial weight	0.0167	0.8242	403.36	1114.90	<.0001

From Table 2.5 it is clear that the length of the testing period in days accounts for most of the variation (67%) in feed intakes, even in the saturated model, where the inter-relationships among variables are taken into account (partial R^2). The second and third most important variables are final and initial weights, which account for 14% and 2%, respectively, of the variation in feed intake. The contributions of ADG, KLB and the age of the animal were lower than 0.2% and were therefore ignored. From this analysis it is therefore possible to draft a regression model to predict a feed intake value for each animal where all of the variables, included in the regression, are known. The

model to predict a feed intake value for Bonsmara centralized tested animals was as follows (only variables included at $p < 0.01$; Total $R^2 = 0.82$):

$$\text{Feed intake} = (-1.872 \times \text{Initial weight}) + (5.988 \times \text{Test length}) + (3.282 \times \text{Final weight}) - 453.535$$
$$\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots(2.3)$$

The Pearson correlation between the measured feed intake values and the predicted feed intake values, (using equation 2.3) for all Bonsmara bulls tested in a centralized growth test is 0.91. This high correlation indicates that the predicted feed intake values can be used as an indication of what the measured feed intake will be.

Equation (2.3) was then used to predict a feed intake value for all on-farm growth tested bulls. By the use of this regression equation, feed intake values between centralized and on-farm growth tested animals, although measured on different diets, can be compared. These feed intakes were then used in equation (2.1) to calculate (predict) profitability values (R-value) for each on-farm growth tested Bonsmara bull.

Table 2.6 presents the general statistics for all bulls tested in a centralized or on-farm growth test from 1975 to 2001 for test length (days), feed intake (kg), predicted feed intakes (kg), R-values and the estimated breeding values (EBV) for R-value.

It can be seen from Table 2.6 that the maximum test length of the centralized and on-farm growth tests differs greatly (140 days for the centralized test and 365 days for the on-farm growth tests). This results in an increase in the average feeding (testing) period of on-farm growth tests of 25 days compared to the centralized tests. This is the reason for the higher average predicted feed intake of 1320.1kg for on-farm growth tested bulls, compared to the average feed intake of 1231.5kg for centralized tested bulls. The average feed intake of the on-farm tested bulls does, however, not differ significantly to the average predicted feed intakes for these centralized tested bulls of 1 232.0kg. The higher feed intake is the reason for a lower average profitability or R-value (average of a loss of R575.76) calculated for bulls tested on an on-farm growth tests. This was however, expected due to farmers only sending selected (perceived "best") bulls to be tested in a centralized growth test while submitting the rest to an on-farm growth test.

Table 2.6 General statistics for centralized and on-farm growth tested animals as well as for pedigree animals'[#] test length (days), feed intake, predicted feed intakes, R-values and the estimated breeding values (EBV) for R-value

Variable	N	Min.	Max.	Mean	Variance	Std Dev	Std Error	Coeff of Variation %
Only the centrally tested bulls								
Test length	9278	84	140	118.16	416.35	20.40	0.188	17.270
Feed Intake	9278	433	2030	1231.53	64932.12	254.82	2.34	20.690
Predicted feed intake	9278	521	1842	1232.02	53715.17	231.77	2.13	18.810
R-value	9278	-1188.27	387.99	-407.26	28188.76	167.90	1.55	-41.225
EBV	9278	-165.96	215.43	16.24	1624.67	40.31	0.40	248.21
On-farm tested bulls								
Test length	67160	84	365	143.14	1143.96	33.82	0.135	23.630
Predicted feed intake	67160	494	3208	1320.10	71041.62	266.54	1.07	20.190
R-value	67160	-2462.45	294.52	-575.76	62922.90	250.84	0.94	-43.567
EBV	67160	-135.84	238.44	15.69	1147.08	33.89	0.13	215.91
Pedigree Animals[#]								
EBV	79204	-165.96	238.44	11.54	935.22	30.58	0.08	265.11

[#] Pedigree animals are parents of tested bulls without own performance

The regression limits the variance around mean values. This could be the reason for the lower standard error of the mean in the on-farm growth tests compared to that of the centralized growth tests.

The mean, standard deviation and coefficient of variation of the EBVs of the pedigree animals were lower than either of the on-farm and/or centrally tested animals. The reason for this could be because these animals often do not have their own measurements and receive an EBV from relatives. BLUP (best linear unbiased prediction) allocates these animals an even more conservative EBV closer to zero.

Figure 2.12 represents the genetic trend for R-value for all bulls tested in the growth tests (Phase C or D) from 1986 to 2001. (As it was decided by the Bonsmara Breed Society to use 1986 as a base year for all genetic traits, the average EBVs of animals born in 1986 was set to zero.)

Figure 2.12 shows an improvement in R-value with an average of R0.81 per annum. This improvement can be explained by the high genetic correlation between feed efficiency traits and profitability (R-value) and also the selection for feed efficiency over years. The genetic trend also shows that the R-value is a trait that can effectively be selected for. Direct selection could even lead to more rapid progress than the indirect correlated response, when selecting for FCR, is only 0.87.
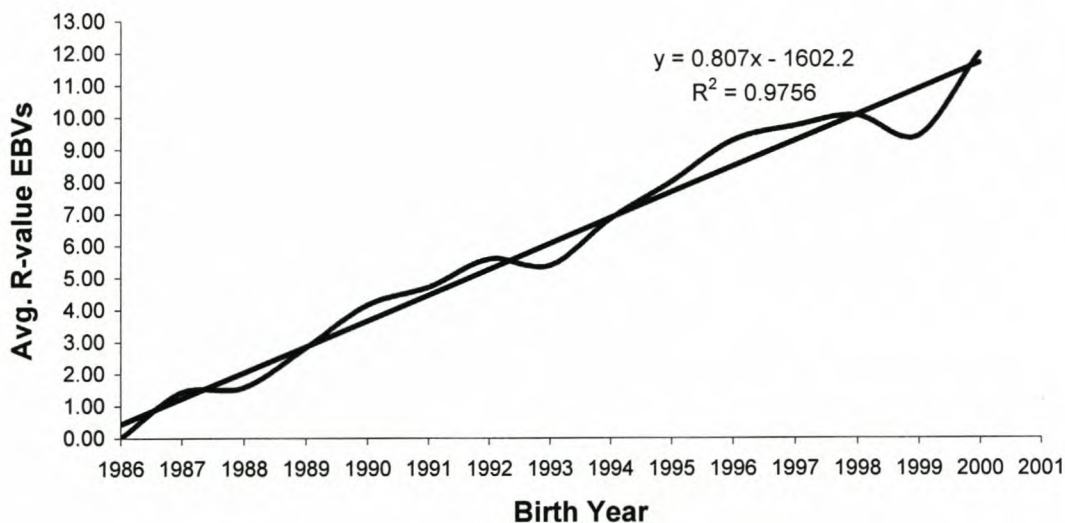

Figure 2.12 Genetic trend for R-value for all performance tested bulls tested in a Phase C or D growth test of the ARC

These calculations of the R-value or profitability were, however, based on a fixed set of economic assumptions. In practice these economic assumptions do change over time. For instance, the feed price might increase or decrease while the carcass price remains the same, or *visa versa*. It is expected to have an influence on the ranking of the animals, based on their R-value EBVs. It would also be of interest to determine which animals will be favoured in rankings when these price ratios change one way or the other and what role an important trait such as feed efficiency will play in these rankings.

Figures 2.13, 2.14 and 2.15 present the feed, weaner and A3-carcass prices from January 1998 to June 2002, respectively.
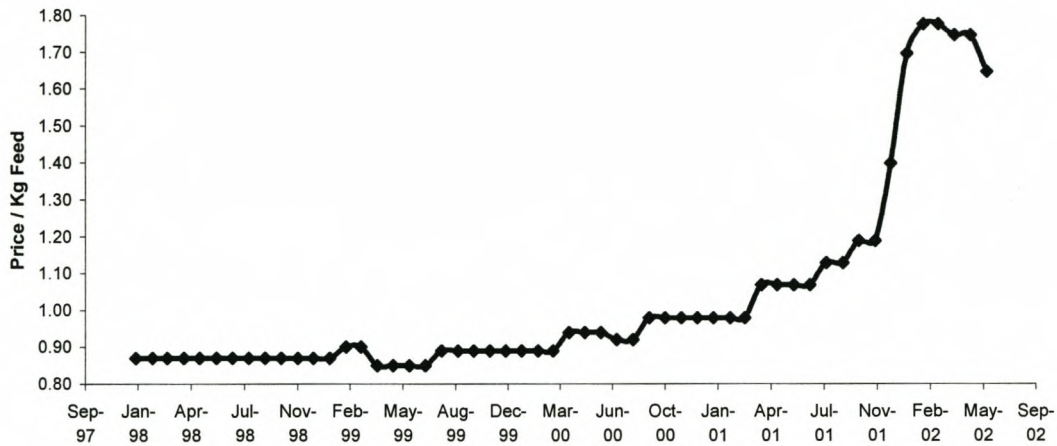

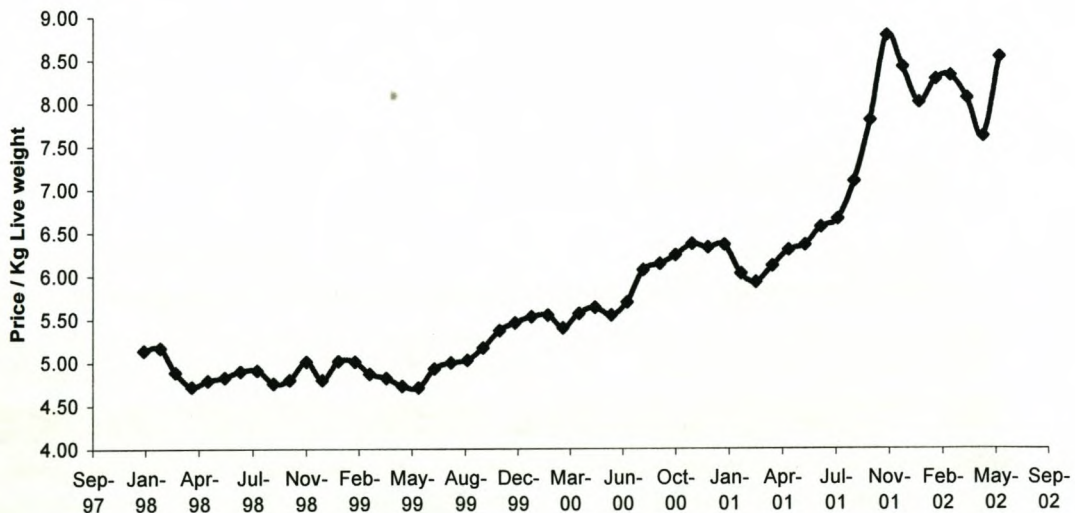**Figure 2.13** Feed prices for the Phase C feed ration from January 1998 to June 2002

Figure 2.14 Weaner prices from January 1998 to June 2002 obtained from The South African Feedlot Association web page
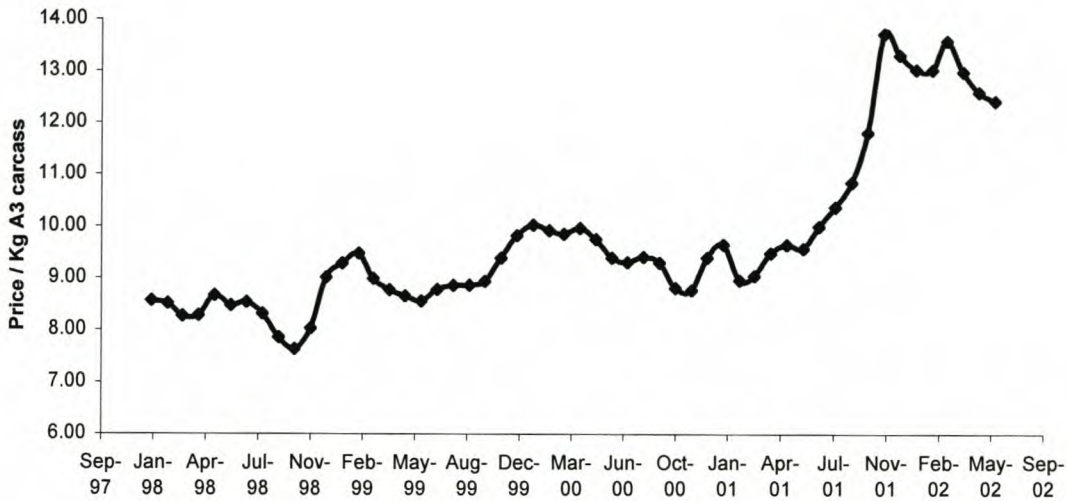
Figure 2.15 A3-carcass prices from January 1998 to June 2002 obtained from SAMIC's web-page

The centralized feed diet price increased gradually by R0.32 per kg from January 1998 (R0.87/kg) to November 2001 (R1.19/kg), thereafter it increased sharply by R0.59 to February 2002 (R1.78/kg) (Figure 2.13). Figure 2.14 and 2.15 shows that the weaner and carcass prices increased from January 1998 to August 2001 by R1.52 and R1.82, respectively, where after the weaner and A3-carcass prices increased sharply by R2.14 and R3.36 per kg in the next three months to reach a maximum in November 2001.

Figure 2.16 presents the A3-carcass/feed price ratio as well as the weaner/feed price ratio between January 1998 and May 2002. The best economic environment to produce beef from the feedlot was in November 2001 (based on positive feed margin) with a carcass price (A3) of 11.6 times that of the feed price (FEE). These animals would have been bought three months earlier (average feeding period) in August 2001 when the weaner price was 5.9 times that of the feed price. The favourable carcass/feed ratio was due to the fact that the carcass and weaner price increased sharply after August 2001 while the feed price only responded a month later. The most unfavourable economic environment for beef production over the time of investigation was in May 2002 with a carcass and weaner price of 7.2 and 4.7 (weaner price of three months earlier (February 2002)) times that of the feed price (UEE), respectively. The average carcass/feed and live weight weaner/feed price ratios over the time under investigation were 9.6 and 5.8 (AEE), respectively.

Figure 2.16 A3-carcass feed price and Weaner feed price ratio from January 1998 to June 2002

Table 2.7 presents the simple Pearson correlations between the R-values for the three different economic environments as mentioned above. From Table 2.7 it is apparent that there is no real difference between R-values in the three different environments as the lowest correlation of 0.80 between FEE and UEE (the two extreme environments) indicates. These different sets of R-values were then used to recalculate EBVs for each centralized tested bull in the different economic environments. Table 2.8 presents the Pearson (above the diagonal) and Spearman (below the diagonal) correlation between the EBVs of the three different sets of R-values.

Table 2.7 Simple Pearson correlation between the R-values in the three different economic environments

	AEE	UEE
FEE	0.92	0.80
AEE		0.97

Table 2.8 Pearson (above the diagonal) and Spearman (below the diagonal) correlations between the EBVs of the three different sets of R-values

	FEE	AEE	UEE
FEE	-	0.94	0.85
AEE	0.93	-	0.96
UEE	0.81	0.96	-

The high Pearson and Spearman correlations between the EBVs amongst the different economic environments (Table 2.8) suggested that the average economic environment could be used to calculate EBVs for R-value or feedlot growth profitability under varying feed/carcass price ratio scenarios. It is therefore not necessary to change the carcass, weaner or feed price on a regular basis to account for possible re-rankings based on R-value EBVs.

2.4 Conclusion

When Bonsmaras are fed under these conditions and assumptions, R-value increases from week one until it reaches an optimum at week ten. By this time all animals have been fed for a period of 98 days (28 days adaptation and 70 days test period). The longer the animals are fed, after 98 days, the less profitable they become and will eventually result in a loss for the feedlot.

The heritability estimate of R-value indicates that this trait is genetically inherited and that it can be selected for.

The genetic correlation estimate of –0.92 between FCR and R-value indicates that R-values can be improved by selection for animals with a favourable feed conversion ratio.

Heritabilities obtained from random-regression methodology were generally higher than heritabilities estimated by multitrait analysis. The advantage of using random-regression models are that random-regression models takes the time lag between measurements into account and that it is now possible to calculate a breeding value for an animal on any given time (age) on the trajectory.

It is possible to predict a feed intake value for performance-tested animals where animals were group fed with the help of a regression equation ($R^2 = 0.82$). Consequently, a feedlot or post-weaning growth profitability value can also be calculated for performance-tested animals with unknown feed intakes. The heritability, breeding values and genetic trend of R-value suggested that this trait should be considered in any beef feedlot system to select for. It is suggested to select for the breeding objective (feedlot profitability) rather than for the individual contributing traits or selection criteria. The high correlations obtained between EBVs for R-value from different economic (favourable to an unfavourable) environments show that the average carcass, live weaner and feed prices over the last 54 months can be used as an indication of economic factors and it is not necessary to change these factors on a regular basis.

CHAPTER 3

GENETIC VARIANCE COMPONENTS FOR RESIDUAL FEED INTAKE AND FEED CONVERSION RATIO AND THEIR CORRELATIONS WITH THE OBJECTIVE

3.1 Introduction

The high feeding cost of animals is a major constraint in profitability in livestock production enterprises. Feed costs represent approximately one-half of the total cost of production for most classes of livestock. Therefore, improvement of feed efficiency should be a major consideration in most breeding programmes (Kennedy *et al.*, 1993). Genetic selection to improve feed efficiency aims to reduce the cost of feeding in beef cattle production and thereby improve profitability.

Traditionally, selection for growth rate has received considerable emphasis in most breed improvement schemes. Its value to the improvement of enterprise efficiency and profitability of ruminant production systems has, however, been questioned, as increased mature size is a direct consequence, resulting in an increased cost of maintaining females (Barlow, 1984; Scholtz & Roux, 1984). Thompson & Barlow (1986) showed that greater improvements in enterprise efficiency would result from improvement in feed conversion efficiency of the growing animal and reduction in feed intake of the mature dam. Evidence for genetic variation in either of these traits was equivocal at the time. Koots *et al.* (1994b) reported highly negative weighted genetic correlations between feed conversion ratio (FCR) and growth rate and size. These correlations indicate that selection to reduce FCR and thus improve efficiency would be accompanied by an increase in growth rate, and an increase in mature cow size.

A second disadvantage of selection on FCR relates to problems inherent with selection on ratio measurements (Gunsett, 1986), involving two different traits (feed intake and growth) with different variances within them.

Considerable variation in feed intake, independent of size and growth rate, exists in beef cattle. This trait is defined as residual (or net) feed intake (RFI) (Archer *et al.*, 1997). There has been considerable interest in RFI as a measure of feed efficiency in animals. Much of that interest has been in quantifying the amount of variability in RFI and determining how much of the variability is genetic (Kennedy *et al.*, 1993).

The biggest advantage of using RFI as an efficiency trait instead of FCR, as stated in the literature by Archer *et al.* (1997; 1998) and Herd & Bishop (2000), is the fact that RFI is not defined as a ratio trait and that selection to reduce RFI offers an opportunity to reduce feed intake, without compromising growth performance, and also without the possible correlated response in maturity type. These arguments are therefore that the inclusion of RFI will contribute towards both pre-weaning as well as post-weaning profitability in beef production.

Unfortunately, little work has been done on RFI and on the genetic correlations between RFI, FCR and other production and reproduction trait in beef cattle under South African production and economical environments. The aim of this study was to estimate genetic (co)-variances (and ratios) between weaning weight and other traits and to compare RFI and FCR with growth (average daily gain (ADG), weaning weight (WW) and shoulder height (SHD)), reproductive (scrotum circumference (SCR)) and profitability traits measured in growth tests of young bulls. These results will serve as a clear indication of the value of inclusion of RFI and FCR in breeding objectives aimed at breeding more profitable feedlot cattle under South African production and economical environments.

3.2 Materials and Methods

The data analysed in this study was collected from the centralized growth test stations of South Africa's Agricultural Research Council (ARC). Records from Bonsmara bulls, tested in centralized growth tests between 1989 and 2001 were used. The data set consists of the individual feed intake and weights of 6 738 bulls. For additional information on the data see Chapter 2.

Traits measured in a centralized growth test are, amongst other, feed intake, weight increase (growth), scrotum circumference (SCR) and shoulder height (SHD). Individual feed intakes and weight increase make it possible to calculate average daily gain (ADG), feed conversion ratio (FCR), residual (or net) feed intake (RFI) as well as a feedlot profitability value for each bull (or a post-weaning growth monetary value). Feed conversion ratio is the amount of feed consumed by the animal in order to gain a kilogram in body (live) weight. Residual (or net) feed intake is defined as the amount of feed eaten by an animal less or more than what would be expected for the growth of the animal and its body weight (used as an indicator of maintenance requirements).

More precisely, RFI is calculated as the error term (e) when fitting the equation:

$$\text{Feed intake} = \mu + (\beta_w \times \text{mean metabolic weight}) + (\beta_g \times \text{weight gain}) + e,$$

Where:

Feed intake = the daily feed intake in kg;

μ = constant;

mean metabolic weight = mean (weight$^{0.73}$) of the animal for the feed intake test period;

weight gain = live weight gain (kg/day) over the feed intake test period;

β_w and β_g = the regression coefficients for metabolic and weight gain;

e = the RFI.

A post-weaning growth monetary value, calculated in Rand (R-value), for each bull was simulated as if the tested bull was fed under feedlot conditions and sold to an abattoir. Equation 2.1, as given in Chapter 2, was used to simulate a profit value (R-value) for each bull at the completion of the test period.

Variance components, heritabilities and genetic correlations for and between weaning weight (WW), ADG, SCR, SHD, FCR, RFI and R-value were estimated simultaneously by multitrait restricted maximum likelihood (REML) procedures using the VCE package developed by Groeneveld (1994). Three multitrait analyses were done. The first multitrait analysis included six traits, namely WW, ADG, SCR, SHD, FCR and R-value. In a subsequent analysis, FCR was removed from the model and RFI was included into the model. The third and last multitrait analysis included all seven traits.

The importance of non-genetic sources of variation on the traits was determined by the PROC GLM procedure of SAS (2000). Non-genetic sources that were included in the models for WW were the linear and quadratic regression of the age of the dam, the linear and quadratic regression of the age of the animal at weaning and the contemporary group for weaning weights (herd, weaning date, treatment code and sex) as fixed effects (1 246 levels). For ADG only the linear regression of the age of the dam and the contemporary group fixed effect for the growth test (which include test centre, test year, test phase and test number) were included in the model (514 levels). For SCR and

SHD the linear and quadratic regression of the age of the animal at the end of the growth test, the linear regressions of the age of the dam and the contemporary group fixed effect for the growth test were included as non-genetic sources. For FCR, RFI and R-value the linear regression of the age of the animal at the end of the growth test and age of the dam were included and the contemporary group effect as a fixed effect. These non-genetic sources were significant (P < 0.001) and were therefore included in the models for FCR, RFI and R-value. Table 3.1 gives a summary of the different models used for each trait.

Table 3.1 Summary for the different models used for different traits

Factor	Effect	Levels	WW	ADG	SCR	SHD	FCR	RFI	R-Value
Age	C				X	X	X	X	X
Age^2	C				X	X			
Dam age	C		X	X	X	X	X	X	X
Dam age^2	C		X						
Weaning age	C		X						
Weaning age^2	C		X						
Growth-test contemporary	F	514		X	X	X	X	X	X
Weaning contemporary	F	1 246	X						

Age = Age of the animal at the end of the growth test, Dam age = Age of the dam at end of test, Weaning age = age of the animal at weaning, C = Covariate, F = Fixed effect, Growth-test contemporary (test centre, test year, test phase and test number), Wean contemporary group (herd, wean date, index code for treatment and sex).

In order to compare the effectiveness of response in R-value based on selection for RFI or FCR, expected correlated responses were estimated. Selection intensities for both traits were assumed to be equal and were therefore cancelled out of the equation of Falconer & Mackay (1996):

$$R_{2.1} / R_2 \quad = \quad r_A \ (h_1 / h_2)$$

where: $R_{2.1}$ = Correlated response on trait 2 when selecting for trait 1;

               R_2 = Direct response on trait 2 under selection for trait 2;

               r_A = Genetic correlation between trait 1 and 2;

               h_1 and h_2 = Square root of the heritability of trait 1 and trait 2, respectively.

Indirect selection will be better than direct selection if $R_{2.1}$ is larger than R_2, therefore ($r_A \times h_1$) must be greater than h_2. Indirect selection can therefore not be expected to be better unless the secondary character has a substantially higher heritability and the genetic correlation is high.

3.3 Results and Discussion

Table 3.2 presents the general statistics for the different traits and covariates included in the different models.

It can be seen from Table 3.2 that the least profitable animal in the growth tests has resulted in a loss of R824.78 while the most profitable animal resulted in a profit of R494.36 under the mentioned assumptions. The average R-value was a loss of R223.93 with a standard deviation of R141.28. This accentuates the necessity of selecting the most suitable animals for feedlotting in order to make a profit. The mean FCR (6.44±0.81) corresponds with the mean FCR of 6.5±0.9 obtained by Arthur et al. (2001). The range of RFI of −3.73 to 3.56 correlates well with the range estimated for Bonsmara cattle by Archer & Bergh (2000) of between −3.76 and 3.72. The mean RFI of 0.11±0.91, however, differs from the mean of 0.00±0.67 presented by Archer & Bergh (2000) as well as the zero mean obtained by both Herd & Bishop (2000) and Arthur et al. (2001). The reason for the difference in the mean of this study is the result of the way the regression coefficients for metabolic weight and gain were applied in the calculations of RFI. These coefficients were obtained from an initial extended data file (11 839 records) before it was reduced to 6 738 records to be able to estimate genetic variance components. Figure 3.1 presents the frequency distribution for RFI. The skewness statistic for this distribution is −0.0429, while the standard error of skewness is 0.0298. Since two times the standard error of skewness is larger than the absolute value for the skewness statistic the distribution is not significantly skewed. The data is leptokurtic ("taller" then a normally distributed population) due to a positive (0.475±0.119) kurtosis statistic.

Table 3.2 General statistics for the different traits and covariances in models

Trait/Covariance	Min.	Max.	Avg.	Std. Dev.
WW (kg)	125	375	234	30.67
ADG (kg)	857	2680	1654	237.60
SCR (mm)	210	470	342	27.70
SHD (mm)	1060	1580	1195	35.13
FCR (kg)	3.67	9.74	6.44	0.81
RFI	-3.73	3.56	0.11	0.91
R-Value (R)	-824.78	494.36	-223.93	141.28
Age (days)	272	410	358	26.61
Age of the dam (days)	669	6032	2195	1008.14
Weaning Age (days)	150	269	205	23.30

Age = Age of the animal at the end of the growth test, Dam age = Age of the dam at the end of test, Weaning age = age of the animal at weaning

Table 3.3 presents the summary of the stepwise regression procedure that was fitted in order to determine to what extend does FRC and RFI contribute to the variances of R-Value.
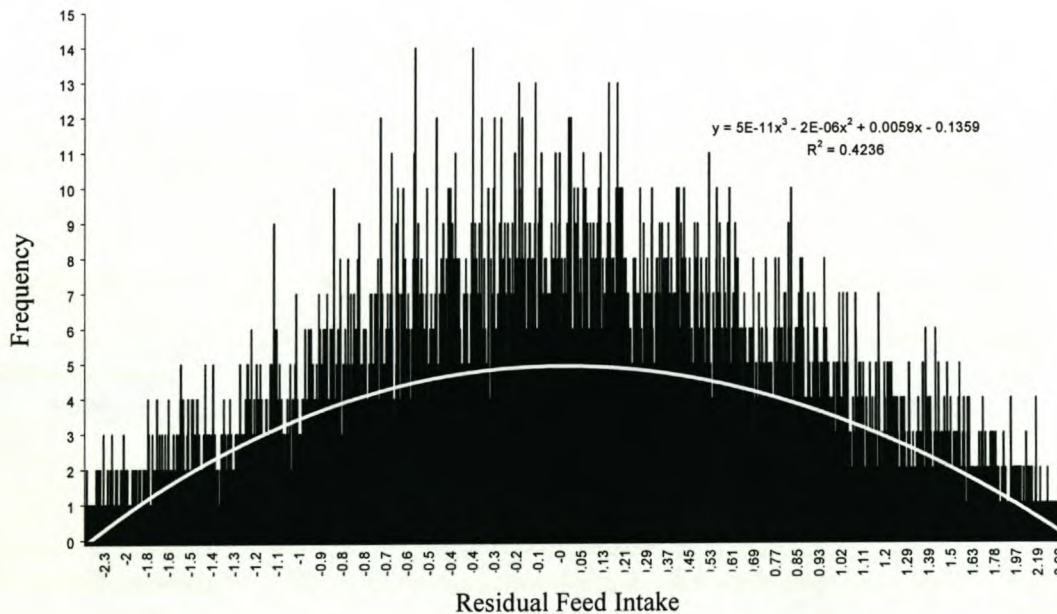

$y = 5E\text{-}11x^3 - 2E\text{-}06x^2 + 0.0059x - 0.1359$
$R^2 = 0.4236$

Figure 3.1   Frequency distribution of RFI

Table 3.3 Summary of stepwise regression model to predict R-Value

Summary of Stepwise Procedure to predict R-Value when FCR was included						
Step	Variable Entered	Partial R-Square	Model R-Square	C(p)	F Value	Pr > F
1	FCR	0.7385	0.7385	1402.08	19022.80	<.0001
2	WW	0.0432	0.7817	61.00	1331.61	<.0001
3	ADG	0.0008	0.7824	39.12	23.75	<.0001
4	SHD	0.0009	0.7833	13.43	27.65	<.0001
5	SCR	0.0003	0.7836	6.00	9.43	0.0021
Summary of Stepwise Procedure to predict R-Value when RFI was included						
Step	Variable Entered	Partial R-Square	Model R-Square	C(p)	F Value	Pr > F
1	RFI	0.3609	0.3609	8918.35	3804.57	<.0001
2	ADG	0.2211	0.5821	3504.33	3563.48	<.0001
3	WW	0.1303	0.7124	313.77	3052.15	<.0001
4	SHD	0.0104	0.7228	61.69	251.97	<.0001
5	SCR	0.0024	0.7251	6.00	57.69	<.0001
Summary of Stepwise Procedure to predict R-Value when FCR and RFI was included						
Step	Variable Entered	Partial R-Square	Model R-Square	C(p)	F Value	Pr > F
1	FCR	0.7385	0.7385	1420.70	19022.80	<.0001
2	WW	0.0432	0.7817	76.55	1331.61	<.0001
3	RFI	0.0016	0.7833	27.85	50.53	<.0001
4	SHD	0.0006	0.7839	10.86	18.97	<.0001
5	SCR	0.0002	0.7841	5.23	7.64	0.0057
6	ADG	0.0000	0.7841	-	-	-

Seventy four percent of the variance of R-value is explained by FCR while RFI only explained 36% of the variance. When FCR and RFI was included simultaneously in a stepwise procedure FCR still explains the biggest part of the variation (74%) in R-value while RFI only explains an additional 0.2%. When FCR and RFI are both included in the stepwise procedure ADG does not contributes to

the variation in R-value. Because FCR is a component of R-value, it was expected that a large portion of the variation is explained by it. A greater improvement in R-value is therefore expected with an improvement in FCR than with RFI.

The heritability and genetic correlation estimates for and between traits of the three different multitrait models were the same up to two decimals. This shows that the co-linearity effect between FCR and RFI has little impact on the performance estimates. Therefore, only results of the seven-trait analysis (third model) will be presented.

Table 3.4 presents the heritabilities and genetic correlation estimates for and among the different traits investigated in this study as well as some estimates from the literature (Koots *et al.*, 1994a; b; Arthur *et al.*, 2001). Unfortunately, when RFI was additionally included in the multitrait analysis, VCE finished with status 3 (Groeneveld, 1994) and therefore, the standard errors of heritabilities were not available.

Table 3.4 Heritability (on diagonal and bold) and genetic correlation estimates (above diagonal) for and among traits

Trait	WW	ADG	SCR	SHD	FCR	RFI	R-Value
WW	**0.32** 0.24[*]	0.28 0.39[#]	0.15 0.30[#]	0.50 0.53[#]	-0.03 0.16[#]	-0.05	-0.24
ADG		**0.37** 0.31[*]	0.21 0.27[#]	0.48 0.41[#]	-0.69 -0.53[#]	-0.09	0.65
SCR			**0.42** 0.48[*]	0.09 0.14[#]	-0.06 -0.04[#]	0.05	0.01
SHD				**0.52** 0.61[*]	-0.24 0.22[#]	-0.02	0.10
FCR					**0.34** 0.32[*]	0.75	-0.92
RFI						**0.31** 0.32[**]	-0.59
R-Value							**0.36**

[*] Koots *et al.* (1994a), [#] Koots *et al.* (1994b), [**] Arthur *et al.* (2001)

The heritabilities for and genetic correlation estimates between WW, ADG, SCR, SHD and FCR are of the same order as those obtained by Koots *et al.* (1994a; b) as shown in Table 3.4. The large difference in heritability estimates for WW, compared to literature values, can be ascribed to the exclusion of maternal genetic effect in the current study (Koots *et al.*, 1994a; b). The only two genetic correlations between weaning weight and other traits that were in the same order as correlations obtained by Koots *et al.* (1994b) were the correlations between WW and SHD (0.50) and between WW and ADG (0.28). However, it should be kept in mind that the estimates reported by Koots *et al.* (1994b) were obtained from two-trait analyses, compared to the seven-trait analysis in this study. This could be a reason for the differences between the genetic correlations obtained in this study compared to the correlations obtained by Koots *et al.* (1994b).

Weaning weight, due to its low genetic correlation with other traits, is a poor predictor of an animal's feedlot post-weaning growth efficiency and profitability.

The heritability estimate of 0.34 for FCR corresponds well with the mean estimate reported by Koots *et al.* (1994a), as well as those obtained by Archer *et al.* (1999), Robinson *et al.* (1999) and Herd & Bishop (2000), but is slightly lower than the 0.42 obtained by Arthur *et al.* (2001). The heritability estimate of 0.31 for RFI corresponds to that of 0.32 estimated by Arthur *et al.* (2001). The heritability estimates for both these two traits are, however, higher than those obtained by Van Bebber & Mercer (1994) for FCR and RFI of 0.12 and 0.21, respectively.

The genetic correlation estimate between RFI and FCR of 0.75 is very close to the estimate of 0.74 in broilers obtained by Van Bebber & Mercer (1994). The correlation estimates between RFI and the other traits were almost zero. This confirms that RFI is genetically independent of ADG and SHD. Selection for growth rate (ADG) has been repeatedly associated with an increase in cow size and its benefit to overall herd productivity has been seriously questioned (Barlow, 1984; Scholtz & Roux, 1984).

The biggest advantage in the use of RFI is therefore its independence from ADG and SHD and, therefore, genetic selection against RFI has the potential to improve feed efficiency in the young animal without increasing cow size. FCR on the other hand is lowly correlated with SHD (-0.24). This indicates that selection for FCR will have a small positive effect on SHD and that it is possible to select animals with a low FCR without a drastic change in SHD, and therefore mature type.

A high genetic correlation estimate of -0.92 between FCR and R-value was obtained. This was expected because for each kg feed an animal consumes less, in order to gain a kg in body weight, the more profitable the animal becomes to the producer (see equation 2.1). The genetic correlation estimate between ADG and R-value of 0.65 also shows an increase in R-value with an increase in ADG. RFI is also genetically correlated with the R-value (-0.59), but to a much lesser degree than FCR.

Table 3.5 Expected correlated response in R-value through selection for FCR, RFI and direct selection for R-value

	Selection for FCR	**Selection for RFI**	**Selection for R-value**
Selection response on R-value	0.87	0.55	1.00
Improvement in R-value per generation, when 30% best bulls are selected	R50.36	R31.84	R57.89

The expected correlated response in R-value through indirect selection for FCR ($R_{FCR-R-value}/R_{R-value}$) relative to direct selection for the R-value was 0.87, while the expected correlated response in R-value through indirect selection for RFI ($R_{RFI-R-value}/R_{R-value}$) was 0.55 (Table 3.5). This means that if the 30% most profitable sires (based on R-values) were selected on profitability (R-value), to be used as parents for the next generation, the response on selection is R57.89 (with a selection deferential of R160.81). When 30% of bulls are selected directly for FCR, the correlated response of selection on R-value therefore will only be R50.36, R7.53 per generation less then direct selection for R-value. When the best 30% of bulls are selected on RFI, the correlated response of selection in the next generation for R-value will only be R31.84, R26.05 per generation less than direct selection on R-value. These results suggest that it would be more efficient to select directly for R-value than through indirect selection on either FCR or RFI. Where the R-value cannot be calculated and direct selection is not possible, it would be better to select indirectly for R-value through the use of FCR rather than RFI.

3.4 Conclusion

For Bonsmara cattle, under South African conditions, the genetic correlations between weaning weight and other traits contributing to feedlot profitability were low to negligible. This suggests that the indirect genetic response in these traits through the direct selection on weaning weight would be small, if any.

The stepwise regression partial R-square values, genetic correlations and expected correlated responses between RFI and FCR with R-value suggest that indirect selection for R-value through the selection for FCR and/or RFI will result in slower genetic gain in R-value than direct selection for R-value. However, where the R-value cannot be calculated and/or direct selection for R-value is not possible, it would be better to select indirectly for R-value through the use of FCR rather than RFI. Faster genetic gain would be achieved by selection for the objective expressed in monitory terms, than selecting for contributing traits.

CHAPTER 4

A PROPOSED SELECTION INDEX FOR FEEDLOT PROFITABILITY BASED ON BREEDING VALUE PREDICTIONS OF SELECTION CRITERIA RELATED TO THE OBJECTIVE

4.1 Introduction

The variable costs of post-weaning growth and finishing cattle in a feedlot play a major role in the ultimate profitability of beef production. It is therefore important that the biological differences amongst animals be exploited and individuals identified that can be used as parent stock to increase the biological, and ultimately economical efficiency of feedlot animals.

Despite manipulation of the environment and cattle management to reduce feed costs, it has also been known for several decades that feed intake and measures of feed efficiency are heritable in beef cattle (Johnston, 2002).

Feed intake and growth (gain) are measured in centralized growth tests of the Agricultural Research Council (ARC) in South Africa. The problem, however, is to use this data in an appropriate way when selection decisions are made so as to select the most profitable feedlot animals.

Profitability is a composite trait involving a number of component traits (Dickerson, 1969). Therefore, an appropriate manner in which to define a post-weaning profitability value or feedlot growth profitability value could be by means of a selection index, which includes the major components determining profitability (e.g. feed intake and gain) as well as their relative economic values.

The aim of this study was to compose a single post-weaning growth (feedlot) index based on the economic values of different components, which determine profitability in a post-weaning growth test or feedlot by using selection index methodology and breeding value predictions.

4.2 Materials and Methods

The dataset, to estimate genetic variance components in this Chapter (after appropriate editing was performed), consists of the individual feed intake and weight recordings of 6 995 Bonsmara bulls. Only bulls tested between 1990 and 2001 were used in the estimation of variance components. The pedigree file represented 26 076 animals with 3 555 sires and 15 783 dams. This dataset only includes bulls measured in the 16 and 12-week growth tests. For additional information on the data see Chapter 2.

The importance of non-genetic sources of variation on the traits was determined by the PROC GLM procedure of SAS (2000). Non-genetic sources (at a significance level of $p<0.001$) that were included in the models for initial weight, final weight and shoulder height were the linear regression of the age of the dam, the linear and quadratic regression of the age of the animal at the end of the growth test and the contemporary group (fixed) effect for the growth test (which include test centre, test year and test number, i.e. the number of the test the animal tested in during that specific test year) (524 levels). Test length was confounded with year and therefore, test length was not included in the model. The linear regression of the age of the dam was not significant for feed intake and therefore only the linear and quadratic regressions of the age of the animal at the end of the growth test and the contemporary group fixed effect for the growth test were included in the final model.

Variance components, heritabilities and genetic correlations for and between initial weight (IW), final weight (FW), feed intake (FI) during the test period and shoulder height (SHD) were estimated through the use of multitrait restricted maximum likelihood (REML) procedures using the VCE package developed by Groeneveld (1994). Shoulder height was included in the multitrait analysis to account for differences in mature size (maturity types) among bulls. This should also enable breeders to select economically fast growers with an appropriate frame size whose daughters could be used as replacement heifers.

The following model equation was used for the analysis:

$$y = Xb + Za + e,$$

where:

y = vector of the observations for the ith trait;

b = vector of fixed effects for the ith trait;

a = vector of random animal effects for the ith trait;

e = vector of random residual effects for the ith trait.

X and Z are incidence matrixes relating records of the ith trait to fixed and random animal effects, respectively.

After the estimation of variance components was performed the components were used to predict breeding values for each animal for the different traits. These breeding values (EBVs) were then used in a selection index to calculate a single economical value, or a gross test value (GTV), for each animal. This economical value is an indication of the gross profitability of the animal in a post-weaning growth test.

It is generally accepted that the selection index is, in most cases, the most accurate method to use. The optimal procedure for selection uses all the information available about each individual's breeding value, combined into an index of merit (Falconer & Mackay, 1996). The aim of a selection index is to combine all relevant information into a single numeric value on the basis of which individuals will be selected. The construction of an index is not easy without the use of matrix methods, particularly if there are more than two sources of information (Nicholas, 1987; Van Vleck, 1993). Lerner (1961) also stated that the accuracy of the selection index, as compared to an independent culling levels procedure, improves as the number of traits in the selection index increase.

This selection index (based on BLUP EBVs) differs from the classic Smith-Hazel selection index method in the sense that in the classic index, phenotypic values are used to calculate the relevant b-values, which also include the correlations between the relative traits. In the constructed selection index in the current study a multitrait animal model was used to calculate breeding values. As all genetic covariances among traits were accounted for in the breeding value predictions, the drafting of the selection index for each animal was thus simply a function of the economic value of each trait.

The following selection index was used to calculate the GTV for each animal:

GTV (in South African Rand) = $(((EBV_{FW} \times 12.35) \times 55\%) - (EBV_{IW} \times 8.25)) - (EBV_{FI} \times R0.90)$

where:

EBV_{FW} = Estimated Breeding Value of Final Weight;

EBV_{IW} = Estimated Breeding Value of Initial Weight;

EBV_{FI} = Estimated Breeding Value of Feed Intake.

The following assumptions were made in order to calculate the GTV:

- Live weight weaner calf price at R8.25 per kilogram
- A3 Carcass price of R12.35 per kilogram (It is assumed that all bulls are classified as A3)
- Dressing percentage at 55%
- Feed cost set at R0.90 per kilogram.

In order to test the normality of the distribution of GTV, the skewness and kurtosis statistics for GTV were obtained by using the PROC MEANS procedure of SAS (2000).

4.3 Results and Discussion

Table 4.1 presents the general statistics (for the 6 995 animals in the edited dataset) for the different traits and co-variances (grouped into the different test lengths) included in the different models for the estimation of variance components, heritabilities and genetic correlations.

The average age of the animals at the end of the growth test was 357.8 days. The youngest animal was 272 days old while the oldest animal was 410 days (a difference of 138 days). The age of the dams varied from one year and 10 months (669 days) to 15 years, with an average of 6 years of age (From Table 4.1).

Table 4.1 General statistics for the initial weight (IW), final weight (FW), feed intake (FI), shoulder height (SHD), age and age of the dam at entering of growth tests

Trait	Min.	Max.	Avg.	Std.
IW (kg)	139	414	260.19	32.21
FW (kg) (16-wk)	280	585	438.12	42.72
FW (kg) (12-wk)	232	568	403.00	48.21
FI (kg) (16-wk)	656	1685	1192.74	137.50
FI (kg) (12-wk)	433	1188	853.18	114.29
SHD (mm) (16-wk)	1070	1580	1202.51	33.81
SHD (mm) (12-wk)	1050	1310	1174.05	32.69
Age (days)*	272	410	357.76	26.81
Dam age (days)*	669	5493	2162.90	1013.90

* = at end of growth test, 16-wk = 16-week growth test (116 days), 12-wk = 12-week growth test (84 days)

Table 4.1 also shows that the weight of the animals at the onset of the growth tests varied between 139kg and 414kg with an average of 260.2kg and a standard deviation of 32.2kg. The minimum and maximum weight of animals at the end of the growth tests for the 16-week testing period were 280kg and 585kg, which were obviously higher then the 232kg and 568kg, respectively, for animals tested in a 12-week testing period.

The general statistics for shoulder height between the two different test periods, however, did not differ significantly. The difference between the average shoulder height for animals tested in a 16-week test compared to animals tested in a 12-week test was only 28.46mm, with a difference in the standard deviation of only 1.12mm. This correlates with the lower standard deviation for final weight for animals tested in a 16-week test period, compared to animals tested in a 12-week test.

Table 4.2 presents the heritability and genetic correlation estimates for and between the different traits. The heritabilities obtained for IW and FW were 0.41 and 0.40, respectively, with a genetic correlation of 0.78 between them. Although these estimates are lower than those obtained from the random-regression models in Chapter 2, they are slightly higher than those reported by Koots *et al.* (1994a) for weaning and yearling weights of 0.27 and 0.35, respectively. The reason for these higher heritabilities compared to those of Koots *et al.* (1994a) could be due to the inclusion of the maternal effects in both weaning and yearling weights. In this study the maternal effects on weights

were ignored. The genetic correlation estimate between IW and FW of 0.78 obtained in this study is exactly the same as the value between weaning and yearling weights as presented by Koots *et al.* (1994b).

Table 4.2 Heritabilities on the diagonal and genetic correlations above the diagonal (± standard errors) for and between traits

Trait	IW	FW	FI	SHD
Initial Weight (IW)	**0.41±0.02**	0.78±0.02	0.41±0.05	0.40±0.03
Final Weight (FW)		**0.40±0.02**	0.70±0.03	0.55±0.03
Feed Intake (FI)			**0.33±0.02**	0.39±0.04
Shoulder Height (SHD)				**0.51±0.02**

The heritability of 0.33 for FI corresponds to the heritabilities published elsewhere in the literature (Archer *et al.* 1998; Arthur *et al.* 2001; Herd & Bishop 2000). Koots *et al.* (1994a), however, presented a mean heritability of 0.41 for feed intake in their review paper. The heritability of 0.33 approximately corresponds to the heritabilities obtained by the random-regression model (varied between 0.28 and 0.45) in Chapter 2. Koots *et al.* (1994b) presented genetic correlations of 0.67 (between FI and weaning weight), 0.79 (between FI and yearling weight) and 0.38 (between FI and yearling height). Besides the higher average correlation of 0.67 between FI and weaning weight obtained by Koots *et al.* (1994b), (compared to the correlation of 0.41 between FI and IW obtained in this study) the correlations between FI and IW and between FI and SHD correspond well to the correlations between FI and yearling weight and between FI and yearling height reported by Koots *et al.* (1994b).

The genetic correlation between FI and FW of 0.70 was higher than the correlation of 0.41 between FI and IW. The heritability of 0.51 for SHD corresponds to heritabilities obtained by the Animal Improvement Institute of the Agricultural Research Council (ARC) for ten different breeds (Anon., 1999).

After fitting the appropriate models, using the estimated genetic (co)variances, BLUP breeding values (EBVs) were obtained for each animal. These EBVs were then used in the selection index to calculate the GTV for each bull. Figure 4.1 presents the distribution of GTVs.
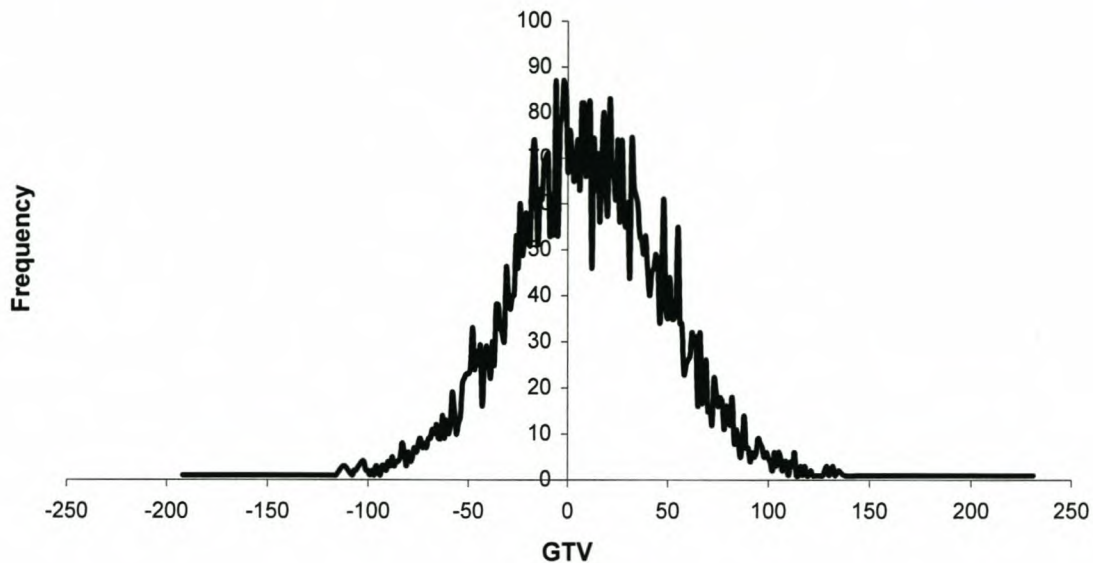
Figure 4.1 Frequency distribution of Gross Test Value (GTV) in SA Rand

The skewness statistic for this distribution is 0.017 while the standard error of skewness is 0.0293. Since two times the standard error of skewness is greater than the absolute value for the skewness statistic, the distribution is not significantly skewed. The data is, however, leptokurtic ("taller" then a normally distributed population) due to a positive (0.845±0.059) kurtosis statistic. Although the data is leptokurtic, it was assumed that GTVs is normally distributed. The GTV-values varied between -R192.17 and R231.38 with an average of R9.31 and a standard deviation of R39.96. The coefficient of variation for GTV was 4.29% indicating that there is variation in this trait and that it can be selected for.

Table 4.3 presents the simple Pearson correlations between the individual GTVs and corresponding estimated breeding values (EBVs) of average daily gain (ADG), shoulder height (SHD), Kleiber ratio (KLB), feed conversion ratio (FCR) and weaning weight (WW), obtained from the 2002 national BLUP (best linear unbiased prediction) analysis for the Bonsmara breed.

Table 4.3 Pearson correlations between GTV and EBV's of other production traits

Production/Reproductive Trait	Pearson Correlation with GTV
Average Daily Gain (ADG)	0.68
Shoulder Height (SHD)	0.29
Kleiber Ratio (KLB)	0.26
Feed Conversion Ratio (FCR)	-0.51
Weaning Weight (WW)	0.31

The Pearson correlations between the EBVs and GTVs ranged from -0.51 to 0.68. The lowest correlation (closest to zero) was 0.26 between KLB and GTV. Correlations of 0.68 and -0.51 were estimated between ADG and GTV and FCR and GTV, respectively. Although these correlations are moderate they indicate that an increase in the GTV can be expected with an increase of ADG or a decrease in FCR.

The Pearson and Spearman correlations between the R-value EBVs (the objective of this study), discussed in Chapter 2, and the index values for post-weaning performance in this Chapter were both very high (0.97). This high correlation indicates that it does not matter which method is used to calculate a genetic post-weaning growth of feedlot profitability value. Table 4.4 presents the breeding values for the objective (post-weaning growth of feedlot profitability value, discussed in Chapter 2) as well as the selection index values for post-weaning or feedlot performance for the bottom and top 10 animals, based on the objective.

Table 4.4 Breeding values for feedlot profitability and selection index values for post-weaning performance for the bottom and top 10 animals based on feedlot profitability EBVs

Animal	Objective (R-value EBVs)	Selection Index (GTV)
40604308	-184.11	-189.03
41608746	-170.62	-163.63
40611923	-163.00	-192.17
42564948	-156.76	-153.56
41608886	-147.69	-158.26
36802106	-144.28	-138.15
36989689	-140.75	-151.37
22587513	-139.99	-175.73
26929042	-134.57	-131.99
42317131	-132.05	-139.53
.	.	.
.	.	.
.	.	.
.	.	.
.	.	.
28679801	153.84	161.00
42977686	160.17	158.25
43800895	165.06	135.20
21491196	165.48	182.38
38802914	167.16	164.37
43845064	167.73	162.33
22282891	169.13	168.44
40085276	170.56	179.84
23075948	175.33	174.86
43796929	218.88	231.38

Figure 4.2 presents the genetic trend of the selection index value (GTV). As shown in Figure 4.2, there was an improvement in GTV over years, but with fluctuation between years. The genetic improvement in GTV over the years could possibly be explained be the favourable correlations between GTV and FCR and GTV and ADG. The fact that breeders have selected for ADG and FCR in the past, together with these favourable correlations with GTV, could be the reason for the genetic improvement of R1.55 per year (Figure 4.2) in GTV over the last 12 years.
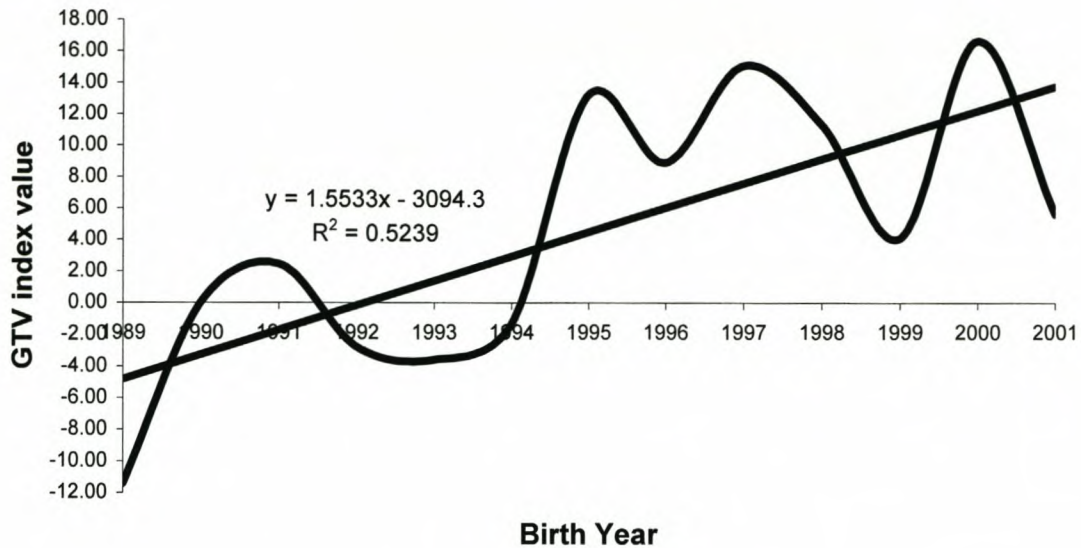
$$y = 1.5533x - 3094.3$$
$$R^2 = 0.5239$$

Birth Year

Figure 2.7 Genetic trend of the GTV selection index value

4.4 Conclusions

It is possible to select for a post-weaning profitability or gross test profitability value. The Pearson and Spearman correlations between the objective (feedlot profitability value) and the post-weaning performance index values indicate that it is not important which of the two methods are used to calculate a genetic feedlot or post-weaning growth profitability value to be used in selection decisions. The selection index value is, however, more simple than the feedlot profitability with less assumptions. It is recommended that the post-weaning selection index value be used as a selection criterion in breeding programmes to improve post-weaning growth profitability rather then the more complex feedlot profitability value (R-value). The selection index can benefit the feedlot industry by selecting offspring of bulls with high GTV values to maximize profitability in a feedlot or in a post-weaning growth test.

CHAPTER 5

GENERAL CONCLUSIONS

The rapid development of computer hardware over the last number of years has made the simultaneous development of more appropriate analytical software possible. These analytical techniques have resulted in the more accurate prediction and estimation of genetic merit for productive and efficiency traits. As such technology is utilized, producers will have the tools to apply direct selection on economically important traits such as post-weaning growth profitability or feedlot profitability traits.

One of these analytical techniques which is of interest is the development of a multitrait analysis. In general, heritability estimates are more accurately computed when a multitrait rather than unitrait model is used for the analysis. A second advantage of using a multitrait analysis is that it is now possible to obtain genetic correlation estimates between traits and take the correlations between traits in account in the calculation of heritabilities. A multitrait analysis also makes it possible to use the BLUP EBVs obtained from the multitrait analyses easily in a selection index. This selection index differs from the classic Smith-Hazel selection index method in the sense that, in the classic index, phenotypic values are used to calculate the relevant b-values (which also include the correlations between the relative traits). As all genetic covariances among traits were accounted for in the breeding value predictions obtained from the multitrait analyses, the drafting of the selection index for each animal was thus simply a function of estimated EBVs and economic value of each trait.

A clearly defined post-weaning growth or feedlot profitability value was calculated based on a simple mathematical method for all bulls tested in a (Phase C) centralized growth test, for which individual feed intakes were known. It was also possible to predict a feed intake value for performance tested animals which were group fed with the help of a regression equation ($R^2 = 0.82$). Consequently a feedlot profitability value can also be calculated for performance tested animals tested in an on-farm (Phase D) growth test where individual feed intakes are unknown.

The heritability estimate of 0.36 for feedlot profitability was moderate and shows that the breeding objective is genetically inherited and that it should be considered in any breeding programme.

The high (favourable) genetic correlation estimate between feed conversion ratio and feedlot profitability of –0.92, indicates that a breeder can improve feedlot profitability through selecting for animals with a favourable feed conversion ratio. The expected correlated response in feedlot profitability, through the direct selection on FCR of 0.87, indicates that a breeder would make a 13% slower genetic improvement in feedlot profitability when selecting on FCR than through direct selection on the objective itself. The genetic correlation between RFI and feedlot profitability was moderately negative (–0.59) with an expected correlated response on feedlot profitability of only 0.55. These genetic correlations and expected correlated responses between residual feed intake and feed conversion ratio with feedlot profitability suggest that indirect selection for feedlot profitability through the selection for feed conversion ratio and/or residual feed intake will result in slower genetic gain in feedlot profitability than direct selection for the objective itself. However, where feedlot profitability cannot be calculated and/or direct selection for feedlot profitability is not possible, it would be better to select indirectly for feedlot profitability through the use of feed conversion ratio rather than residual feed intake or net feed intake.

Heritabilities estimates obtained from random-regression methodology were generally higher than those estimated by multitrait analysis. The advantage of using random-regression models are that these models take the time lag between measurements in account and that it is now possible to calculate a breeding value for an animal on any given time (age) on the trajectory.

The high correlations obtained between EBVs for feedlot profitability from different economic (favourable to an unfavourable) environments show that the average carcass, live weaner and feed prices over the last 54 months can be used as an indication of economic factors and that it isn't necessary to change these factors on a regular basis.

The genetic correlations between weaning weight and other production and efficiency traits were low to negligible. This suggests that the indirect genetic response in these traits through the direct selection on weaning weight would be small, if any, and that weaning weight, although important in terms of cow efficiency, is a poor indication of post-weaning growth or feedlot profitability.

A simplified selection index for post-weaning performance, including all selection criteria that are closely related to the objective (feedlot profitability), was constructed. Both the Pearson and Spearman correlations between the objective (feedlot profitability value) and the post-weaning

performance index values were 0.97. These high correlations indicate that it is not important which method (mathematical objective or the post-weaning performance index methodology) is used to calculate a genetic feedlot or post-weaning growth profitability value to be used in selection decisions. The selection index value is, however, more simple than the feedlot profitability value with less assumption. Therefore, it is recommended that the post-weaning selection index value be used as the selection criterion in breeding programmes to improve post-weaning growth profitability rather then the more complex feedlot profitability value. This index should be introduced as standard evaluation procedure into Phase C and D of the National Beef Cattle Performance Testing Scheme of South Africa.

Beef breeders in South Africa, and especially the feedlot industry, will now be able to select offspring of bulls with high feedlot profitability index values to maximize profitability in a feedlot or in a post-weaning growth test.

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