Animal recording as a tool for improved genetic management in African beef cattle breeds

By

Samuel Atanasio Abin

Dissertation submitted in partial fulfilment of the requirements for the degree

MSc(Agric) Animal Breeding and Genetics

In the

Department of Animal and Wildlife Sciences

Faculty of Natural and Agricultural Sciences

University of Pretoria-Pretoria

Republic of South Africa

Supervisor: Prof. Esté VanMarle-Köster
Co-supervisor: Dr. Helena Theron

October 2014

Declaration

I declare that the thesis/dissertation, which I hereby submitted for the degree MSc(Agric) Animal Breeding and Genetics at the University of Pretoria, is my own work which I did under the guidance of my supervisors and has not previously been submitted by me for a degree at this or any other tertiary institution.

.... Date…………………………

Samuel Abin

…………………………….. Date…………………………

Prof. Esté VanMarle-Köster

……………………………… Date…………………………

Dr. Helena Theron

DEDICATION

This work is dedicated to my wife Mrs. Elmuhajer Hania for her unceasing love, support and encouragement as well as to our daughter Rozeta Chadu, a beautiful gift God has given us during this study.

Acknowledgement

Initially I would like to say thank you God for your guidance and blessing on me. It is because of your love that I made it through to this end.

I would like to express my deepest appreciation and gratitude to my supervisors Prof. Van Marlé-Köster Esté and Dr Theron Helena for giving me the opportunity to work with them. Thank you for your excellent guidance, caring, patience and understanding. You have provided me with the necessary knowledge in animal science that entrenches a brighter future. I would like to extent my gratitude to Dr. Visser Carina, Dr. Van der Westhuizen Japie and Miss. Garritsen Christy for the knowledge, advice and assistance they offered me during this study. I would not miss this chance to thank Prof. Webb Edward Cottington and Mrs. Mulder Elydia who are always willing to serve.

Many thanks and appreciations goes to the SA Stud Book and the South African Breeders' Society of Afrikaner, Boran, Drakensberger, Nguni and Tuli breeds for giving me the data for this study. This study would not have been materialized without this substantial supports.

I would like to acknowledge the University of Pretoria and Department of Animal and Wildlife Sciences in particular for the award of the UP postgraduate research bursary.

Many thanks and appreciation goes to the USAID embodied in RHEA Project in collaboration with Virginia Polytechnic Institute and State University (USA) and University of Juba (South Sudan) for granting me the study sponsorship. Collective and individual acknowledgments are also owed to RHEA Staff especially Prof. Theo Dillaha and Brannan Christina (USA) and Prof. Aggrey L. Abate (Principal investigator of RHEA Project, University of Juba).

I would like also to thank all my sisters and brothers especially Abini Butrus, and my intimate friend Uman Paul for their love and support throughout my life.
My deepest gratitude goes to my father Abini Atanasio and mother Rinda Rozeta, who sincerely raised me with special caring and tender love.

Special thanks and gratitude goes to my enthusiastic wife Mrs Elmuhajer Hania, who always cheering me throughout hard and good times. Really it is a blessing to have you in my life.

Finally, I would like to thank and also apologize to everybody who was instrumental in the success of this thesis/dissertation but not personally mentioned.

ANIMAL RECORDING AS A TOOL FOR GENETIC MANAGEMENT IN AFRICAN BEEF CATTLE BREEDS

By

Samuel Atanasio Abin

Supervisor: Prof. Esté VanMarle-Köster

Co-supervisor: Dr. Helena Theron

Department: Animal and Wildlife Sciences

Degree: MSc(Agric) Animal Breeding and Genetics

October 2014

Abstract

Population structure in five African beef cattle breeds in South Africa was investigated, to assess the effect of animal recording in management of genetic diversity and genetic improvement. Pedigree records of 247,173 Afrikaner, 57,561 Boran, 198,557 Drakensberger, 256,692 Nguni and 55,309 Tuli breed were analysed using the online POPREP software system. Pedigree completeness over six generations varied with the lowest completeness in the Boran and the highest in the Afrikaner.The average generation interval ranged between 6.0 to 6.4 years. The rates of inbreeding per year were 0.03%, 0.04%, 0.06%, 0.07% and 0.08% in Boran, Nguni, Afrikaner, Drakensberger and Tuli respectively. Effective population sizes were 89, 107, 122, 191 and 364 in Tuli, Afrikaner, Drakensberger, Nguni and Boran respectively. Inbreeding and effective population size for the Boran was not a true reflection due to poor pedigree recording. These results indicate that none of the breeds are in critical limits of endangerment. Breeding values were regressed on birth year of each breed for weight traits; Kleiber ratio and scrotal circumference from 1986 to 2012. Genetic trends were stable for birth weights except the Afrikaner and Tuli. Genetic progress has been made in weaning and post weaning weights for all the breeds except for limited progress in the Nguni. Kleiber ratio and scrotal circumference in all measured breeds have shown good progress. The results of this study confirmed that recording of pedigree and performance records are effective in maintenance of genetic diversity and genetic improvement through selection based on EBVs of recorded traits.

Table of contents

List of Tables

List of Figures

Abbreviations

AI	Artificial Insemination
AGR	Additive Genetic Relationship
AMUL	Anand Milk Union Limited
AnGR	Animal Genetic Resources
ARC	Agricultural Research Council
BCBS	Boran Cattle Breeders Society
BIF	Beef Improvement Federation
BLUP	Best Linear Unbiased Prediction
BMPCUL	Bangladesh Milk Producers Co-operative Union Limited
DADGRIS	Domestic Animals Diversity Information System
DNA	Deoxyribonucleic Acid
EBVs	Estimated Breeding Values
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária
ET	Embryo transfer
F	Inbreeding coefficient
f	Additive genetic relationships
ΔF	rate of inbreeding
Δf	rate of additive genetic relationships
FAO	Food and Agriculture Organization of the United Nations
FABRE	Farm Animal Breeding and Reproduction
FLI	Federal Research Institute
GEBVs	Genomic breeding values
L	generation intervals
h^2	Heritability
ICAR	International Committee for Animal Recording
ICBF	Irish Cattle Breeding Federation Society Ltd.
ILRI	International Livestock Research Institute
INTERGIS	Integrated Registration and Genetic Information system
ISO	International Organization for Standardization
Kg	Kilogram
Klb	Kleiber Ratio

MARF	Ministry of Animal Resources and Fisheries
MLC	Meat and Livestock Commission
mm	Millimetre
NBCEC	National Beef Cattle Evaluation Consortium
Ne	Effective population size
r_g	Genetic correlation
RFID	Radio Frequency Identification
RTU	Real-Time Ultrasound
SA	South Africa
SNP	Single nucleotide polymorphism
UK	United Kingdom
USAID	United States Agency for International Development

Chapter 1

1.1 General introduction

Livestock is an important component of food, socio-economic and cultural aspects in most developing countries. It approximately accounts for 30% of the agricultural gross domestic product, with a projected increase of up to about 40% by 2030 due to recurrent demand for animal products (FAO, 2010). This increase in demand for animal products can be attributed to continuous increases in population sizes, urbanization and individual income (Delgado, 2003; Thornton, 2010). In Sub-Saharan Africa indigenous cattle form the largest part of livestock resources which were mostly developed for beef production (Rewe *et al.*, 2009). Based on the World Bank assessment, there is a need to increase meat production by about 80% between 2000 and 2030 and this require more efficient and sustainable animal production systems (FAO, 2010).

Animal recording is the first practical step towards genetic improvement programs of livestock species worldwide. The genetic progress achieved in beef cattle thus far was obtained mainly through recording and evaluation of weight, fertility, feed efficiency and carcass related traits (Miller, 2010). Recording of these performance traits provide objective information for sound decision-making and is crucial for selection and breeding (FAO, 1998a/b). However, modern selection tools that include improved quantitative genetic methods and artificial reproductive techniques have favoured the use of few superior genotypes which would be detrimental to global domestic animal genetic diversity in the long run (FAO, 2007a; Groeneveld *et al.*, 2009). Livestock diversity is a prerequisite for selection and sustainable genetic improvement towards achieving various breeding goals in unpredictable future production environments (Notter 1999; Okeyo *et al.*, 2010). Despite the continuous advances in molecular genetics there are still national and international needs for pedigree information to evaluate inbreeding, effective population size, generation interval and other important genetic structure parameters of a population (Martinez *et al.*, 2008; Groeneveld *et al.*, 2009; Malhado *et al.*, 2010). Knowledge about the genetic diversity and genetic trends in a population is crucial for genetic interventions as well as evaluation of the results of the adopted selection program (Malhado *et al*., 2010). The information on genetic structure combined with genetic trends in a population under selection can be used to guide future management actions to counteract any threats to genetic diversity and promote genetic improvement and adaptation of a breed as well as ensuring sustainable food security (FAO, 2007a; Malhado *et al.*, 2008).

1.2 Motivation and aim of the study

Animal recording is not only an essential tool for the livestock breeder, but also provides the data required for genetic evaluation. Information with regard to the genetic structure and genetic trends for cattle breeds under selection is of utmost importance to guide selection decisions. Animal Recording forms a platform for genetic analyses that aimed for organized selectrion program. It also offers an opportunity to monitor the genetic changes that occurred within a population/breed as a result of different breeding practices and averts risks associated with loss of genetic diversity (Boichard *et al.,* 1997; Carolino and Gama, 2008). Thus, the aim of this study was to investigate different African indigenous beef cattle breeds of larger and smaller population numbers in South Africa that are subjected to animal recording and to assess the potential of animal recording in genetic management.

1.4.1 Objectives

I. To investigate the population structure of five indigenous African beef cattle breeds using pedigree records.

II. To explore the genetic trends for recorded traits of economic economic importance which include; reproductive, growth and feed efficiency based on EBV.

Chapter 2
Literature review

2.1 Introduction

Animal recording provides databases and systems for inventory, characterization, conservation, monitoring of population trends and threats, as well as genetic improvement of animal genetic resources (Kosgey *et al.*, 2011). Over the past five decades, animal breeding has witness a remarkable progress, which was the result of domestication, natural selection and a combination of conventional techniques, such as breed substitution, crossbreeding and within breed selection (Thornton, 2010). Developed countries have been using animal recording for many purposes that include estimation of breeding values for selection of bulls and bull mothers to produce bulls and replacement heifers, development of extension systems, and national strategies for livestock development and appropriate decision making (Trivedi, 1998; Djemali, 2004). The organised animal recording system and intense selection for production traits in these countries had resulted into a relatively small number of well-defined and efficient specialized breeds producing relatively good quantity and quality products (Simm *et al.*, 2004; FAO, 2010). In developing countries, animal breeding programs are more diverse ranging from conventional pastoral system to livestock production system in transition and the commercially oriented industrial production systems (McDermott *et al.*, 2010).

The implementation of animal recording however offer both opportunities and challenges to countries that need to engage in or are already engaging in animal recording, selection and improvement programs. The increase in demand for livestock products offer an opportunity of making profits and would potentially contribute to poverty alleviation. The challenges in countries that have to implement animal recording for the first time lies in the need to understand the nature of animal recording and selection before adoption of any available systems. Countries that have a recording infrastructure in place are often challenged by the consequence of selection as selection leads to change in traits, but not all traits change in the preferred way. Moreover selection of elite animals tends to increase homozygosity within a population and thereby increase the chance for inbreeding depression in the long term (Sørensen *et al.*, 2005; Hiemstra *et al.*, 2010).

An animal recording system is fundamental in animal breeding program, it aids in identification, registration and measurement of various indicators of animal performance or production system criteria, processing of data to extract the desired information for decision making (Flammant, 1998; Bowman *et al.*, 2010). The aim of this review was to discuss the prerequisites for the planning and compilation of selection programs for sustainable beef production with specific reference to different animal recording systems, benefits and use in both developed and developing countries.

2.2 African cattle breeds

A breed can be defined as either a sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity (Köhler-Rollefson, 1997; FAO, 1999). African cattle breeds are part of the prestigious inherited resources that largely contribute to agriculture, economic, social, cultural, and spiritual aspect of most African people on the continent. The previous available archaeological, anthropological, historical, linguistic evidence on the origins of the African domestic cattle was complex and unresolved (Blench, 1993). However, the current developments in the field of molecular genetics with comprehensive gene mapping and determination of genetic distances based on highly polymorphic DNA markers is unravelling this complexity. Recent evidence include that African cattle breeds have originated from Asia, where they entered Africa in three main phases via the Nile valley in Egypt or the Horn of Africa (MacHugh *et al.*, 1997; Rege, 1999; Hanotte *et al.*, 2002) and the native African *taurine* breeds, centred in the Saharan Belt of Africa (Wendorf and Schild, 1994; Hanotte *et al.*, 2002). Modern African cattle breeds can be grouped into five major categories: the Taurine (humpless Bos *taurus*); Zebu (humped Bos *indicus*); Sanga (Bos *taurus* x Bos. *indicus*); Zenga a combination of

Sanga x Zebu (Rege, 1999; Reisti-Marti *et al.*, 2003) and African composite breeds (combination of two or more breeds).

Taurine cattle: The African Taurine cattle comprised of the humpless Shorthorns and Longhorns of West and Central Africa. The humpless Shorthorn breed further includes 14 humpless ecotypes that are widely distributed in the humid and sub-humid zones while the humpless Longhorn breeds included two ecotypes namely N'Dama and Kuri breed (Rege, 1999). These breeds are characterized by small body size, hardiness and resistance to many endemic diseases particularly trypanosomosis (Bosso *et al,* 2009).

Zebu cattle: Zebu is the most abundant and widely distributed cattle in the African continent that include about 75 breeds. Zebu is highly adaptable to the varying environmental condition and is characterized by thoracic humps that are placed over the shoulders or the posterior part of the neck (Rege, 1999). The majority of Zebu, about 61 breeds, is found in Eastern Africa and neighbouring countries in southern-central Africa while the rest are found in the Western part of Africa. The East African Zebu dominated the areas that extended from Northern Sudan to the Zambezi River bordered by the rain forest in the west. They are sub-divided into small East African Zebu that embraced 49 breeds and large East African Zebus that comprised 13 breeds. The West African zebu consists of Gudali breed represented by two sub-groups (Sokoto with only one strain, and Adamawa with 3 strains); Fulani breed (having six strains) and the non Gudali/Fulani breed comprised Azoauak, Shuwa and Maure (Rege, 1999).

Sanga cattle: Sanga cattle are also known as Bos *taurus africanus* and are distinguished by a small cervico-thoracic hump located posteriorly on their neck (Strydom *et al.*, 2001). Sanga cattle are composed of 30 breeds/strains that are further sub-divided into different ecotypes in accordance to their location as Sanga of Eastern Africa and Sanga of Southern Africa (Rege, 1999). The Sanga of Eastern Africa consist of three groups namely the Nilotic Sanga of South Sudan (previous Southern Sudan) and South-western Ethiopia; the Abyssinian Sanga of Ethiopia and Eritrea; and the Ankole group with its ecotype found in Uganda, Rwanda, Burundi, Tanzania and Democratic Republic of Congo. The Sanga of Southern Africa are represented by six groups namely the Shona represented by the Mashona of Zimbabwe; the Nguni group; the Zambia/Angola group; the Ovambo and South-western group; the Setswana group; and the Afrikaner breed as a group (Rege, 1999).

Zenga cattle: The Zenga is a collective name for the groups of cattle breeds that were developed from interbreeding between Zebu-Sanga or vice versa. These cattle originated in East Africa and they act as buffer zone between the zebu country in the North and the predominantly sanga country in the South (Rege and Tawah, 1999). The Zenga type cattle include the Arado, Fogera, and Horro in Ethiopia; Jiddu in Southern Somalia; Alur, also called Nyoka or Blukwa cattle in DRC; Nganda in Uganda; Sukuma in Tanzania and Bovino de Tete in Mozambique (Rege, 1999).

Composite breeds: Unlike the other types of cattle, composite breed is the result of a planned mating scheme designed to combine the desirable traits of two or more breeds into one composite as purebred with static heterosis maintained in the established generations without crossbreeding (Bourdon, 2000). There are about six commercial composite breeds in Sub-Saharan Africa with each having distinct proportions of exotic blood (Rege and Tawah, 1999; DADGRIS, 2007). These breeds include the Bonsmara and Drakensberger in South Africa (Meyer, 1984; Rege and Tawah, 1999), Rentilo and Manjani Boina in Madagascar; Mpwapwa in Tanzania and Wakwa in Cameroon (Rege and Tawah, 1999).

2.3 Genetic diversity of livestock

Conservation and sustainable utilization of farm animal genetic diversity is a global obligation under the Convention on Biological Diversity (CBD) and the Global Strategy for the Management of Farm Animal Genetic Resources (Gibson *et al.*, 2006; FAO, 2007a). This is to ensure sustainable agricultural production to meet the present and future human needs for food and livelihood security as well as to preserve cultural heritage across the production environments (Gibson *et al.*, 2006; FAO, 2007a/b). The term animal genetic resource (AnGR) is inclusive to those animal species that are of social-economic and scientific importance and are used, or may be used, for the production of food and agriculture (Rege and Gibson, 2003; FAO, 2007b; Alderson, 2010). Domestic animal genetic diversity referred to the genetic or allelic differences among and within breeds of species used for food and agriculture (Cardellino and Boyazoglu, 2009).

The need for increased selection pressure has intensified the application of improved quantitative genetic methods and artificial reproductive techniques. These led to an increase in production efficiency at the expense of genetic diversity and the survival of many breeds across the world. The total global domestic animal was about 8054 breeds since domestication of the first livestock species (FAO, 2011). From this huge number of breeds, a total of 631 breeds (compared to 695 in 2008 and 690 in 2006) breeds are classified as extinct and another total of 1710 breeds (21%) are classified as being at risk (compared to 1 649 in 2008 and 1 491 in 2006) with cattle having the highest number of breeds (194) that are extinct and also at risk among the mammalian species (FAO, 2011). The status of risk or endangerments for domestic animal population has been proposed by Bodo, (1989) as shown in table 2.3.1. The concerns with regard to the loss of genetic diversity are however, not only concerned with the extinction of indigenous breeds, but also the loss of genetic diversity within breeds. Loss of genetic diversity within of some these breed has negatively affected some production and fitness traits as observed in dairy breed (Sørensen *et al.*, 2005; Oltenacu and Broom, 2010) and beef cattle breed (Burrow, 1998; Santana *et al.*, 2010).

Table 2.3.1 Categories for endangered status of domestic populations

Status	No of breeding females	Description
Critical	<100	A breed is close to extinction, Because the genetic variability has already reduced below that of the ancestral population. Therefore, action must be done to increase the effective population size to ensure the survival of the population.
Endangered	100–1,000	A breed is in danger of extinction, because its effective population size is inadequate to prevent genetic loss through inbreeding in future generations. The methods of Preservation must be enacted o save such breed.

Vulnerable	1–5,000	This implies that some disadvantageous effects have endangered the existence of the breed and need precautionary measures must be taken into consideration to prevent further decrease in the population of the concerned breed.
Insecure	5–10,000	The number of breeding animals is decreasing rapidly indicating an escalation in the loss the genetic variation in future.
Normal	>10,000	The breed is not in danger of extinction. Can reproduce without genetic loss and there are no visible changes in population size.

Proposed basic terms of reference for uniparous populations adapted from Bodo, (1989).

Conservation of farm animal genetic resources can be done either in situ or ex situ, but the in-situ conservation is the preferred conservation approach since it has the advantage of allowing continued improvement of the genetic resources within the prevailing environment and thereby meeting the demands of both the farmers and consumers (Geerlings *et al.*, 2002; Gibson *et al.*, 2006). Moreover, effective management of farm animal genetic resources depend on comprehensive knowledge of breed characteristics, including data on population size and geographical distribution (Groeneveld *et al.*, 2010). It will be difficult if not impossible to conserve animal diversity without understanding the characteristics embedded in these breeds and their production systems. The availability of pedigree and production data in the formal animal breeding schemes offer great opportunity to investigate and assess the risk associated with diversity within breeds (Groeneveld *et al.*, 2010; Leroy *et al.*, 2013). Maintenance of within breed diversity is crucial for genetic improvement by selection as it influences the reproductive viability of a breed and its adaptability to adjust to the changing environmental conditions and contributes to the total diversity within a species (Simianer, 2005; Hoffmann, 2010). Therefore, genetic diversity is instrumental in mitigating any unpredictable change in socio-economic needs, environment condition and production objectives (Hoffmann, 2010). There are several factors that threaten the diversity of animal genetic resources and are used as key parameters in monitoring any associated risk. These parameters include genetic drift which is a temporal changes in allele frequencies leading to variance of effective population size, increase in homozygosity (inbreeding effective population size), the rate at which unique alleles are lost (eigenvalue effective population size) and average genetic relationships (Caballero and Toro, 2000; Groeneveld *et al.*, 2010; Leroy *et al.*, 2013).

Both inbreeding and additive genetic relationship are quantified in term of a coefficient. The inbreeding coefficient of an individual is defined as the probability of identity by descent of the two genes carried by an individual at a given locus (Bourdon, 2000). Inbreeding coefficient quantifies the expected reduction in proportion of heterozygous loci in the inbred individual, compared to the proportion of heterozygous loci in a typical individual from the non-inbred population from which the individual descended (Hohenboken *et al*, 2005). It implies mating of related individuals and is associated with decline in performance and fitness due to the reduction of genetic variation and usually known as inbreeding depression (Falconer and Mackay, 1996). Inbred animals are those individuals with an inbreeding coefficients ≥0.0625 which corresponds to mating between first cousins. The degree of measurement of inbreeding coefficient ranged between zero for non-inbred and one (or 100%) for inbred individual (Northcutt *et al.*, 2004; Hohenboken *et al.*, 2005).

The coefficient of additive genetic relationship (coancestry) is the probability of identity by descent of two genes taken at random from each individual at a locus (Toro *et al.*, 2011). It is the representation of the animal in the whole pedigree, regardless of the knowledge of its own pedigree (Malhado *et al.*, 2010). The knowledge about additive genetic relatedness is essential to estimate genetic parameters such as heritability, repeatability and genetic correlation that are necessary for genetic evaluations (Falconer and Mackay 1996; Bourdon, 2000; Aynalem, 2006). The information obtained from genetic evaluation will therefore guide proper mating decision, efficient selection strategies and sustainable breeding programs (Falconer and Mackay 1996; Van der Werf, 1999; Bourdon, 2000). Moreover, additive genetic relatedness is central in the estimation of inbreeding and optimization of genetic management in a conservation program (Toro *et al.*, 2011).

The effective population size is defined as the size of an idealized population which would give rise to the rate of inbreeding (ΔF) or rate of change in variance of gene frequencies observed in the population under consideration (Wright, 1923). The rate of loss of genetic diversity over time depends on the effective population size which is linked to age structure and mean generation interval of the breeding animals (Engen *et al.*, 2005). It is therefore necessary to consider all those factors when predicting the expected rate of loss of heterozygosity in a population.

Effective population size (Ne) is computed on the basis of the size of both female and male breeding populations making it a reliable tool for assessment of risk status (Gandini *et al.*, 2004; Groeneveld *et al.*, 2009). Knowing the effective population size (Ne) allows the rate of inbreeding and hence the loss of genetic diversity within the population to be inferred (Harmon and Braude, 2009; Groeneveld *et al.*, 2010). Moreover, the status of risk depends on current and predicted future population trends; as a rapid downward trend is an indication of a high level of risk (Groeneveld *et al.*, 2010). In animal breeding, it is recommended to maintain an effective population size (Ne) of at least 50 (short-term Fitness) to 100 (long-term Fitness) that corresponds to a rate of inbreeding coefficient of 0.5 to 1% per generation (FAO, 1998b; Bijma, 2000). Small effective population sizes will indicate rapid loss of genetic variability (Sørensen and Norberg, 2008).

2.4 Breeding objectives and selection criteria

In developing countries livestock production is still mostly low input-low output production systems and fulfils multiple objectives of economic, cultural, social and environmental aspects (Moll, 2005; Wurzinger *et al.*, 2006). Development of efficient means to increase production and productivity of livestock is important. This will relatively increase profit and improve farmers' livelihood. The establishment of breeding programs therefore can assist here, but proper definition of breeding objectives and recording of related traits are required (Groen, 2000; Miller, 2002). The set of traits in the breeding objectives should be linked to characteristic in selection criteria, have economic value, heritable, easy and cost effective to record by the breeders/farmers (Hetzel and Seifert, 1986; Goddard, 1998; Olesen *et al.*, 2000; Kluyts *et al.*, 2003). In Sub-Saharan Africa with its challenging environmental conditions, the selection criteria of beef cattle mostly include fitness; growth and to a lesser extend carcass traits (Steyn, *et al.*, 2009; Kugonza, 2012; Tada *et al.*, 2013). The inclusion of each trait in the selection program and its potential benefits is therefore, determined by its economic importance, heritability and genetic correlation with other traits.

2.4.1 Fitness traits

Fitness traits could be described by reproductive, survival/adaptability, mothering ability and longevity/stayability of individual animals in a population (Barker, 2009; Fuerst-Waltl and Fuerst, 2010). They have low heritability, unfavourable genetic correlations with performance traits, difficult and expensive to record (Koots *et al.*, 1994a/b; Philipsson and Lindhe, 2003). This resulted in failure to directly include fitness traits in some selection criteria (Fuerst-Waltl and Fuerst, 2010). The heritability estimates for fitness traits in African beef cattle and some crossed breeds are relatively low with the exception of scrotal circumference as shown in table 2.4.1.1.

Table 2.4.1.1 Summary of heritability estimates (h^2) for fitness traits in beef cattle

Trait	Breed	h^2	Reference
Age at first calving	Bonsmara cross	0.13	Corbet *et al.*, 2006.
	Afrikaner	0.27	Rust and Kanfer, 1998.
Calving date	Afrikaner	0.09	Beffa, 2005.
	Bonsmara cross	0.02	Corbet *et al.*, 2006.
Calving success	multibreed composite	0.03	Van der Westhuizen *et al.*, 2001.
	Afrikaner	0.08	Beffa, 2005.
	Afrikaner	0.27	Rust and Groeneveld, 2002.
Calving rate	SA beef cattle	0.04	Rust and Groeneveld, 2002.
Calving interval	Boran Cross	0.08	Demeke *et al.*, 2004.
	Bonsmara cross	0.04	Corbet *et al.*, 2006.
	multibreed composite	0.02	Van der Westhuizen *et al.*, 2000.
Days open	Boran Cross	0.04	Demeke *et al.*, 2004.
No service/conception	Boran Cross	0.08	Demeke *et al.*, 2004.
Scrotal circumference	Bonsmara	0.44-0.46	Maiwashe *et al.*, 2002; Van der Westhuizen *et al.*, 2004; Nephawe *et al.*, 2006.
Longevity	multibreed composite	0.08	Van der Westhuizen *et al.*, 2001.
Tick resistance	Bonsmara	0.05-0.17	Budeli, 2010.
		0.26	Schoeman, 1989.

Efficient reproduction is necessary for profitable and efficient beef cattle production, but fertility trait is complex and governed by the underlying genetic potential that expresses the endocrine and physiological functions that cannot be fully defined by phenotypic measurements made directly on the animals (Eler *et al.*, 2002). In females, fertility could be defined as the cow's ability to conceive normally, calve down and suckle the calf to weaning successfully (Davis, 1993; Nino-Soto and King, 2004), while in males, it could be defined as the ability of a bull to produce semen that will result in a successful pregnancy (Foote, 2003; Nino-Soto and King, 2004). Traits that are relatively easy to record at low cost in most management systems to measure reproductive efficiency of female beef cattle are age at first calving, calving success, calving interval, calving rate, calf survival, days to calving and calving date (Rust and Groeneveld, 2001).

Natural service is used in most beef cattle operations and therefore, acceptable bull fertility is also critical to the success of these operations (Carpenter *et al.*, 1992). Bull fertility and performance would be determined by a number of factors including; plane of nutrition (Chase *et al.*, 1994), structural soundness, capability of the reproductive organs, quality of semen, level of libido (the number of cows a particular bull is expected to service, the length of the mating period), the serving capacity of the bulls (Godfrey and Lunstra, 1989; de Araujo *et al.*, 2003). Scrotal circumference has however been advocated as an easily measurable, moderately to highly heritable trait in beef bulls and it is favourably correlated to semen quality and output (Meyer *et al.*, 1990; Brinks, 1994; Morris *et al.*, 2000; Parkinson, 2004). Moreover, scrotal circumference has been found to be a useful indicator for age at puberty both in bulls and related heifers (Toelle and Robison, 1985; Brinks, 1994). Therefore, selection based on scrotal circumference is an indirect means to improve female fertility because of the strong additive genetic relationship with age at puberty in heifers (Smith *et al.*, 1989; Van Melis *et al.*, 2010). Genetic correlations between the reproductive traits are shown in table 2.4.1.2 to illustrate the complexity of these traits.

Table 2.4.1.2 Genetic correlations (r_g) between reproductive traits in beef cattle

Trait	r_g	Reference
Age at first calving /Calving date	0.88	Corbet *et al.*, 2006.
	0.09	Van der Westhuizen *et al.*, 2001.
	0.60	Van der Westhuizen *et al.*, 2000.
Age at first calving /Calving interval	0.44	Corbet *et al.*, 2006.
	-0.03	Van der Westhuizen *et al.*, 2001.
Calving date /Calving interval	0.01	Corbet *et al.*, 2006.
	0.75	Van der Westhuizen *et al.*, 2001.
Calving success/Calving date	-0.95	Beffa, 2005.
Days to calving /Pregnancy rate	-0.99	Corbet *et al.*, 2006.

Despite low heritability estimates and variable genetic correlations between female reproductive traits in beef, these traits can be used as genetic indicators to improve female reproduction in tropical breeds (Johnston *et al.*, 2013). The birth weight of an animal and pre weaning growth are determined not only by its own genetic potential but also by the maternal environment which is represented mainly by the uterine environment, dam's milk production and nursing ability (Meyer, 1992; Newman and Coffey, 1999). An increased proportion of calve surviving to weaning is of great economic importance and their mortality reduce beef income and add significantly to beef production costs (Meijering, 1984; Melton, 1995). It is therefore necessary to integrate calf survival traits in the definition of the breeding objective in beef cattle selection programs (Goyache *et al.*, 2003; Prayaga, 2004). Recording of survival traits in extensively managed range beef cattle is challenging; survival data are often derived from presence or absence of animal at certain ages/weights in the course of the animals' life, with survival from birth to weaning being commonly reported (Beffa *et al.*, 2009).

Mothering ability is one of the critical factors that determine the efficiency of beef production especially in the tropical rangelands (Mason and Buvanendran, 1982). It encompasses the protective ability, maternal instincts and milkability that a cow offers to her calf. The traits related to mothering ability of cows could be recorded and evaluated through the weaning weight of their calves (Campêlo *et al.*, 2004; Du Plessis *et al.*, 2006) and it defines the overall productivity of the cowherd (Du Plessis *et al.*, 2006). It also determines the stayability of a cow. Cows that consistently wean lighter calves are culled from the herd (Eler *et al.*, 2008). However, under extensive pastoral systems, recording of such traits are sometimes complicated by voluntary cross-suckling i.e. a calf suckle on other cow than its own mother (Prayaga *et al.*, 2008).

2.4.2 Growth traits

Growth rate and efficiency of gain are of major economic importance to the beef industry and the first trait to receive selection emphasis in beef cattle breeding due to its early expression, ease of measurement and positive association with a profit per unit change in the growth rate (Parnell *et al.*, 1994; Prayaga, 2003). Moreover it is of moderate to high heritability (Table 2.4.2.1).

Table 2.4.2.1 Summary of heritability estimates (h^2) for growth traits in beef cattle

Trait	Breed	h^2	Reference
Birth Weight direct	Gudali	0.39	Ndofor-Foleng *et al.*, 2012.
	SA Brangus	0.21	Neser *et al.*, 2012.
	Boran	0.34	Wasike *et al.*, 2009.
	Bonsmara cross	0.23	Corbet *et al.*, 2006.
	Afrikaner	0.39-0.4	Beffa, 2005; Beffa *et al.*, 2009.
	Nguni	0.36	Norris *et al.*, 2004.
		0.26	Van Niekerk *et al.*, 2004.
Birth Weight maternal	Gudali	0.05	Ndofor-Foleng *et al.*, 2012.
	SA Brangus	0.05	Neser *et al.*, 2012.
	Bonsmara cross	0.10	Corbet *et al.*, 2006.
	Afrikaner	0.14	Beffa, 2005; Beffa *et al.*, 2009.
	Nguni	0.13	Norris *et al.*, 2004.
Weaning Weight direct	Gudali	0.25	Ndofor-Foleng *et al.*, 2012.
	SA Brangus	0.23	Neser *et al.*, 2012.
	Boran	0.12	Wasike *et al.*, 2009.
	Bonsmara cross	0.14	Corbet *et al.*, 2006.
	Afrikaner	0.19	Beffa, 2005.
	Nguni	0.29	Norris *et al.*, 2004.
		0.17	Van Niekerk *et al.*, 2004.
Weaning Weight maternal	Gudali	0.11	Ndofor-Foleng *et al.*, 2012.
	SA Brangus	0.11	Neser *et al.*, 2012.
	Bonsmara cross	0.19	Corbet *et al.*, 2006.
	Afrikaner	0.21	Beffa, 2005.
	Nguni	0.16	Norris *et al.*, 2004.
Yearling Weight	Gudali	0.21	Ndofor-Foleng *et al.*, 2012.
	SA Brangus	0.22	Neser *et al.*, 2012.
	Boran	0.19	Wasike *et al.*, 2009.
	Tuli	0.18	Assan and Nyoni, 2009.
	Bonsmara cross	0.26	Corbet *et al.*, 2006.
	Afrikaner	0.19	Beffa, 2005.
	Nguni	0.25	Norris *et al.*, 2004.
		0.13	Van Niekerk *et al.*, 2004.
Final weight	Gudali	0.18	Ndofor-Foleng *et al.*, 2012.
	SA Brangus	0.29	Neser *et al.*, 2012.
	Bonsmara cross	0.42	Corbet *et al.*, 2006.
	Afrikaner	0.36	Beffa, 2005.
	Nguni	0.13	Van Niekerk *et al.*, 2004.
Mature weight	SA Brangus	0.24	Neser *et al.*, 2012.
	Bonsmara	0.41	Nephawe, 2004

Body measurements and weights at different ages and production stages are the most common measurement for growth traits in beef cattle (Van Marle-Köster *et al.*, 2000). These traits are positively and strongly correlated with efficiency of weight gain (Crews *et al.*, 2010) as shown in table 2.4.2.2.

Table 2.4.2.2 Genetic correlations (r_g) between pre and post weaning growth traits in beef cattle

Trait	Genetic correlation	Reference
Birth and weaning weights	0.78	Neser *et al.*, 2012.
	0.70	Corbet *et al.*, 2006.
	0.45	Maiwashe *et al.*, 2002.
Birth and yearling weights	0.57	Neser *et al.*, 2012.
	0.28	Bosso *et al.*, 2009.
Birth and final weights	0.60	Neser *et al.*, 2012.
	0.45	Maiwashe *et al.*, 2002.
Birth and mature weights	0.63	Neser *et al.*, 2012.
Weaning and yearling weights	0.86	Neser *et al.*, 2012.
Weaning and final weights	0.99	Neser *et al.*, 2012.
	0.71	Maiwashe *et al.*, 2002.
Weaning and mature weights	0.94	Neser *et al.*, 2012.
Yearling and final weights	0.85	Neser *et al.*, 2012.
Yearling and mature weights	0.43	Neser *et al.*, 2012.
final and mature weights	0.75	Neser *et al.*, 2012.
Birth weight and average	-0.04	Bosso *et al.*, 2009.
weight gains from weaning to after yearling	0.28	Maiwashe *et al.*, 2002; Van der Westhuizen *et al.*, 2004
	0.29	Van der Westhuizen *et al.*, 2009

The recording of feed intake and its utilization are also important due to the association with growth rate and subsequently the influence on cost of feeding and profit of the industry. However this trait is seldom included in selection objectives due the difficulty associated with its direct measurement in large herd (Arthur *et al.*, 2001; Carstens *et al.*, 2006). The Kleiber ratio was found to be highly correlated (e.g, -0.81) with feed conversion efficiency in beef cattle (Arthur *et al.*, 2001). Consequently, it is often used as indirect way of selection for feed efficiency and expressed as post-weaning average daily gain/mature mass $^{0.75}$ (Kleiber, 1947; Scholtz *et al.*, 1990; Köster *et al.*, 1994).

2.4.3 Carcass traits

Carcass quality has become one of the important determinants of price and purchasing earning particularly in developed countries (Bredahl *et al.*, 2001; Seroba *et al.*, 2011). In developing countries, the interest in carcass traits is mostly limited to researcher and most of the breeding programs do not directly include carcass trait in their breeding objective and criteria. The traits used to assess carcass quality include marbling score, fat thickness, kidney, pelvic and the heart fat percentages, rib eye area and yield grade, hot carcass weight and dressing percentage (Pariacote *et al.*, 1998; Rios Utrera and Van Vleck, 2004). These traits can generally be grouped into two major quality classifications; cutability traits which include muscling and leanness and quality traits represented by marbling (Anderson and Lewis, 1990). Carcass quality differs between breeds (Chambaz *et al.*, 2003) and is influenced by the plane of nutrition and production system (Keane and O'Ferrall, 1992). Although carcass traits have moderate to high heritability estimates, its inclusion in selection criteria is hampered by the antagonistic genetic correlations between cutability and marbling (Anderson and Lewis, 1990; Koots *et. al.*, 1994a/b; Marshall, 1994), recording of traits on large numbers of carcass is expensive, increase the likelihood of errors and may reduce beef producers' and processors' interest in participating (MacNeil and Northcutt, 2008; Crews *et al.*, 2010). Moreover, there are no reliable tools to record these traits except for Real-Time Ultrasound (RTU) which are still expensive as it required trained personnel to be contracted. The genomic selection for carcass traits would be useful and act as an additional tool for carcass evaluation in future (Garrick and Saatchi, 2011; Montaldo *et al.*, 2012).

2.4.4 Genetic evaluation

In order to successfully select beef cattle, preliminary information on the expected performance of the progenies of the selected animals is required. The next step after the measurement of phenotypic traits is the development of statistical methods and computer hardware capable of storing and processing large data sets of one or more of the recorded traits from a particular breed to predict the breeding values of individual animal (Rauw *et al.*, 1998; Johnston *et al.*, 2007). The Best Linear Unbiased

Prediction (BLUP) Animal Model has proven to be an effective evaluation technique. The BLUP animal model combines information collected on individual animals, its known relatives, the heritability of the performance traits and the correlations between them to predict the genetic potential of individual animals for specific traits. The predicted genetic potential of individual animal is shown as Estimated Breeding Values (EBVs) that are expressed in units of measurement for each particular trait such as kg; mm and days. This process involves partitioning of observed performance into several effects, according to a model equation that describes the factors that influence performance for a particular trait (Garrick and Golden, 2009). The EBV therefore indicates the genetic potential of the animal for the specific traits. It indicates the genetic difference between the individual animal and the herd or breed standard to which the animal is being compared (Holloway, 2005).

The more performance tested relatives of an animal that are included in the BLUP analysis, the more accurate the EBVs of that animal will be (Bergh, 2008a). Correct assignment of a calf to its parents is therefore, one of the most important factors for genetic evaluations, selection program and estimate of population structure parameter. Incorrect recording of parentage/pedigree influences the accuracy of the EBVs (Bergh, 2008a; Pollot, 1998) and inbreeding related parameters that may result into reduce genetic progress (Van Eenennaam, 2012). The calculated EBVs are tools that guide towards breeding objectives in pure breeding, crossbreeding and formation of the composite breeds (Bill, 2007). The EBVs generated by the BLUP Animal Model could be used to determine genetic trends as a response of selection by regression of the average EBVs on the year of birth (Nicholas, 2003).

The need for pedigree recording in an animal recording program for breed improvement becomes extremely critical when reproductive technologies such as artificial insemination (AI) and embryo transfer (ET) are used to propagate the desired genes across herds/populations. These reproductive technologies create powerful opportunities for breed improvement by increasing intensity of selection through increases in the number of offspring produced by selected sires and by providing access to elite sires across many herds/populations. Therefore, objective animal recording will help in monitoring the results of selection and improvement programs and avoid the associated risks (FAO, 1998a). These parameters are however unique to the population in which they are estimated and they may change over time due to selection and management decisions (Pico *et al.*, 2004). Pedigree and performance recordings are importance practical step towards genetic evaluation and selection process and are conducted following some guidelines as discussed herein below.

2.5 Animal recording process

The converging goal in beef cattle industry is to genetically improve one or more traits of economic importance as defined in the breeding objective. The first step after the development of a breeding objective and selection criteria is to device appropriate means for the recording of traits related to the breeding objectives. In practice, livestock industries and their infrastructure for genetic improvement have developed from historical foundations as systems for animal identification, pedigree recording, performance recording, and genetic evaluation (Garrick and Golden 2009). This will enable selection of superior candidates and optimize production efficiency in the subsequent generation. Recording for beef cattle selection and improvement follows some basic principles that start with a unique and permanent identification of individual animals for efficient recording of parentage, performance data, storage, management and use of the these data (ICAR, 2001). Animal identification is the marking of individual animal or group of animals with a unique individual or group identifier composed of records that ascertain animal ownerships and link animal to its own profile (Besbes and Hoffmann, 2011). It is crucial and serves many purposes including farm management, genetic improvement, biodiversity management, prevention and control of zoonosis and other animal diseases, trade opportunities, proof of ownership and theft control (Besbes and Hoffmann, 2011; Olori, 2012). The main techniques used for permanent animal identification in the current livestock industry include: branding (by fire or freezing), ear marking (by notching, tattooing and ear tagging); electronic identification (radio frequency identification "RFID" chips ear tag, & bolus) and natural characters, mainly DNA genotyping and retinal images (Caja *et al.*, 2004). Identification systems in Africa ranged from traditional branding and ear marking in most of countries (ICAR, 2004a) to modern electronic bolus in Botswana (Moreki *et al*, 2012).

Internationally, an alphanumeric code is used, as a combination of two leading characters or three numerical digits as country identification following the ISO standard and a subsequent national alphanumeric or numeric sequence, providing a unique identification within country. After unique identifications, other types of animal related data by principle are required for efficient recording program as summarized in table 2.5.1 (ICAR, 2001; 2012):

Table 2.5.1 Standard format for data recording program

Data	Format
Invariable animal data	• The internationally unique ID of the animal (containing the code of the country of origin) • The breed or breed composition of the animal • Date of birth of animal • Sex of the animal • The ID of the animal's genetic parents • ID of recipient mother, in case of embryo transfer, • ID of foster mother, in case of fostering • ID of the other genetically identical animal(s), if the animal is an identical twin or a clone.
Life history data	a- The animal's physical location • Animal ID • Date of recording • Recording person • Actual location: farm ID (management-group within farm if applicable) • Changing to: farm ID (management-group within farm if applicable) • Code(s) for special events (e.g. weaned, died, slaughtered etc.) b- The animal's reproductive status, • Animal ID • Date of recording • Recording person • Actual location: farm ID (management-group within farm if applicable) • Code of the reproductive event • ID of other animal(s) involved (e.g. mating partner, calf, foster calf etc. if applicable)
Recorded data	• Animal ID or group of animals (if applicable) • Date of recording (start/end of test period etc.) • Recording person • Actual location: farm ID or management-group within farm (if applicable) • Trait code • Trait value • Additional information pertaining to the animal (e.g. Age of thr animal) • Additional information pertaining to the recording procedure

Source: ICAR, 2012

Invariable animal data are the animal's own specific data that are unchangeable from birth throughout its lifetime such as date of birth and sex of the animal. The standard format of such types of data is presented in table 2.5.1.

Life history data includes information on the status of the animal (alive or dead, suckling or weaned) and its environmental management. These data are time critical as they permit the retrieval of all information pertaining to management condition, reproduction status and other relevant information from a specific animal at particular date. Other performance related data like calving date and calving ease are assessed concurrently with the relevant event in the life history and reported on the same format. Adequate information on the general features of the system are included along with life history as animal productivity is influenced by a range of inter-related factors such as health and nutritional status, technical equipment used and contemporary group which may set limits on the level of output. The animal's physical location and reproductive status are the two main areas of data that are needed to be collected and permanently updated (ICAR, 2001; 2012). This data encompasses events such as mating, insemination, embryo transfer and birth for females, and castration for males (ICAR, 2012). The information on possible mates and mating dates should also be recorded especially if the females were kept with one or several bulls during the mating period.

Recorded data are directly recorded on an animal or animal group, which includes both objective and subjective assessments (ICAR, 2001). The objective valuation of information such as birth date, birth weight, weaning weight, yearling weight, heights and length of body, scrotal circumference and other traits are measured using international technical equipment like kilograms and metric system (ICAR, 2012). Subjective assessments are used to obtain values on traits/characteristics that could be measured, but exact measurements may not be possible because they are too difficult or too expensive to record such as carcass dressing percentage and quality (Hui, 2012; ICAR, 2012). This assessment requires trained personnel to ensure its accuracy and also needs regular base verification for the data quality purpose. In any recording scheme, it is critical to define each recordable trait with two or three uniform letters to specify trait codes for international standard. Regardless of the type of recorded trait, the possible standard format is illustrated in table 2.5.1. Principally, the value of recorded traits should strictly reflect the actual measurement, count or subjective score. However, if traits need to be standardized, the raw data are adjusted to a defined age, weight, or length of testing period to comply with the defined standard. For example a number of performance traits are derived from a combination of recorded traits such as daily gain in the test period which is the difference between weight at the end and weight at the start of the testing period, divided by the difference of age at the end and the age at start of testing period, expressed as gram per day or Kg per year. The recording of such type of performance traits could be conducted either on-farm or station depending on trait definitions (ICAR, 2012).

Animal recording could therefore, be defined as the process by which data pertaining parentage, performance, characteristics and other relevant data are collected and systematically stored for appropriate use (Besbes and Hoffmann, 2011). This information could be grouped in to three types of data namely pedigree, performance and management data that form the profiles of individual animal's and their ancestries' and are usually kept by the breed society or studbook. The information included in Pedigree, Performance and management records are animal identification, birth date, breed, sex, owners, traits EBVs, health, feed consumption and other related information. In order to establish successful animal recording scheme, certain activities are needed to define the overall structure of the scheme and its success as shown in the figure 2.5.1 (FAO, 1998a).

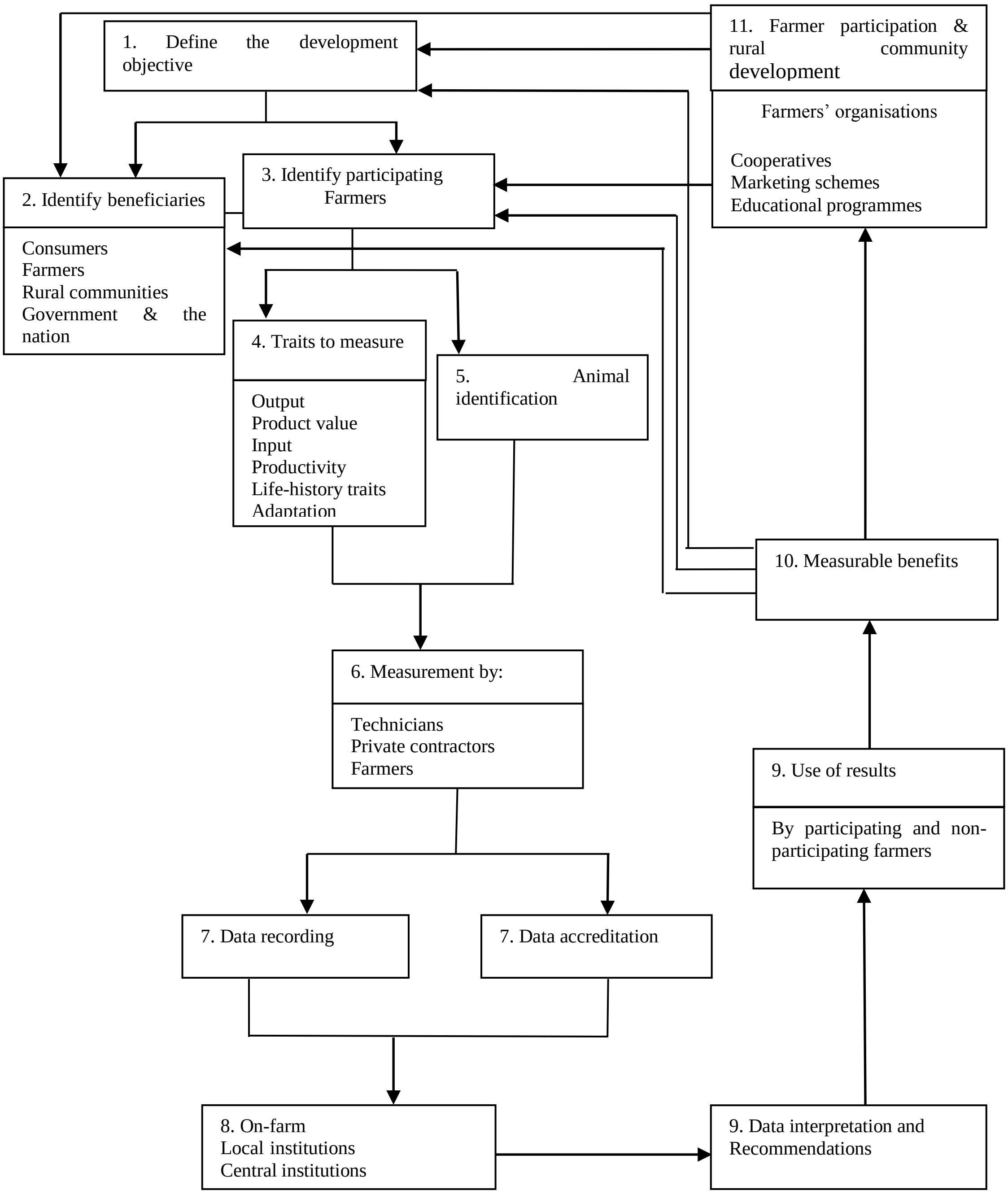

Figure 2.5.1: Planning of Animal Recording Systems (FAO, 1998a)

2.5.1 Animal recording systems in developed countries

Animal recording systems evolved in developed countries over several decades in high input animal production systems as the primary tool of pure breed genetic improvement programmes (Flamant, 1998; Djemali, 2004). It was one of the practical steps for the development of the present modern breeds characterized by high production efficiency (Flamant, 1998; Guellouz *et al.*, 2004). Developed countries have specialised organisations that undertake and supervise livestock recording and evaluation effectively. These organisations maintain large animal pedigree and performance data bases structured according to the latest scientific developments and computing systems for analysis (FABRE, 2006). The recorded data are collected and submitted electronically to the central data base for genetic evaluation. The organizations run the genetic evaluations and provide EBVs for growth, reproduction, carcass (Mason and Buvanendran, 1982) and composite traits (Mwansa *et al.*, 2002) to guide farmers in the selection process. The data used to derive EBVs are collected from different testing stations such as on farm performance testing, progeny testing and Nucleus or group breeding schemes (Mason and Buvanendran, 1982). The EBVs and other management information derived from recorded data are used for selection of bulls and bull mothers to produce bulls and replacement heifers, development of extension systems, and national strategies for livestock development and appropriate decision making (Trivedi, 1998; Djemali, 2004).

With the current development in DNA-based technology, accurate selections based on genomic breeding values (GEBVs) are now possible in developed countries. Several organizations in North America are in the process of implementing genomic breeding values for quantitative growth and carcass traits in beef cattle using Bovine SNP50 genotypes and phenotypic or EBV data (Van Eenennaam *et al.*, 2009; Weber *et al.*, 2012b; Pollak *et al.*, 2012). This DNA technology therefore offers an additional tool for accurate genetic evaluation. Genomic breeding values (GEBVs) have potential for traits that have been more difficult to measure by the existing recording techniques (Williams, 2012; Weber *et al.*, 2012a). Moreover using DNA microsatellites or SNPs to determine parentage allows seed-stock farmers to produce their own young sires by developing bull-breeding herds and resolve the discrepancies of paternity of calves produced by multi-sires in AI or natural breeding systems (Dodds *et al.*, 2005; Pollak, 2005; Weber *et al.*, 2012b).

In spite of all these advances, recording systems in beef cattle schemes are not as uniform as that of the dairy industry due to the diversity in environment, management and production systems (Mason and Buvanendran, 1982; Journaux *et al.*, 2006). The specialised organisations that monitor collection and evaluation of beef cattle pedigree and performance records in developed countries include the National Beef Cattle Evaluation Consortium (NBCEC) in the USA and Canada (Garrick and Golden, 2009; Bullock *et al.*, 2003), BREEDPLAN genetic evaluation system in Australia, New Zealand and Canada (Reverter *et al.*, 2002), Irish Cattle Breeding Federation Society Ltd. (ICBF) in Ireland, (Wickham and Durr, 2011), Meat and Livestock Commission (MLC) in UK and Institute de l'Elevage in France (Phocas *et al.*, 2004).

2.5.2 Animal recording system in developing countries

In contrast, animal recording systems have not been used efficiently in most developing countries and Sub-Saharan Africa in particular. In a survey conducted to assess the status of animal identification and recording systems in developing countries and countries with economies in transition, the majority of countries surveyed have simple ownership identification systems (e.g. branding) with very few having electronic systems in place (e.g. microchip bolus system). Unfortunately, the majority of these countries only used animal identification for traceability rather than performance recording systems (Banga *et al.*, 2010). The lack of such schemes in most developing countries is one of the hindrances affecting the contribution of the livestock sector to food production and income generation (Scholtz *et al.*, 2010). Several efforts were made to improve indigenous breeds through importation of exotic breeds from developed countries. The promotions of these indigenous breeds and their crosses have seldom proved successful owing to the diverse and harsh environments in Sub-Sahara Africa (Mpofu, 2002). Cross breeding or breed upgrading predisposes the local breeds to the risk of genetic dilution or replacement and ultimately less adaptability and resiliency. Temperate breeds lack the genetic characteristics of heat tolerance, resistance against many of the tropical diseases and ability to survive long periods of feed and water shortage (King *et al.*, 2006). All these genetic properties are crucial for successful animal production in the tropics (Syrstad, 1992).

Development of proper improvement schemes in Sub-tropical Africa is a challenging task, due to lack of policy frameworks to support sustainable breed improvement programs (Scholtz *et al.*, 2010; Wasike *et al.*, 2011), lack of human capacity (Kahi *et al.*, 2005; Philipsson *et al.*, 2006; Rege *et al.*, 2011; Ojango *et al.*, 2010), absence of well-structured breeding programs (e.g. recording systems, breeders organisations), and implementation strategies (Philipsson *et al.*, 2006; Ojango *et al.*, 2010), small herd size and poor recording of accurate pedigree and performance data (Martojo, 2003; Kosgey and Okeyo, 2007; Burrow, 2012).

It has been advocated that gradual introduction of an animal recording program into low-input extensive production systems through the establishment of open nucleus breeding schemes would overcome some of these problems (Cunningham, 1980; Smith, 1988; Bondoc and Smith, 1993; Trivedi, 1998). The introduction of animal recording programs should be conducted through extension programs and encouragement of stakeholders in the recording management and promotion of farmer groups or cooperatives (Trivedi, 1998). The few effective genetic improvements programs in Sub-tropical Africa are found in Southern Africa, where the improvement programs are being managed and supervised by SA Studbook (Scholtz, 2010), BreedPlan (Reverter *et al.*, 2002) and the Kaonafatsho ya Dikgomo improvement Scheme for small and upcoming farmers that is being supported by the government and managed by the ARC (Banga, 2002). The Kenyan Boran breeding scheme in Eastern Africa is being run by private farmers initiatives under the umbrella of breed society in corporation with other government institutions and national agricultural research organizations such as livestock recording centre (Rewe *et al.*, 2008; Koskey *et al.*, 2011) and the Ndama cattle breed of Western Africa is being managed by private farmers or a private Company like International Trypanotolerance Centre (Dempfle and Jaitner, 2000; Bosso *et al.*, 2009). Brazil is one of the exemplary countries in Latin America; which have successful beef breeding schemes that are run by universities together with private companies such as EMBRAPA 'Brazilian Corporation for Agricultural Research (Scholtz *et al.*, 2010). In most of the South Asian and Pacific countries the successful improvement programs are being managed by non-governmental organizations, cooperatives and private companies such as AMUL in India and BMPCUL in Bangladesh (Herath *et al.*, 2009).

2.6 Design of a breeding program for beef cattle

The first important step towards the establishment of animal selection program for genetic improvement is the setting of breeding objectives. Definition of breeding objectives will help in deciding what traits of relevant importance should be recorded. This will be followed by development of a breeding structure. Breeding structure is the organizing component that enables regular recording of traits, genetic evaluation to derived EBVs, selection and dissemination of the improved animals to establish broad based improvement program. The traditional breeding structure for most breeds of livestock is commonly represented by a pyramid which was initially characteristic to pig and poultry breeding structures (Newman, 2011). The pyramid may consist of two or more tiers namely nucleus and multiplier or commercial herds or all the three (Bourdon, 2000; Nicholas, 2003). In beef cattle industry straight breeding programs is mostly applied at the nucleus which composed mainly of breeders who generate sires to produce sires (SS pathway) and dams to produce sires i.e. DS pathway (Bill, 2007; Newman, 2011). The nucleus composed of small number of elite animals (seed stock) from the national cattle population and it is where basic recording of performance and pedigree data, as well as selection take place (Pollak, 2005). At the nucleus, individual animals with desirable traits are used for breeding to produce offspring with improved characteristics, which may in turn be selected for breeding future offspring or are sold (usually males) to multipliers or directly down to commercial tiers (Nicholas, 2003; Bourdon, 2000). The general design of the traditional breeding pyramid is shown in the figure 2.7.1.

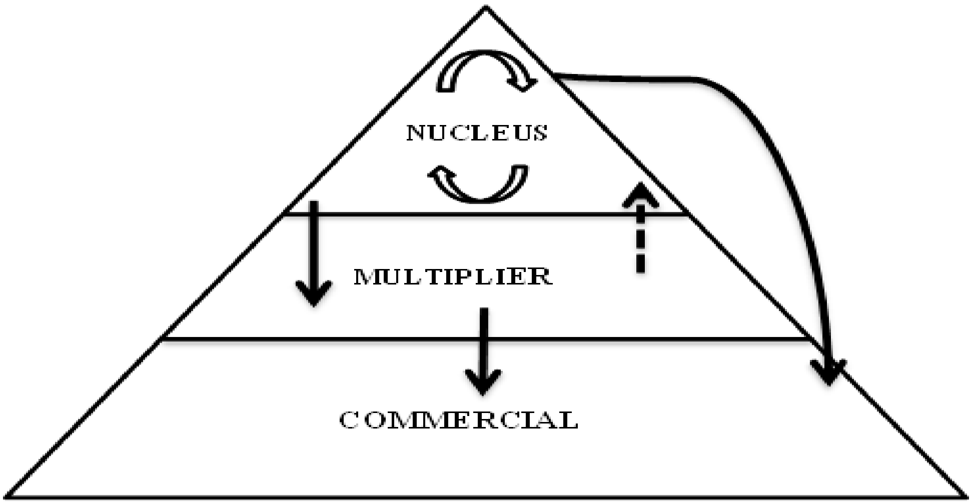

Figure 2.7.1: Trditional Breeding structure for livestock adapted from Nicholas, (2003)
Curved arrows: Selected breeding animals in the nucleus; **Downward arrows:** Transfer of genetic material from nucleus to multiplier or direct to commercial in case of two tiers; **Specked upward arrow:** Movement of information and outstanding female animals from lower tiers to the nucleus in case of open nucleus.

There are two types of nucleus breeding herds; closed and opened nucleus systems. The closed nucleus breeding system is characterised by one way genes flow within the pyramid from top to bottom making it the only source of genetic progress for other tiers (Nicholas, 2003). The open nucleus breeding scheme is a reciprocal breeding system in which females with good performance could flow from the lower tiers to the nucleus where they are mated with the best available sires and at the same time they receive improved genetic material from the top tier leading to a two-way flow of genes. Such type of breeding scheme would result in a better breed improvement than would be possible in individual herds (Köhler-Rollefson, 2004).

In a well organised open nucleus breeding scheme, the response to selection would increase by 10-15 percent, and the rate of inbreeding would be halved compared with a closed nucleus scheme of the same size (Nicholas, 2003). Additionally it will integrate farmers' resources, reduce overhead costs and encourage more farmer participation (Bondoc and Smith, 1993). However, this will be more feasible and efficient only if performance recording had been conducted in lower breeding tiers (Van der Werf, 2000). Open nucleus system could therefore; concurrently increase selection intensity and within breed genetic diversity as a result of the new genotype introduced from the lower tiers.

The primary function of the multiplier herd is to expand or replicate the genetic material of the elite sires of the nucleus herd in to greater numbers and to pass them on to the commercial herds (Intaratham, 2002). The multiplier may consist of either one or more tiers of purebred or cross bred animals as males and sometimes females from one or more nucleus could be obtained with the aim of producing sufficient breeding stock to satisfy the demands in the commercial tier (Nicholas, 2003). The recording of performance and pedigree data could also take place in the multiplier tiers (Newman, 2011). The progress in the improvement of the national herd therefore, depends on the efficiency of selection in the nucleus and multiplier segments. It takes time for genetic improvement in one tier to be transmitted to the next tier and the resultant difference in average performance between any two adjacent tiers is called the improvement lag which is expressed in terms of the number of years of the genetic improvement represented by the difference in performance between adjacent tiers. Improvement lag is affected by the age structure in the lower tiers, and the merit of sires and dams used in the lower tiers (Nicholas, 2003).

The commercial herds large commercial producers and smallholder farmers. They need good sires and usually their sources for genetic materials are the commercial bulls bred by stud breeders (Intaratham, 2002). The majority of the existing organized cattle breeding programs in developing countries are implemented by government institutions through nucleus herds on state farms and only few countries in this region have governmental breeding programs that involve direct participation of the breeders

2.8 Conclusion

Animal recording is a systematic, highly interlinked and interdependent process that cements the baseline information on animals' performance, facilitates comparison of production alternatives, and reinforces animal management decisions as well as genetic improvement programs (FAO, 1998a). Animal recording offers several benefits to various animal stakeholders which include:

- The Government and indirectly the world, through characterization of livestock production potential to enhanced food security, more competitive trade and greater social stability.

- The farmers, through increased income, better management and maintenance of a sustainable rural economy and by extension the consumers, through improvements in quantity and quality of animal products.
- Animals, through conservation of biodiversity between and among breeds for sustainable utilization.

Accordingly, animal recording constitute one of the major indispensable prerequisites towards any developmental decision aimed at improvement, management and conservation of animal genetic resources in any country.

Chapter 3
Materials and Methods

3.1 Introduction

Modern beef cattle breeding is characterised by interlinked activities which include recordings of pedigree and performance data, genetic evaluation, selection of superior candidates and production management. These recorded data are means to drive change in cattle populations and could also be used to monitor the dynamics occurring in the population under selection program. The aim of this study was to investigate population parameters of different African beef cattle breeds of larger and smaller population numbers in South Africa that are subjected to animal recording program and assess the potential of animal recording in maintenance of genetic diversity and genetic improvement.

3.2 Data

The South African breeds used for this study are indigenous to the African continent namely Afrikaner, Boran, Drakensberger, Nguni and Tuli. Brief histories about these breeds are given herein below. The data used comprised pedigree and EBVs (Estimated breeding values) of measured economic importance traits of the selected breeds. The data were obtained from SA Studbook with consent of the breeders. Moreover, approval from the Ethics committee (Faculty of Natural and Agricultural Sciences) was obtained to ensure compliance with the research ethics and Integrity of the University of Pretoria (EC130424-038).

3.3 Synopsis of the studied breeds

The indigenous African cattle breeds comprised of Sanga, Taurine, Zebu, Zenga and composite breeds as documented by many studies (e.g. Meyer, 1984; Rege, 1999; Strydom et al., 2001; Hanotte et al., 2002 and others). Five indigenous African beef cattle breeds representative of Sanga, Zebu and composite breeds in South Africa were used in this study.

The Afrikaner breed: The Afrikaner breed (also known as Africander) is a Sanga type cattle and one of the most pivotal beef breeds. It was developed from Hottentot cattle in the Cape Province of South Africa (Rege and Tawah, 1999; Scholtz, 2010). The Afrikaner is one of the oldest recognized indigenous breeds as well as the first indigenous South African breed to form a breed society in 1912 (www.afrikanerbees.com; Scholtz, 2010). The Afrikaner was initially used for draught, meat and milk; however in the past few decades its breeders have extended their effort on recording economically important traits to meet the dynamics in the modern beef industry (Scholtz, 2010). The Afrikaner is much desired for crossbreeding due to their hardiness, calving ease and grazing efficiency (Scholtz, 2010). It is a medium-framed animal with dark to light red colour, brawny thighs, well-muscled withers, and deep broad chest with round ribs and spread horns or polled head in the newly developed types (Rege and Tawah, 1999). The male's and female's average birth weight, weaning (210 days) weight and mature weight are 34kg, 210kg, 820-1090kg and 32kg, 195kg, 550-730kg respectively (www.indigenousbreeds.co.za/indigenousbreeds/cattle).The Afrikaner cattle breeders' society is among the active cattle breed societies that engaged in pedigree and performance recording with SA Stud Book and the ARC (Scholtz, 2010).


Figure 3.3.1: Afrikaner cattle breed (www.afrikanerbeed.com)

The Nguni breed: The Nguni is a Sanga type cattle breed which was originally bred along the east coast of Southern Africa by the Nguni tribes in Mozambique, Swaziland, Zimbabwe and Zululand in South Africa (Scholtz, 2010). It is characterised by medium size, multi-coloured skin, resistant to infection, tolerant to heat, good mother line, good fertility under harsh conditions with low calf mortality, good temperament, and ability to thrive on low quality grazing (www.ngunicattle.info; Scholtz, 2010). The male's and female's birth weight, weaning (210 days) weight and mature weight are 27kg, 165kg, 600-800kg and 24kg, 148kg, 350-500kg respectively (www.indigenousbreeds.co.za).

The first effort to breed Nguni cattle in South Africa was initiated by the late Professor HH Curzon in 1932 which culminated with the establishment of the Bartlow Combine breeding station in the late 1940's (Nguni Facts at www.nguni.info). In 1985 the Nguni Cattle Breeder's Society was accepted as a member of the South African Stud Book and Livestock Improvement Association after the appreciation and acknowledgement of the of breed (Nguni Facts at www.nguni.info). The Nguni was originally being used for beef, milk and as draft animal, and then later it progressively became a popular beef breed after the establishment of the breeders Society. The role of Nguni Cattle Breeders' Society is to endeavour the conservation and enhancement of the unique characteristics of the Nguni breed, promote the growth and proliferation of Nguni herds in Southern Africa, and to serve the needs of society members in achieving this mission (www.ngunicattle.info).

Figure 3.3.2: Nguni cattle breed (www.ngunicattle.info)

The Tuli breed: The Tuli is an indigenous Southern African Sanga beef cattle breed. It is widely spread even beyond the African continent to Australia, Canada, USA and South America as commercial herds (www.studbook.co.za; Mpofu, 2002). This breed was developed and improved from Twsana cattle indigenous to Zimbabwe under the auspices of Mr Len Harvey while working as land development officer at the Ministry of Internal Affairs in around the end of 1940s (www.studbook.co.za). Mr Len Harvey's reservation on the viability of upgrading indigenous breeds with European breeds in the harsh ecological conditions of Africa and his observation of the better adaptability and superiority of the Tuli breed to other breeds in the local environmental conditions, had led to the establishment of Tuli Breeding Station in 1945 at Guyu in Zimbabwe (Mpofu, 2002). The initial idea of the Tuli Breeding Station was to breed bulls to assist in improving African stock, but later the commercial farmers developed interest in the breed and started purchasing bulls from the station (www.studbook.co.za; Mpofu, 2002). The Tuli cattle Breeder's Society of Zimbabwe was formed in 1961 and Tuli as a breed was imported into South Africa in the 1970's. The South African Tuli cattle breeder's society was officially formed only later in 1994 and is linked to South African Stud Book (www.studbook.co.za; Scholtz, 2010).

The Tuli breed is a descendant of Sanga cattle, naturally polled, hardy, adaptable, short haired and naturally resistant to both internal and external parasites. Its colours are white, yellow, red and blends of these colours. It has medium size with a long, deep and broad body, strong legs and a docile temperament (www.studbook.co.za; Scholtz, 2010). The male's and female's birth weight, weaning (210 days) weight and mature weight are 35kg, 210kg, 750-1000kg and 31kg, 185kg, 450-550kg respectively (www.indigenousbreeds.co.za).

Figure 3.3.3: Tuli cattle breed (www.studbook.co.za)

The Boran breed: The Boran is a Zebu cattle breed that was developed in the semi-arid and arid pastoral Borana plateau of southern Ethiopia and then spread to the eastern rangelands in Ethiopia, northern Kenya and south western Somalia (Haile *et al.,* 2011). The Boran cattle population is composed of unimproved groups, namely the Borana and Orma Boran and improved group known as the Kenyan Boran (Rege *et al.,* 2001; DAGRIS, 2007). The unimproved Boran is found in subsistence and semi-commercial production systems in Ethiopia, Kenya and Somalia (DAGRIS, 2007; Haile *et al.,* 2011), whereas the improved ones was developed in Kenya and are found in commercial beef ranching systems (Rewe, 2009). The unimproved Boran are typical Bos *indicus* type cattle while the improved Boran genetic makeup was found to consist of 64% Bos *indicus*, 24% European Bos *taurus* and 12% African Bos *taurus* (Hanotte *et al.,* 2002). It is has a good body conformation, multiple colours mainly white, light grey, fawn or light brown with grey, black or dark brown shading on head, neck, shoulders and hindquarters. The horns are thick at the base, very short, erect and pointing forward and the humps are pyramidal in shape and overhanging to the rear or to one side and are well developed in the male (Haile *et al.*, 2011).

The Boran breed is one of the most important indigenous cattle breeds in Kenya that has establish an organised management and strategic breeding program under the Boran Cattle Breeders' Society since 1951 (www.borankenya.org; Rewe *et al.*, 2008). The Boran Cattle Breeders Society (BCBS) activities involved administration, maintaining breed standards, and searching for new markets for both genetic material and beef (Rewe, 2009). The combined efforts of the Boran cattle farmers and the Boran Cattle Breeders Society (BCBS) have led to the spontaneous Boran improvement program and distribution in Kenya and other countries such as Zambia, Tanzania, Uganda, South Africa, Australia and USA (www.boranKenya.org; Mpofu, 2002; BCBS, 2013). It has become a popular choice for breeders in Eastern and Southern Africa due to its superior adaptive, productive traits and mothering ability (Kios *et al.,* 2012). It is characterised by greater ability to survive, grow and reproduce in ambient temperature, poor feed quality and high pathogen incidence than Bos *taurus* and other Bos indicus breeds in their native areas (Mwandoto *et al.,* 1988; Davis, 1993; Herlocker, 1999). At birth, male Boran calves weighed an average of 28kg and females, 25kg whereas the average weaning weights for both male and female are 220kg and 210kg respectively (BCBS, 2013). The mature weight of the male Kenyan Boran ranges from 550 to 850 kg, while female weight is from 400 to 550 kg (Rege *et al.*, 2001). The Boran cattle was accepted as a breed by the South African Department of Animal Improvement in 1995 and the Boran Cattle Breeder's Society of SA was founded in 2003 (www.boran.org.za).

Figure 3.3.4: Boran cattle breed (www.boranKenya.org)

The Drakensberger breed: The Drakensberger is a composite breed developed from unknown proportions of three local breeds namely Africander, Basuto and Zulu as well as Friesian cattle (www.cdad-is.org.cn.) It was previously called Uys cattle, a name given after the Uys family who started farming them in the Volksrust area. This name was only changed to Drakensberger in 1947 when the Drakensberger Cattle Breeder's Society of South Africa was established. The name Drakensbergers was preferred due their widespread concentration in the sour-veld Drakensberg region (Drakensberger Handbook, 2011). In 1969 the Drakensberger Cattle Breeder's Society was annexed to the SA Studbook as an associate member, and in 1972 as full member. In 1980 the breeder's society decided to make performance testing compulsory for membership confirmation. This decision had enabled them to be the first cattle breeder's society to launch BLUP (Best Linear Unbiased Prediction) analysis in South Africa, as the whole breed was subject to performance testing (Scholtz, 2010; Drakensberger Handbook, 2011).

The present day smooth black coat; medium to large, sturdy and well-muscled Drakensberger of good temperament was developed as the results of a total shift to beef production through emphasis on economically important traits such as adaptability, fertility, milk production, longevity, growth ability, feed efficiency and carcass quality alongside with the uniformity and general appearance (Scholtz, 2010;

Drakensberger Handbook, 2011). The Drakensberger has also proved to be a good dam line for crossbreeding (Scholtz, 2010; Drakensberger Handbook, 2011). The male's and female's birth weight, weaning (210 days) weight and mature weight are 36kg, 240kg, 850-1100kg and 34kg, 210kg, 450-650kg respectively (www.indigenousbreeds.co.za). The Drakenberger is widely disseminated in South Africa and also have presence in other countries such as Namibia, Swaziland, Zimbabwe, Equatorial Guinea and Australia (Scholtz, 2010; Drakensberger Handbook, 2011).

Figure 3.3.5: Drakensberger cattle breed (Drakensberger Handbook, 2011)

Conservation and sustainable use of animal genetic resources form the integral part of modern animal breeding programs in sub-Sahara Africa. The contrasting environments of Africa, natural and artificial selection have developed adapted indigenous cattle breeds that embrace a unique reservoir of genetic resources necessary for sustainable improvement of livestock (Hanotte *et al.,* 2000; Woolliams *et al.*, 2008). Therefore, conservation or maintenance of the genetic diversity of these cattle breeds will be an insurance against unpredicted future change in demand for livestock products, environmental changes, threats of diseases (Woolliams *et al.*, 2008; Hoffman, 2010), preservation of indigenous livestock gene pool diversity, cultural and social values of rural people (Mendelsohn, 2003; Anderson, 2010).

3.4 Methods

The parameters used to investigate the consequences of selection program on beef cattle breeds include analyses of genetic structure based on pedigree information (Boichard *et al.*, 1997; Gutiérrez *et al.*, 2003; Van Doormaal *et al.*, 2005; Leroy *et al.*, 2013). The genetic trends can be assessed from the averages of the estimated EBVs of economically importance traits (Snelling *et al.*, 1995; Plasse *et al.*, 2004; Johnston, 2007; Barwick, *et al.*, 2013).

3.4.1 Genetic structure

The total numbers of animals with pedigree records available from SA Stud Book are presented in table 3.4.1.1. Pedigree records were available from as early as 1912 for the Afrikaner. Limited pedigree information was available before establishment of breed societies. The breed societies of the five breeds were established in different year as shown in table 3.4.1.1.

Table 3.4.1.1 Total number of animals in the pedigree of five indigenous African beef cattle breeds

Breed	Establishment of Breeders society	No of animals with pedigree records
Afrikaner	1912	247 173
Boran	2003	57 561
Drakensberger	1972	198 557
Nguni	1985	256 692
Tuli	1994	55 309

The pedigree records for each breed was uploaded separately into a POPREP software system online through the website http://popreport.tzv.fal.de provided by the Institute of FLI-Farm Animal Genetics in Germany. The input data consisted of unique identification of all animals, the sire ID, dam ID, birthdate, and sex. These data sets were in a format required by POPREP software for computation processes (Groeneveld *et al.*, 2009). This study concentrated on a number of population parameters namely pedigree completeness, generation intervals (GI), inbreeding, additive genetic relationship (AGR), Age structure of parents by birth of offspring, distribution of dams by parity number, number of breeding animals and effective population size (Ne). These parameters were computed as follows:

3.4.1.1 Pedigree completeness

Pedigree completeness is a parameter used to examine the quality of a pedigree and was measured as the extent to which individual animal ancestries are known to some defined generation over a period of time in the past (Groeneveld *et al.*, 2009). The pedigree completeness was calculated based on algorithm index proposed by MacCluer *et al.*, (1983) and adapted by Groeneveld *et al.*, (2009) using the formulae:

$$Id = 4Id_{pat}Id_{mat}/Id_{pat} + Id_{mat} \text{ And } Id_k = \frac{1}{d}\sum_{i=1}^{d} a_i \qquad k = \text{pat, mat.}$$

Where k represents the paternal (pat) or maternal (mat) line of an individual, a_i is the proportion of known ancestors in identified generation, whereas d is the number of generations considered in the calculation of the pedigree completeness. The values for pedigree completeness were expressed as percentage per generation range from 0 to 100.

3.4.1.2 Generation interval

Generation interval (L) was defined according to Falconer and Mackay, (1996) as the average age of the parents at the birth of their selected offspring. It was calculated by taking the age of each of the parents at the birth of its offspring and averaging it over the age of all parents (Groeneveld *et al.*, 2009). Selected offspring and those who produced at least one progeny were the only ones considered during computation. The generation intervals for each of the four selection paths (i.e. Sire to son, Sire to daughter, Dams to son and Dam to daughter), males, females and the whole population in the pedigree records were calculated for each respective breed.

3.4.1.3 Age structure of parents and distribution of dams by parity number

To determine the rate of genetic progress in the population, the total number of sires and dams contributing to the cohort/group of individual in the successive generation was broken down by age. Moreover, the total number of dams contributing to the cohort was broken down by parity to distribute them by parity number (Groeneveld *et al.*, 2009).

3.4.1.4 Numbers of breeding animals and effective population size

The numbers of breeding animals influence the dispersion of allele frequencies in a population and thereby determine the effective size. The numbers of breeding animals were counted on the year of birth. Animal is considered as a breeding animal when having a service record or showing up as parent in a birth record of an offspring (Groeneveld *et al.*, 2009).

Effective population size (Ne) was referred to as the number of breeding animals in an idealized population, which would give rise to the same rate of calculated or observed inbreeding (ΔF), as observed in the real population (Falconer and MacKay, 1996). It was estimated from individual increase in inbreeding according to Falconer and Mackay (1996) using the formula:

$$Ne = 1/\ 2\Delta F$$

Where ΔF is the rate of inbreeding coefficient

3.4.1.5 Inbreeding

The inbreeding coefficient (F) and its rate of change (ΔF) are means to quantify the increase in pairs of homozygous genes in an individual relative to its population (Groeneveld *et al.*, 2009). The inbreeding coefficient was computed for all animals in the whole pedigree of each respective breed to estimate the average rate of changes as described by Falconer and Mackay, (1996):

$$\Delta F = (F_t - F_{t-1}) / (1 - F_{t-1})$$

Where F_t and F_{t-1}; are the average inbreeding of offspring and their parents, respectively.

3.4.1.6 Additive genetic relationships

The additive genetic relationship (AGR), as the total average genetic relationship between individuals in a contemporary group of animals in the whole pedigree file, within each breed, was computed using the PEDIG Fortran package of Boichard, (2002). The additive genetic relationships coefficients were used to compute the rate of change of the AGR (Δf) per generation using the equation:

$$\Delta f = (f_t - f_{t-1}) / (1 - f_{t-1})$$

Where f_t and f_{t-1}; are the average additive genetic relationships of the cohort born in generation t (Groeneveld *et al.*, 2009).

3.4.2 Genetic trends

The estimate of breeding values for pre-weaning and post weaning growth traits of the five breeds **(**Afrikaner, Boran, Drakensber, Nguni and Tuli) were used to estimate the genetic trends. The EBVs were available for all traits for all breeds except Boran breed where only birth and growth weight data were available. The reference year considered in the EBVs data was 1986 in respect to the start of INTERGIS (Integrated Registration and Genetic Information System Database). The SAS software (SAS, 2010) was used to retrieve the animals with EBVs and measurements for selected traits between 1986 and 2012. The EBVs for each trait was averaged on birth year using SAS software (SAS, 2010) to investigate the genetic trend. In table 3.4.2.1 the available numbers of animals with EBVs of traits measured for five indigenous African beef cattle breeds are shown.

Table 3.4.2.1 Available number of animals with EBVs of traits measured for five indigenous African beef cattle breeds

Trait (EBV)	Number of animals				
	Afrikaner	Boran	Drakensberger	Nguni	Tuli
Birth weight direct (kg)	201 247	48 400	113 703	47 499	54 207
Birth weight maternal (kg)	232 941	69 080	113 748	48 329	56 917
Weaning weight direct (kg)	216 386	42 734	114 025	48 403	52 583
Weaning weight maternal(kg)	188 943	42 174	114 021	48 400	43 575
Yearling weight direct (kg)	204 248	36 028	113 644	47 044	49 921
Final weight direct (kg)	199 365	31 399	113 026	46 355	47 662
Mature weight direct (kg)	117 169	25 020	102 229	45 229	41 920
Kleiber ratio (kg)	194 950	-	111 229	43 393	37 533
Scrotal circumference (mm)	193 708	-	111 560	43 225	43 190

3.4.2.1 Description of traits

Traits used in this study include traits that were described by Bergh, (2008b) and Rust *et al.*, (2010) and are grouped into reproduction, growth and feed efficiency.

Reproduction

- Birth weight direct EBV (kg): This EBV is an indication of the calf's genetic ability for birth weight. Animals with lower breeding values will possibly breed progeny with lighter birth weights and consequently a smaller chance of calving problems in the mothers. Bulls with higher EBV values for birth weight are expected to sire calves heavier at birth than bulls with lower EBVs.

- Birth weight maternal EBV (kg): This EBV measures the cow's genetic ability to limit the growth of a calf until birth avoiding calving problems naturally. The maternal EBV of a bull is an indication of its daughters' ability to limit the birth weight of their offspring. Lower birth weight maternal EBV reflects good maternity for easy delivery and vice-versa.

- Scrotal Circumference EBV (mm): This EBV is an indication of the animal's genetic ability for scrotal size as measure of fertility. Bulls with small scrotum or low values for scrotal circumference are probably sub-fertile as compared with bulls of a large scrotal circumference or high values for scrotal circumference.

Growth

- Weaning Weight Direct EBV (kg): This EBV is an indication of the animal's own genetic ability to grow until weaning age. Bulls with above average weaning weight direct EBVs are optimum since their calves will likely attain high weaning weights. Bulls with higher EBV values for weaning weight are expected to sire calves heavier at weaning than bulls with lower EBVs.
- Weaning Weight Maternal EBV (kg): This EBV is an indicator of a cow's (the calf's mother) genetic ability (primarily milk production) to create an environment in which her calves can grow optimally. The weaning weight maternal EBV of a bull is an indication of his daughter's maternal ability to wean heavy calves. Bulls with above average weaning weight maternal breeding values are favoured to breed daughters with good maternal ability that could wean heavy calves. Thus this EBV values reflect both the milking ability of daughters and growth potential of their calves.

- Yearling Weight (12 months weight) EBV (kg): This EBV is an indication of the animal's genetic ability to grow until one year of age. Bulls with average to slightly above average yearling weight EBVs for average sized animals are favoured. Bulls with higher EBV values for yearling weight are expected to sire calves heavier at one year of age than bulls with lower EBVs.

- Final weight (18 Months weight) EBV (kg): This EBV is an indication of the animal's genetic ability to grow until 18 months of age. Like yearling Weight, bulls with average to slightly above average 18- month weight EBV for average sized animals are ideal. The 18 Months weight EBV also determines to some extent the mature weight of an animal.

- Mature Weight EBV (kg): This EBV is an indication of the animal's genetic ability for mature weight. Mature animal with average breeding values is likely to breed average sized animals. The mature weight EBV was the combination of 3 EBVs (mature weight 1, mature weight 2 and mature weight 3) at weaning of the first three calves.

Feed efficiency

- Kleiber Ratio: This EBV is an indirect indication of the animal's genetic ability for feed conversion efficiency, measured in extensive post wean growth test. Animals with a higher breeding value are more efficient.

Chapter 4
Results and Discussions

4.1 Introduction

The aim of this study was to investigate different African indigenous beef cattle breeds that have been participating in animal recording and assess the effectiveness of animal recording in genetic management of beef cattle.This assessment was conducted through analysis of both pedigree and performance data of Afrikaner, Boran, Drakensber, Nguni and Tuli breeds from South Africa. The five breeds differed in population size and level of participation in official animal recording. The results of the above analysis have given insight with regard to the effect of the recording system for genetic improvement in the five breeds studied.

4.2 Genetic structure

The population parameters considered in the analysis of genetic structure in this study were pedigree completeness, inbreeding, additive genetic relationships, number of breeding animals and effective population size considering the whole pedigree of each breed. The trends for these population parameters were presented for the time period from 1986 to 2012. This is due to the small numbers of animals in the pedigree before the year 1986.

4.2.1 Trends of number of offspring and pedigree completeness

The evolution in the number of offspring born in the original pedigree file is illustrated in figures 4.2.1.1 for each breed per year of birth. The pedigree completeness for the offspring in the original pedigree file was investigated up to six generations deep as the percentage of known ancestors per parental generation in the whole data set of Afrikaner, Boran, Drakensberger, Nguni and Tuli breeds. The evolution in the pedigree completeness is illustrated in figures 4.2.1.2 to 4.2.1.6 and table 4.2.1.1 and 4.2.1.2 for each respective breed.

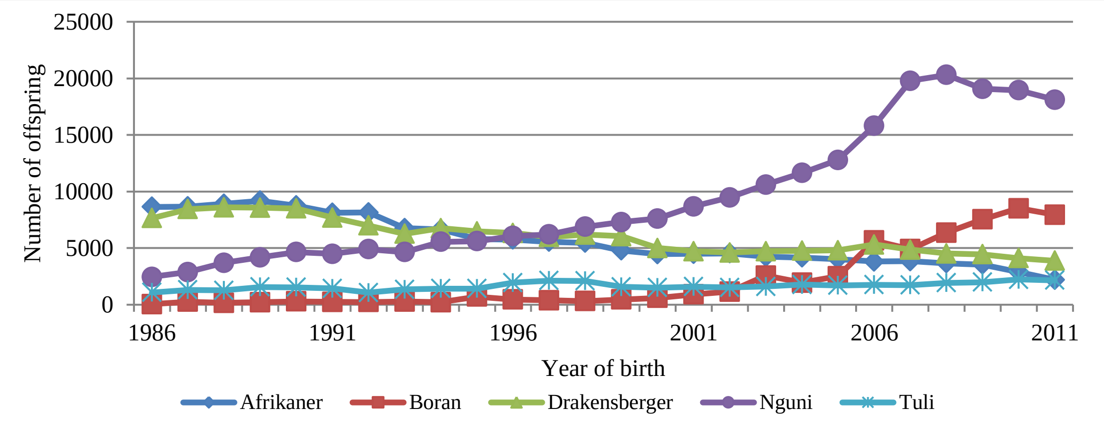

Figure 4.2.1.1: Trends of number of offspring for five indigenous African beef cattle breeds

The number of offspring in the pedigree file of the Afrikaner and Drakensberger breeds have decreased drastically since late the nineteen nineties from 8 000 and 7 643 to approximately 2000 and 3 874 offspring in 2011 respectively. The number of animals registered in the pedigree of Boran breed has increased, gaining momentum after the year 2000 and reached approximately 8 000 animals. The trend of the number of offspring in the pedigree file of Nguni breed has increased steadily and reached about 20000 in mid-2000’s, then stabilized and declined to about 18000 animals in 2011. The numbers of offspring in the pedigree file of Tuli breed has increased slowly and stabilized.

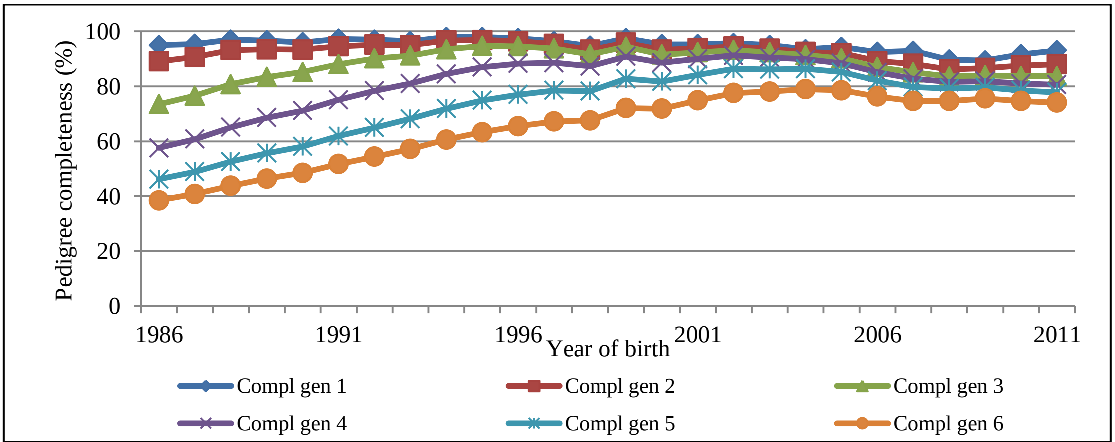

Figure 4.2.1.2: Trend of pedigree completeness for the Afrikaner breed

From the figure 4.2.1.2, the trend for pedigree completeness six generation deep is above average and has improved over the specified period for Afrikaner breed. The average pedigree completeness has reached the peak of 98.5% first generation and

82.2% six generations deep in 2012. The number of offspring (4.2.1.1) for this breed has decreased while pedigree completeness has greatly improved.

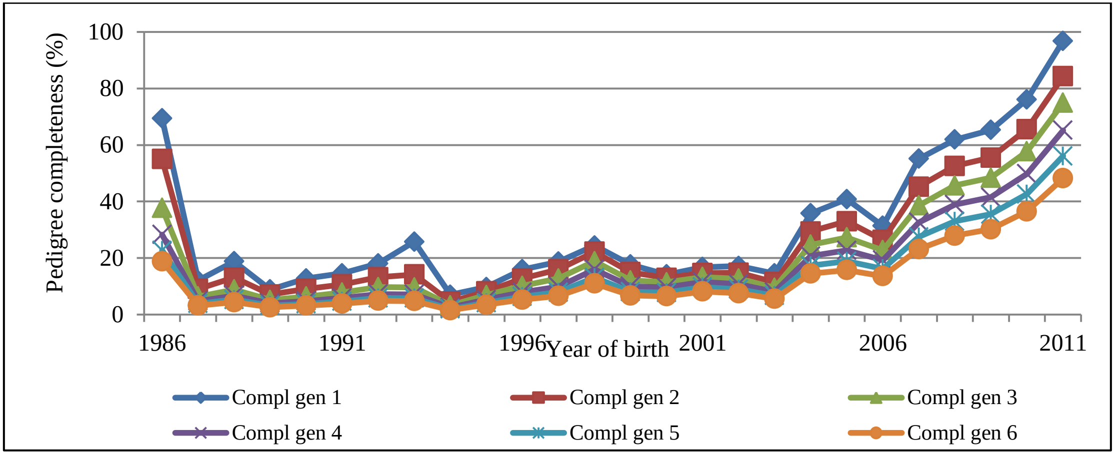

Figure 4.2.1.3: Trend of pedigree completeness for the Boran breed

The Boran breed has shown meagre, but inconsistent progress in the trend for pedigree completeness with steady improvement attained in the last ten years of this study. This is due to limited pedigree records in the years prior 2000 as well as its late introduction to South Africa. Due to continuous improvement, the proportions of known ancestors have increased to 99.5% in the first generation and 53.7% in the six generation in 2012. The number of offspring (4.2.1.1) in the pedigree of this breed has increased sharply after 2000 followed by improved pedigree completeness.

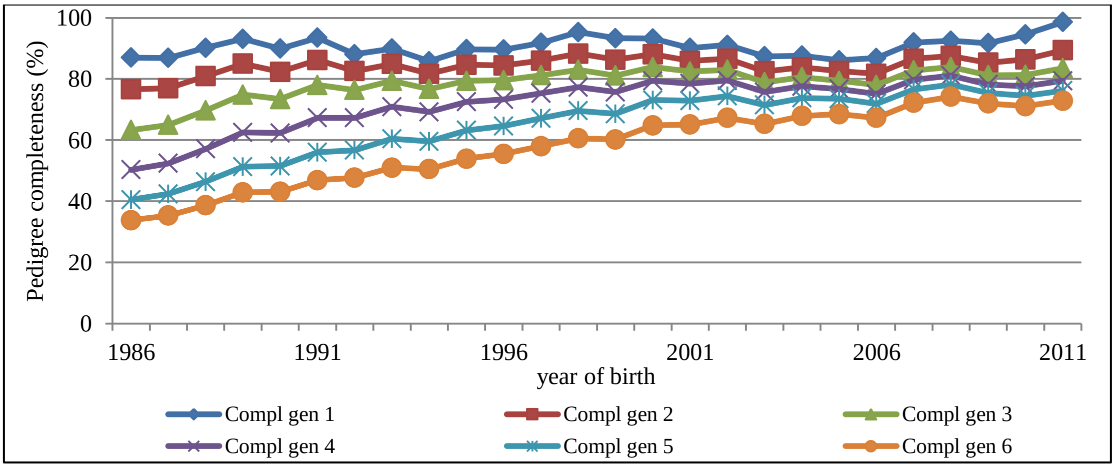

Figure 4.2.1.4: Trend of pedigree completeness for the Drakensberger breed

The trend for the pedigree completeness for the Drakensberger is above average with average completeness of almost 100 in the first generation and 69.2% in the sixth generations deep in 2012. However, contrary to improvement in pedigree completeness, the trend of the number of offspring (4.2.1.1) in the pedigree file has decreased.

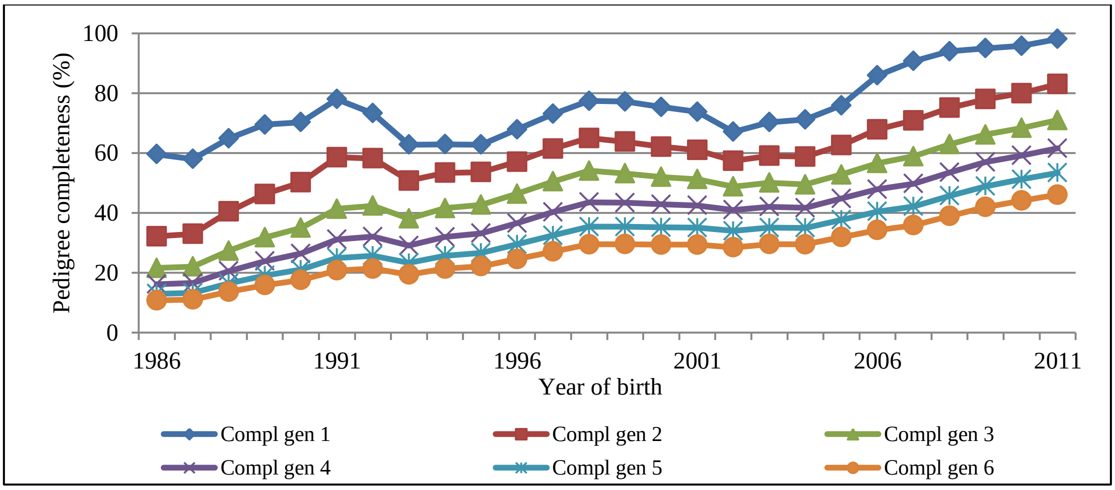

Figure 4.2.1.5: Trend of pedigree completeness for the Nguni breed

The trend of the pedigree completeness over six generations deep for the Nguni breed has gradually improved with average pedigree completeness ranging from 98.7% in six generations deep to 46.5% in the first generation in 2012. The trend of the number of offspring (4.2.1.1) in the pedigree of this breed has increased steadily.

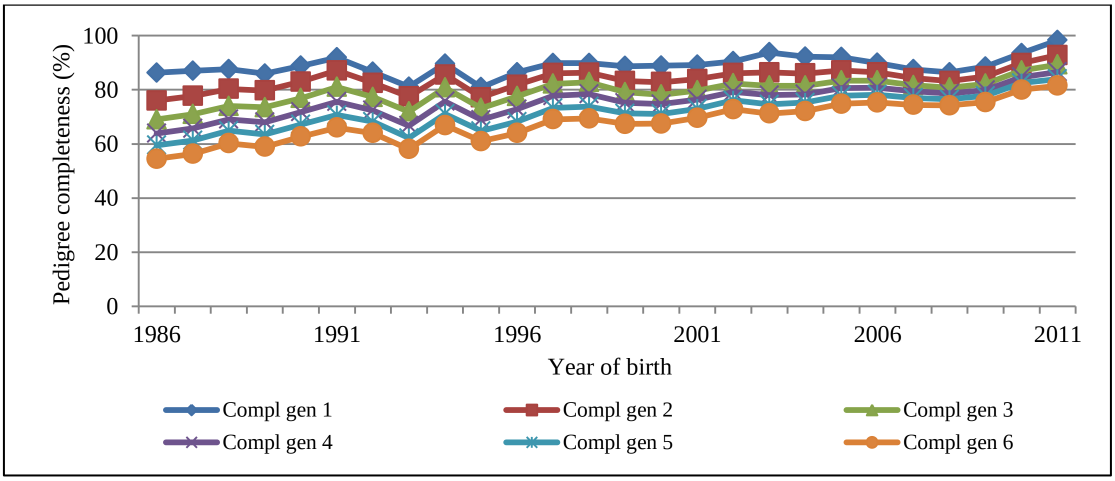

Figure 4.2.1.6: Trend of pedigree completeness for the Tuli breed

The Tuli breed has improved in the average pedigree completeness for the six generations ranging between 96.3% for first generation and 77.5% for six generations in 2012. The number of offspring (4.2.1.1) in the pedigree files of Tuli breed has stabilized with improved trend of pedigree completeness.

Average pedigree completeness for all animals and animals born in the past 25 years (1986 to 2012) are presented in table 4.2.1.1and 4.2.1.2 for each breed respectively.

Table 4.2.1.1 Estimated average pedigree completeness (%) six generations deep for all animals in the pedigree of five indigenous African beef cattle breeds

Breed	Gen 1	Gen 2	Gen 3	Gen 4	Gen 5	Gen 6
Afrikaner	56	51.2	46.1	41.3	36.7	32.3
Boran	22.5	16.8	13.4	10.9	9.1	7.8
Drakensberger	49.5	43.3	38.3	34	30.2	26.7
Nguni	44.5	34.8	27.9	22.8	18.9	16
Tuli	68.8	63.7	58.2	53	48.2	43.9

Gen: generation

The Tuli and Afrikaner breeds had a higher level of completeness six generation deep compared to other breeds in the original pedigree records. More than 50% of genealogical ancestors of animals in the original pedigree records in first generation for the Tuli and Afrikaner breeds were known. These proportion decreases with deeper generation up to 43.3% and 32% at six generation deep for the Tuli and Afrikaner breeds respectively. The Boran, Drakensberger and Nguni breeds have completeness level of less than 50% in the first generation which decrease with increased depth of completeness up to 7.8%, 26.7% and 16% respectively.

Table 4.2.1.2 Estimated average pedigree completeness (%) six generations deep for animals born over the last 25 years for five indigenous African breeds

Breed	Gen 1	Gen 2	Gen 3	Gen 4	Gen 5	Gen 6
Afrikaner	95.2	92.6	88.2	81.6	73.8	65.6
Boran	33.3	27.6	23.2	19.4	16.3	13.8
Drakensberger	91	84.5	78.5	72.1	65.3	58.4
Nguni	75.9	60.2	48.5	39.7	33	27.8
Tuli	89.2	84	79.5	75.6	72	68.3

Gen: generation

For the animals born from 1986 to 2012, the pedigree completeness was higher and showed an improvement for all five breeds. The Tuli, Afrikaner and Drakensberger breeds have completeness levels of more than 50% in all investigated six generations. The Nguni breed has a completeness level of more than 50% in the first and second generations and only 27.8% in the six generations deep. The least complete pedigree for the specified period was for the Boran breed.

The accuracy of the rate of inbreeding and relatedness depend on the extent of pedigree completeness (Groeneveld *et al.*, 2009; Boichard *et al.*, 1997; Sørensen *et al.*, 2008; Steyn *et al.*, 2012) and computational method (Van Doormaal *et al.*, 2005; Leroy *et al.*, 2013). Pedigree completeness is the sum of the percentage of known ancestors over all traced generations in the past (Boichard *et al.*, 1997). The trends of the pedigree completeness observed in the breeds studied can be attributed to their establishment in South Africa as shown in table 3.4.1.1. Older breeds have better pedigree completeness compared to the most recent established breeds.

Studies conducted to investigate pedigree completeness of beef cattle populations have revealed similar variable degree of pedigree completeness in different breeds. In Italian beef cattle breeds, Chianina had the best pedigree completeness of 62% and 16.4% at six and eight generations respectively (Bozzi *et al.*, 2006); for Irish beef cattle, Simmentals had the lowest pedigree completeness with only 43% four generation deep (Mc Parland *et al.*, 2007a) and for Slovak beef cattle breeds, Blonde d`Aquitaine and Simmental had the highest pedigree completeness in the first generation and Limousine had the lowest pedigree completeness through all the studied generations (Kadlečík and Pavlík, 2012).

The numbers of offspring registered in the pedigree files have increased in Boran, Nguni and Tuli breeds, while it decreased in Afrikaner and Drakensberger breeds. The continued decrease in the numbers of offspring for Afrikaner and Drakensberger indicate that these two breeds are losing their popularity and should be of a concern to the breed. The presence of an anoestrus gene in Afrikaner which interrupt heat period in cows could be a reason that contributed to their reduction in numbers and led to infusion with other breeds (www.afrikanerbees.com; Matjuda, 1997) The reduction in the population of the Drakensberger breed could be attributed to farmers' preference for red cattle in South Africa (Pentz, 2009; Bisschoff and Lotriet, 2013). The Boran breed is the youngest breed in South Africa and is gaining popularity and increasing its numbers.

From the results of the pedigree completeness under the current study, it is noted that pedigree information have variably changed and became more complete over the last 25 year in all five breeds. This improvement in the pedigree quality can mainly be credited to the improvement in animal recording organization through computerization and centralization of the animal recording system (i.e. establishment of INTERGIS) that produced good pedigree and performance records for national livestock.

4.2.2 Generation interval

Figure 4.2.2.1, showed the trends of average generation intervals for five indigenous African beef cattle breeds. The estimated average generation intervals for four gametic pathways (sire-son, sire-daughter, dam-son and dam-daughter), males, females and population of the five indigenous African beef cattle breeds are presented in table 4.2.2.1.

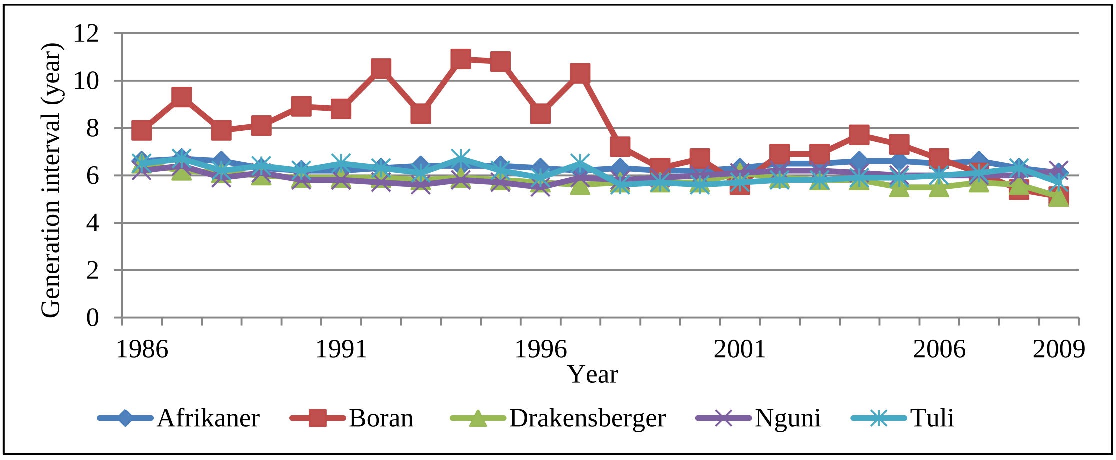

Figure 4.2.2.1: Trends of average generation intervals for five indigenous African beef cattle breeds

From figure 4.2.2.1, the Afrikaner, Drakensbereger, Nguni and Tuli breeds have almost similar and constant average generation interval with slight tendency to reduce from mid-2000. The generation interval for the Boran breed initially increased till mid-1990's and then gradually reduced almost levelling with the other four breeds.

Table 4.2.2.1 Estimated average generation intervals (year) for the four gametic selection pathways, male, female and the breed of five indigenous African beef cattle

Breed	Generation interval (year)						
	SS	SD	DS	DD	Male	Female	Breed
Afrikaner	6.2	6.3	6.6	6.6	6.3	6.6	6.4
Boran	7.6	6.5	7.9	6.1	6.6	6.4	6.3
Drakensberger	5.6	5.6	6.6	6.4	5.6	6.4	6.0
Nguni	6.1	6.2	6	5.8	6.2	5.8	6.0
Tuli	6.4	6.4	6.2	5.9	6.4	5.9	6.2

SS: sire to son; SD: sire to daughter; DS: dam to son; DD: dam to daughter; population: breed

The average generation intervals for the four gametic selection pathways in the current study slightly differed within each breed. The generation interval for male's line is shorter than female's line in the Afrikaner and Drakensberger breeds and longer in the Boran, Nguni and Tuli breeds. The shortest weighted average generation interval for the breeds in this study was 6 years estimated for Drakensberger and Nguni breeds, followed by 6.2 years and 6.3 years for Tuli and Boran breeds respectively. The longest weighted average generation interval was 6.4 years estimated for Afrikaner breed.

The estimated generation intervals obtained in this study are within the ranges reported by studies conducted on other beef cattle breeds. The reported shorter generation intervals for dam's offspring pathways (DS and DD) compared to sire-offspring pathways (SS and SD) for Angus, Hereford, Limousine and Simmental beef cattle (Mc Parland *et al.*, 2007a), Marchigiana cattle breed (Santana *et al.*, 2012) and Brown Swiss population (Worede *et al.*, 2013) are well comparable to the estimates for the Tuli and Nguni breeds. The estimates for the four selection pathways for the Afrikaner and Drakensberger breeds where the sire-offspring pathways are shorter than the dam's offspring pathways are similar to those reported for the Casina and Carreñana breeds (Cañon *et al.*, 1994), Costeño con Cuernos, Romosinuano and Blanco Orejinegro cattle breeds (Martínez *et al.*, 2008) and Alentejana cattle breed (Carolino and Gama, 2008). The estimated generation intervals for the four selection pathways for the Boran breed, where the two sire-offspring pathways are longer than dam to son (DS) pathway but shorter than dam to doughter (DD) pathway is similar to the reported result for the Bonsmara cattle breed (Groeneveld *et al.*, 2009).

Carolino and Gama, (2008) have reported comparable result to those found for the Afrikaner and Drakensberger breeds, where the generation intervals for male's line are always shorter than female's lines. Contrary, Biedermann *et al.*, (2009) has reported a longer generation intervals for male's line than female's lines which is comparable to the estimates found for the Boran, Nguni and Tuli breeds. This could be attributed to early replacement of females, use of proven males for longer time and selection of breeding males only after progeny testing.
The overall weighted average generation intervals for the population of Afrikaner, Boran, Drakenberger, Nguni and Tuli breeds are within the range of 6 years and are consistent with the reported weighted average generation intervals in literature. Similar results were found in the Charolais (6.17), Hereford (6.03) and Angus (6.09) cattle (Mc Parland *et al.*, 2007a) and shorter than reported average generation interval in Japanese Black (9.30) cattle (Nomura *et al.*, 2001); Limousin (6.71) and Semmental (6.54) cattle (Mc Parland *et al.*, 2007a); Sanmartinero (6.8) cattle (Martínez *et al.*, 2008); Marchigiana (7.02) cattle (Santana *et al.*, 2012) and Brown Swiss (6.90) population (Worede *et al.*, 2013). However, the estimated weighted average generation interval in all five breeds in the current study are longer than the reported results in Casina (5.30) and Carreñana (5.40) breeds (Cañon *et al.*, 1994); US Herefords (4.88) (Cleveland *et al.*, 2005); Chiana (5.35), Marchigiana (4.93) and Romagnola (5.15) cattle (Bozzi *et al.*, 2006); Blanco Orejinero (4.70), Costeño con Cuernos (5.40) and Romosinuano (5.7) cattle (Martínez *et al.*, 2008); Bonsmara (5.6) cattle (Groeneveld *et al.*, 2009) and Brangus (5.17) cattle (Steyn *et al.*, 2012).

These results showed relatively constant average generation intervals throughout the studied period for all five indigenous African beef cattle breeds. These average generation intervals can be considered intermediate although it may still compromise the rate of genetic progress. A longer generation intervals will result in minimum rate of genetic change and thereby affect the rate of genetic progress (Comstock *et al.*, 1998; Bourdon, 2000; Márquez and Garrick, 2007). More effort is therefore needed to slightly shorten the generation interval in order to increase the rate of genetic progress in the five breeds under the current study.

4.2.3 Age structure of parents and distribution of dams by parity number

The genetic structure of a population at a specific time is influenced by the age structure of parents and the number of breeding males and females in the preceding herd/population that would eventually determine the effective population size (Groeneveld *et al,* 2009). For a beef herd to be more profitable, a cow should remain in production for several years to compensate for the culled ones and counterbalance the development and maintenance costs (Snelling *et al.,* 1995). However the main reason for culling a cow earlier is her failure to become pregnant or to give offspring (Van der Westhuizen *et al.,* 2001; BIF, 2010). The age structure of sires and dams can determine the effective population as the variance in lifetime span (longevity) due to reproductive success (Groeneveld *et al.,* 2009). The average age of parents (sires and dams) by birth of offspring in the whole pedigree file is present in table 4.2.3.1 for the all five selected breeds. The age distributions of parents (sires and dams) by birth of offspring in the whole pedigree file of each breed are presented figures 4.2.3.1 to 4.2.3.5 for each respective breed.

Table 4.2.3.1 Average age of sires and dams by birth of offspring for five indigenous African beef cattle breeds

Average age	Breed				
	Afrikaner	Boran	Drakensberger	Nguni	Tuli
Sires	6	5.3	5.1	5.9	5.5
Dams	6.2	5.5	4.9	6.1	5.4

There is slight difference between the average age of sires and dams when their offspring are born in all five breeds. The youngest average age of sires and dams by birth of offspring was in the Drakensberger breed, while the oldest average age of sires and dams by birth of offspring was in the Afrikaner breed.

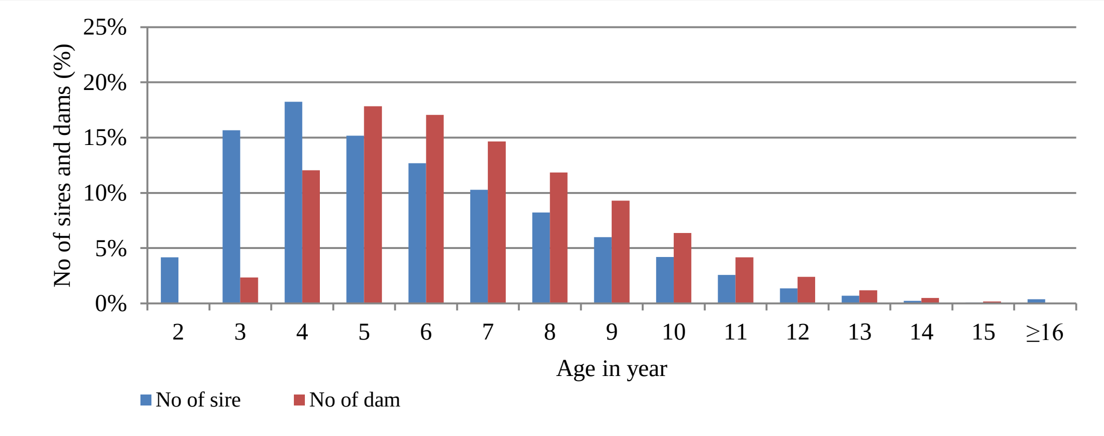

Figure 4.2.3.1: Age distributions of sires and dams for the Afrikaner breed

In the Afrikaner breed; the average age of sires and dams that produced offspring are 6 and 6.2 years respectively. The majority of males used in reproduction were 4, 3 and 5 years of age, while the females were at 5 years of age at reproduction followed by 6 and 7 years of age. The majority of sires and dams produce offspring at the age of four years with a steady decline thereafter. Less than 0.1% of parents with a slightly higher proportion sires remain in reproduction at ≥16 year of age in the population of Afrikaner breed.

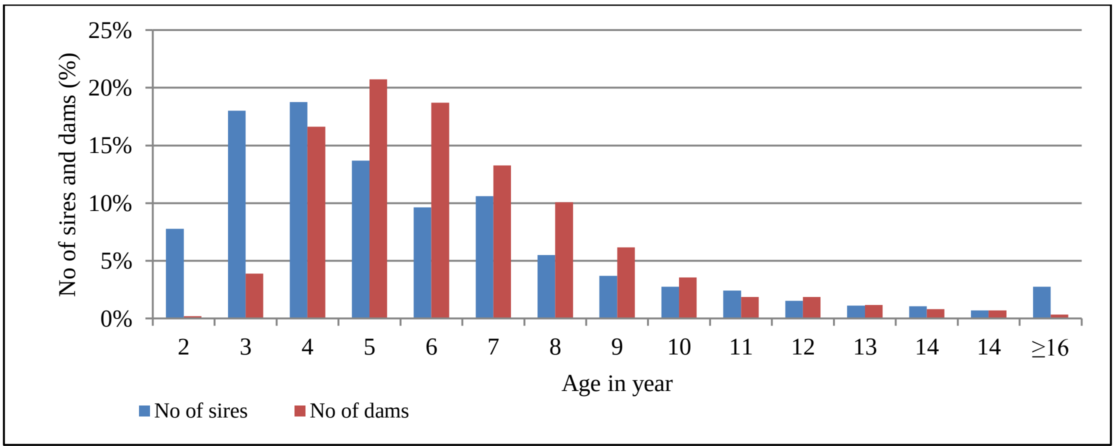

Figure 4.2.3.2: Age distributions of sires and dams for the Boran breed

The proportion of sires in reproduction at the age of 4 years was higher followed by 3rd and 5th years of age. The majority of dams in reproduction were at 5th year of age. Only about 0.3% of males and <0.1% of females were still producing offspring at ≥16 year of age in population of the Boran breed. The average age of sires and dams that produced offspring was 5.3 and 5.5 years respectively.

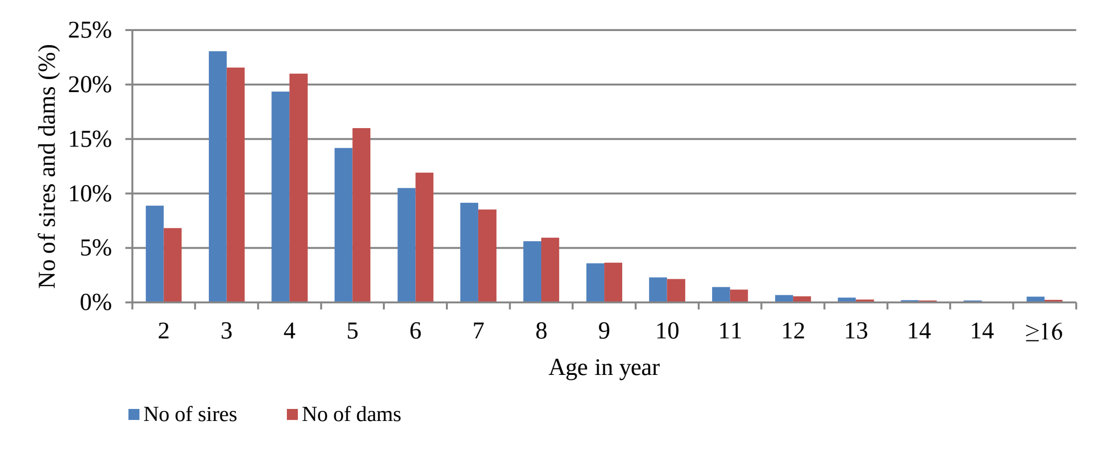

Figure 4.2.3.3: Age distributions of sires and dams for the Drakensberger breed

The majority of sires and dams calved at the age of four years and then followed by a steady decline. The average ages when the offspring are born are 5.1 years for males and 4.9 years for females. The proportion of sires and dams that successfully remained in reproduction till the age of ≥16 year in the population of Drakensberger breed was less that 1%.

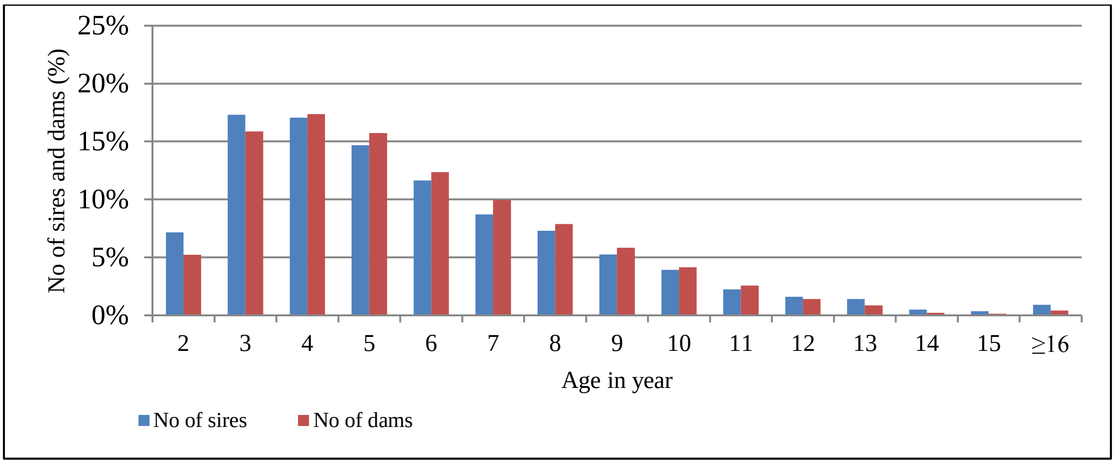

Figure 4.2.3.4: Age distributions of sires and dams for the Nguni breed

The majority of sires and dams produced offspring at the age of four years and then followed by a steady decline. The average ages of males and females by the birth of offspring are 5.9 for sires and 6.1 for dams. The proportion of sires and dams that remained in reproduction till the age of ≥16 year of age in the population of Nguni breed was less than 1%.

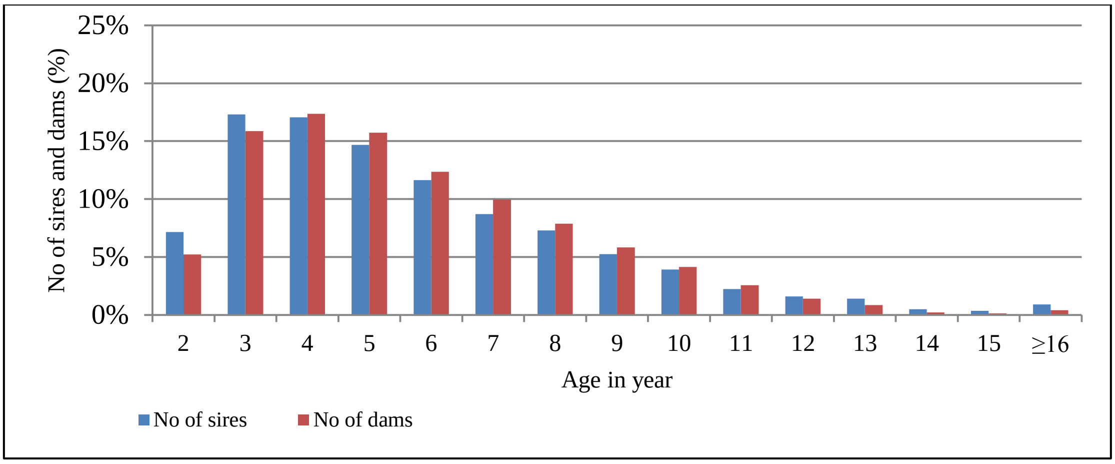

Figure 4.2.3.5: Age distributions of sires and dams for the Tuli breed

The majority of sires produced offspring at the age of 3 years and dams calved at the age of four years. The average ages of sires and dams by birth of offspring are 5.5 years for sires and 5.4 years for dams. The percentage of sires and dams that continue to produce offspring till the age of ≥16 year in the population of Tuli was approximately 1% for sires and less than 1% for dams.

Table 4.2.3.1 and figures 4.2.3.1 to 4.2.3.5 indicate that most of the sires and dams of all the five breeds in this study produced offspring between three and four years of age with males producing offspring earlier than females in most cases. Moreover, the proportions of sires producing offspring in their older ages are greater than dams. This indicated that males are used in reproduction longer than females with Boran having the highest and Tuli the second highest proportion of older males in the population. It will therefore be more profitable if the calving age of the dams is reduced while increasing the proportion of males producing offspring at an earlier age. The calving age of the dams could be reduced by mating heifers right after puberty (Nuñez-Dominguez *et al.,* 1991). This will probably increase the number of offspring per dam and ultimately the economic efficiency of farm. It was reported that, genetic variation in age at puberty in beef cattle do exists; and efficient utilization of such variation in selection would potentially influence production efficiency (Day and Nogueira, 2013).

The overview of the distribution of dams by parity number gives an idea about the rate of turnover of the breeding animals. The rate of turnover is one the aspects that influence the rate of genetic progress in livestock selection and improvement program, since animals with good longevity tend to leave more offspring in the population (Groeneveld *et al.*, 2009). Therefore, female production and reproduction is essential as it quantify the output from the breeding females that were selected to breed future generations and thereby ensuring the sustainability of beef cattle production and robustness of the enterprise.

Figure 4.2.3.6 presents the distribution of parities attained by dams in Afrikaner, Boran, Drakensberger, Nguni and Tuli breeds. For simplicity the dams were placed into three groups as G1, G2 and G3 for each respective breed. Dams with parity number 1 to 5 were put together in group one (G1), 6 to 10 in group two (G2) and 11 to ≥16 in group three (G3) respectively.

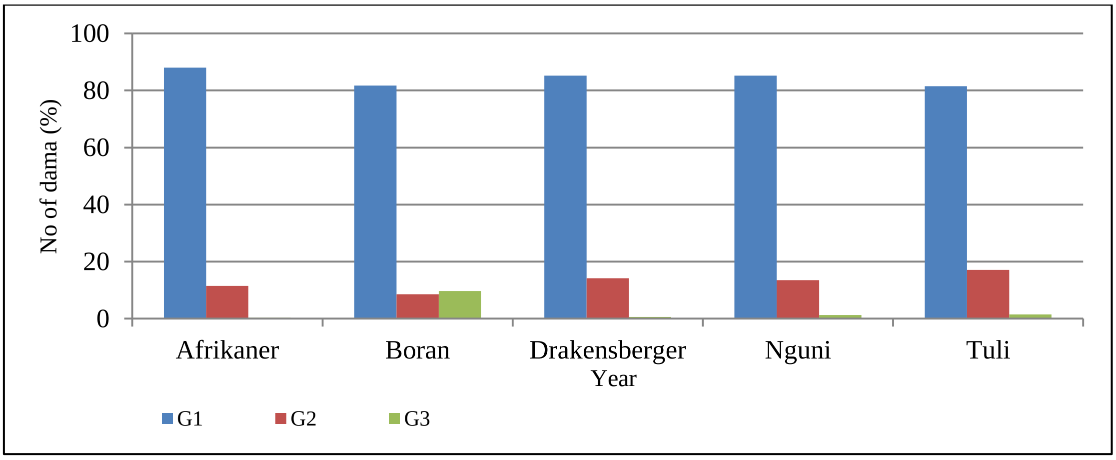

Figure 4.2.3.6: Distribution of dams by parity number for five indigenous African beef cattle breeds
G1: Dams with parity number 1 to 5; G2: Dams with parity number 6 to 10; G3: Dams with parity number 11 to ≥16

Generally group one has the highest proportion of dams in the all five breeds. The number of dams' subsequent decrease with increase in the number of parity over time. That is why it is better to group dams by number especially those with parity number greater or equal to sixteen (Groeneveld *et al*, 2009). The breed with the highest proportion of dams in groups one was Afrikaner with 87.5% and then followed by Drakensberger, Tuli, Nguni and Boran. Group two had shown to be the second highest in Afrikaner with 12%, Drakensberger with 13, Nguni with 13.3 and Tuli with 13.4. The percentage of dams in group 3 (9.8) is greater than group 2 (8.6) in Boran. Only 0.5%, 0.6%, 1.3% and 0.8% of dams were in group 3 for Afrikaner, Drakensberger, Nguni and Tuli respectively.

The average number of offspring per dam increases for breeds having more cows in G2 and G3 parity than ones having more number of cows in G1 parity. Accordingly, the higher numbers of animals with more parity correspond to the higher rate of turnover and apparently good longevity of the respective breed. It was argued that longevity will increase the generation interval and increase the accuracy of the predicted breeding value from the additional data (Nwakalor *et al.*, 1986). However this could be realized only when there is accurate and consistent recording system.

4.2.4 Breeding animals and effective population size

The number of breeding animals at specific time determines the effective population size which is the principal factor that influences the rate of genetic drift and inbreeding in a population over a period of time (Nicholas, 2003; Groeneveld *et al.*, 2009). The trends for the number of animals used in reproduction representing all the animals in the available pedigree data for the Afrikaner, Boran, Drakensberger, Nguni and Tuli breed are presented in Figure 4.2.4.1 and table 4.2.4.1. The calculated values for the effective population size (Ne) are presented in table 4.2.4.1.

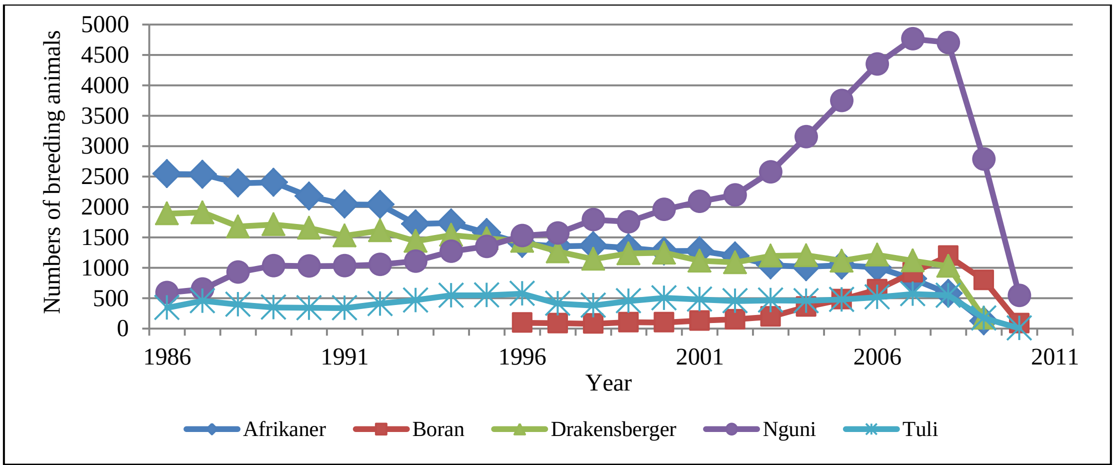

Figure 4.2.4.1: Trends of numbers of breeding animals for five indigenous African beef cattle breeds

The numbers of breeding animals for the Afrikaner and Drakensberger breed have gradually declined. The Nguni and Boran breeds have shown persistent increases in the number of breeding animals. The drop observed in the trend of breeding animals towards 2011 in the five breeds was caused by the presence of young animal as only animals having a service record or appearing as parent in the birth record when considered in the calculation of breeding animals.

Van der Westhuizen and Groeneveld, (2004) have reported that the numbers of breeding animals for the Afrikaner and Drakensberger breed are declining. Only 48% and 55% of the number of sires and 50% and 54% of the number of dams that were used in 1990 were again used in 2002, respectively, while the number of breeding animals for the Nguni breed was still in an increasing phase. This trend was also found in the current study.

Table 4.2.4.1 Number of Breeding animals, offspring born and effective population size for all animals in the pedigree of five indigenous African beef cattle breeds

	Breed				
	Afrikaner	Boran	Drakensberger	Nguni	Tuli
Base population	41 129	24 805	31 015	50 933	7 830
Reference population	206 044	32 756	167 542	205 757	47 479
No of sires used in reproduction	5 452	1 177	4 172	4 568	1 055
No of dams used in reproduction	69 444	11 956	50 581	66 825	13 762
Average no of offspring/sire	45.3	48.9	47.6	56.2	52.4
Average no of offspring/dam	3.6	4.8	3.9	3.8	4.0
Effective population size	107	364	122	191	89

Sires: total number of sires with offspring in the whole pedigree of each breed. **Dams:** total number of dams with offspring in the whole pedigree of each breed.

Base population or animals relatively contribute to the genetic structure of reference population and were defined as the animals with one or more unknown parents. Reference population or animals are those animals with two of their parents/ancestors are known. The highest number of offspring per sire is the result of intense use of popular sires. This will simultaneously increase sire effects and the variance in family sizes as a result of unequal genetic contribution which will adversely affect the effective population size (Falconer and Mackay, 1996).

The effective population size measures genetic variation within livestock populations and is a useful measure due to its direct relationship with the rate of inbreeding and loss of genetic diversity over a period of time (Caballero and Toro 2000; Sørensen *et al.*, 2005). Reduction in effective population size may increase selection response through selection intensity but conversely may lead to inbreeding depression and the loss of genetic variance that limits selection response from new mutations in the long term (Toro and Lopez-Fanjul, 1998). The effective population size between 50 and 100 will lead to an increase in the rate of inbreeding coefficient by 0.5 to 1% per generation which is sufficient to maintain the genetic diversity within a population (FAO, 1998b; Bijma, 2000). A drop in the effective population size below this limit would result to decline in population fitness as a result of mutation and genetic drift (Meuwissen, 1999).

The effective population size for all the five breeds in the present study varied in magnitude (Table 4.2.4.1). The lowest value of effective population size of 89 was found in the Tuli breed which is within the minimum effective population sizes defined by FAO, (1998b) and Bijma, (2000). The Afrikaner breed was having a slightly higher effective population size (107) compared to the Tuli breed. The effective population size for the other populations was found to be relatively good with Boran having the highest effective population size of 364 in whole pedigree followed by Nguni (191) and Drakensberger (122).

The estimated effective population sizes of the breeds in this study are comparable to other cattle populations; 39 and 30 for US Holstein and Jersey cattle respectively (Weigel, 2001) and 47 to 53 for Danish dairy cattle Sørensen *et al.*, (2005). In a number of studies on beef cattle Ne varied from as low as 21 in Spanish beef cattle (Gutierrez *et al.*, 2003) to as high as 167 for South African Brangus cattle (Steyn *et al*, 2012).

From these results, it could be advised that mating policy should be adjusted to increase effective population sizes and reduce the rate of inbreeding particularly in Tuli and Drakensberger breeds. This is extremely important as it will efficiently preserve genetic variability which is a source to developed genetically superior individuals capable to respond to variable future demands. The estimated effective population size for the Boran breed has been overestimated due to under estimation of inbreeding as a result of poor pedigree recording. This study therefore highlights the importance of pedigree recording in beef cattle production.

4.2.5 Inbreeding and additive genetic relationships

Both inbreeding and additive genetic relationships are related to consanguinity and are among the key parameters used in measuring the status of genetic diversity within a population. The average inbreeding coefficient and additive genetic relationship coefficient were calculated for the whole pedigree to determine the level of inbreeding and relatedness in each breed. The estimated rate of addititive genetic relationships (Δf) and inbreeding (ΔF) are summarized in table 4.2.5.1. The trends of addititive genetic relationships and inbreeding coefficients as well as the proportion of inbred animals are shown in figures 4.2.5.1 to 4.2.4.5 and 4.2.5.6 to 4.2.5.7 respectively.

Table 4.2.5.1 Estimated average rate of inbreeding and additive genetic relationships per year and generation for five indigenous African beef cattle breeds

Breed	Average Δf per year (%)	Average Δf per generation (%)	Average ΔF per year (%)	Average ΔF per generation (%)
Afrikaner	0.02	0.14	0.06	0.38
Boran	0.006	0.04	0.03	0.18
Drakensberger	0.03	0.16	0.07	0.44
Nguni	0.004	0.02	0.04	0.23
Tuli	0.03	0.17	0.08	0.52

Δf: Rate of additive genetic relationships; ΔF: Rate of inbreeding

From table 4.2.5.1, the average rates of inbreeding and additive genetic relationships based on the slope of regression have changed with different magnitudes in all five breeds. The highest average rate of inbreeding was observed in the Tuli breed followed by the Drakensberger, the Afrikaner, and the Nguni breeds respectively, while the lowest average rate of inbreeding was in the Boran breed. The highest average rate of additive genetic relationships was in the Tuli breeed followed by the Drakensberger, the Afrikaner and the Boran breeds respectively. The lowest average rate of additive genetic relationships was revealed in the Nguni breed.

Figures 4.2.5.1 to 4.2.5.5 showed the trends of average additive genetic relationship coefficient for all offspring, inbreeding coefficient for all and inbred offspring computed by year of birth of the individual offspring in the whole pedigree of Afrikaner, Boran, Drakensberger, Nguni and Tuli breeds respectively.

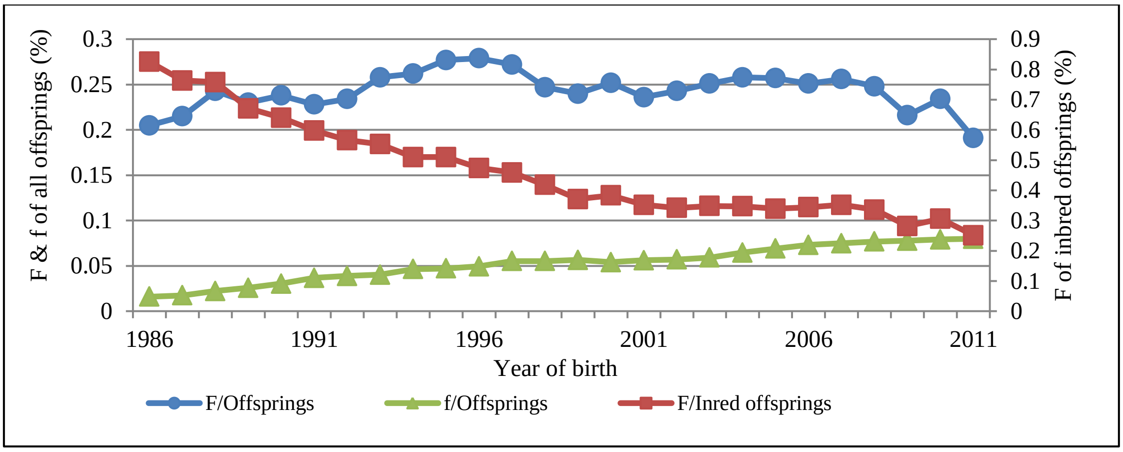

Figure 4.2.5.1: Trends of average inbreeding coefficients for all and inbred offspring and coefficient of additive genetic relationships for the Afrikaner breed

In the Afrikaner breed, the average inbreeding coefficient has increased steadily till it reached 0.28% in mid-1990's and then gradually decreased to 0.2% in 2011. The average inbreeding coefficient for inbred animals has decreased substantially from more than 0.8% before 1986 to 0.25% in 2011. The coefficient of additive genetic relationship has increased gradually and reachd 0.08% in 2011. This indicates that the coefficient of relatedness among the offspring is increasing and will relatively contribute to increase inbreeding in the future.

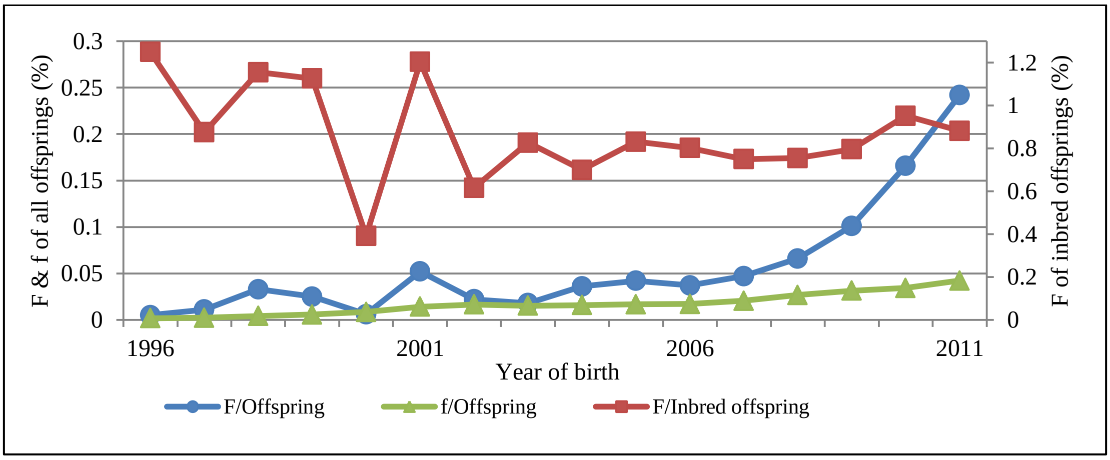

Figure 4.2.5.2: Trends of average inbreeding coefficients for all and inbred offspring and coefficient of additive genetic relationships for the Boran breed

Due to poor recording in the pedigree of Boran breed, the trend of the average inbreeding coefficients and the coefficient of additive genetic relationship are presented from 1996. The trend of inbreeding coefficient and the coefficient of average additive genetic relationship of all offspring in the pedigree have increased steadily especially since 2006. The average inbreeding coefficient and the average additive genetic relationship were 0.04% and 0.025 in 2005 and later increased to 0.24% and 0.4% respectively. The average inbreeding coefficient of inbred offspring has increased at greater rate till late 1980 and then decreased and stabilized. These trends indicated that there is high use of related animals especially after the year 2000. This estimate of inbreeding coefficient is however probably an under estimation due to limited pedigree records. Limited pedigree records will biasedly underestimate the level of inbreeding and overestimate the effective population size (Boichard *et al.*, 1997; Márquez *et al.*, 2010).

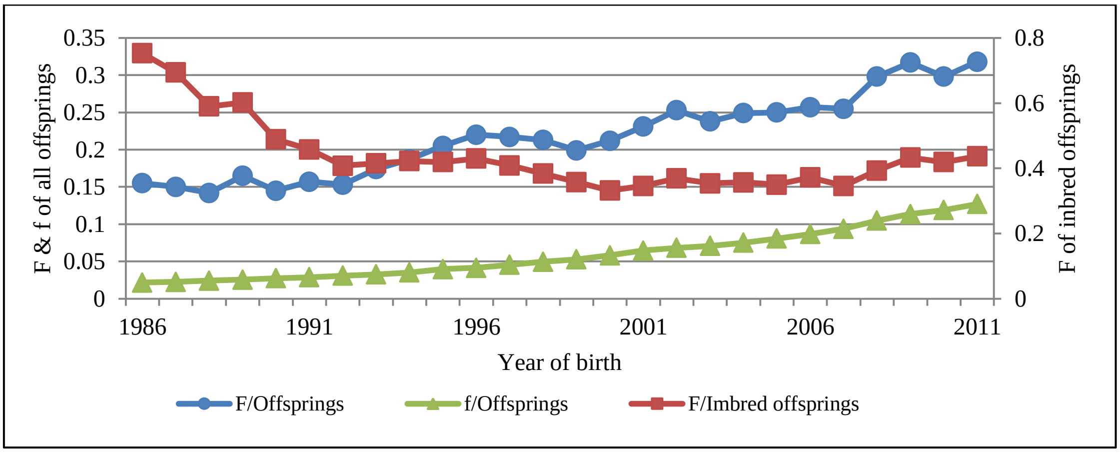

Figure 4.2.5.3: Trends of average inbreeding coefficients for all and inbred offspring and coefficient of additive genetic relationships for the Drakensberger breed

The inbreeding coefficient for the whole population of Drakensberger breed has increased sharply until it reached 0.3% in 2011 with average rate of change of 0.07% per year and 0.44% per generation. The trend of the inbreeding coefficient for inbred offspring has decreased, but started to increase again after 2000. The coefficient of additive genetic relationship has increased steadily. The increased tendency in the level of inbreeding of bred offspring coupled with sharp increase in additive genetic relationships indicates re-intensification of closely related individuals. Therefore, continuous mating of closely related individuals should be restricted to avoid further increase in the level of inbreeding in this breed.

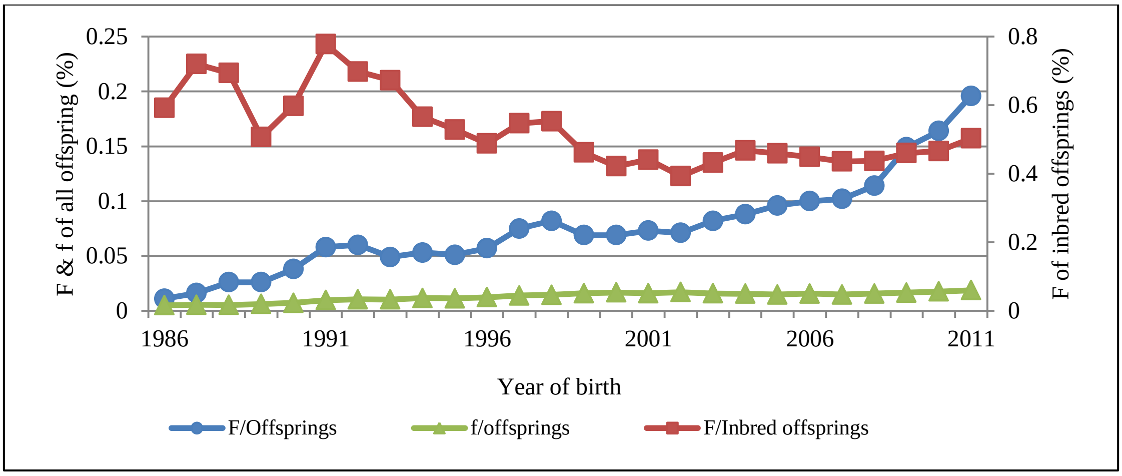

Figure 4.2.5.4: Trends of average inbreeding coefficients for all and inbred offspring and coefficient of additive genetic relationships for the Nguni breed

The inbreeding coefficient for the whole population of Nguni breed has increased persistently till it reached 0.2% in 2011with average rate of 0.04% per year and 0.23% per generation. The trend of inbreeding coefficient for inbred offspring increased to reach the highest level at 0.8% in 1991. Afterwards it decreased gradually and reached the level of 0.5% in 2011. The trend of the coefficient of additive genetic relationship has increased subtly until it reached 0.004% in 2011. The additive genetic relationship is quite low in this breed when compared to inbreeding. This could be attributed to mating of few closely related individuals within Nguni breed.

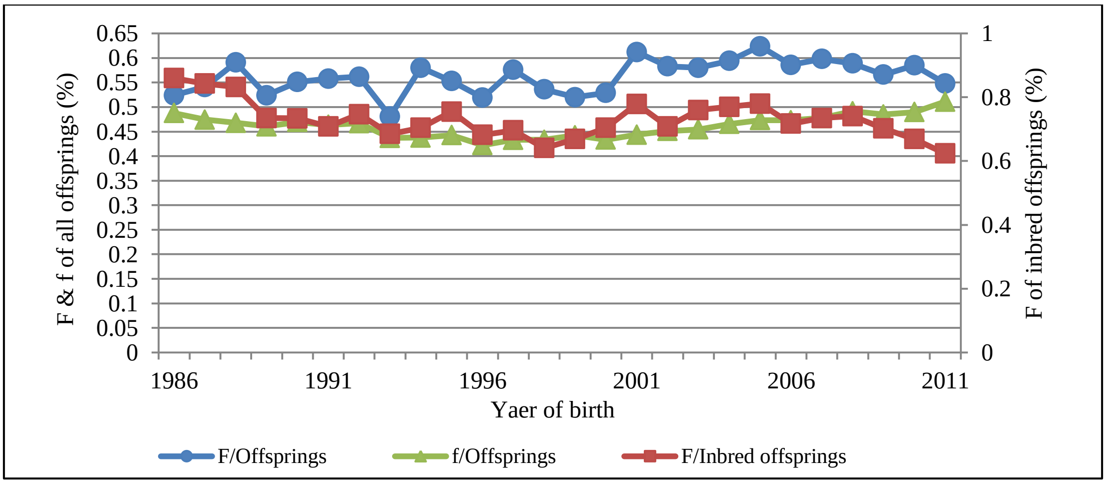

Figure 4.2.5.5: Trends of average inbreeding coefficients for all and inbred offspring and coefficient of additive genetic relationships for the Tuli breed

The trends of inbreeding coefficient for all and inbred offspring and the coefficient of additive genetic relationships for the Tuli breed remained nearly unchanged ranging between 0.5 and 0.63%. The trend of the coefficient of additive genetic relationship has slightly decreased but with an increased trend after 1995. The trend of the average inbreeding coefficient of inbred offspring initially increased and reached the highest before 1986 and then decreased slowly to 0.6% in 2011. This high level of inbreeding and relatedness is serious as it will result in an increase in the level of homozygosity which in turn will increase the risk of the appearance of undesirable effects. A balanced mating policy that favoured best unrelated individuals is primarily needed at this stage to correct the possible effect of such high levels of inbreeding in the population of this breed.

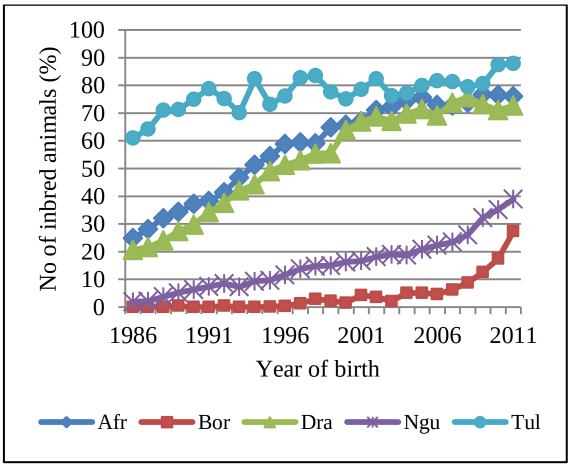

Figure 4.2.5.6: Trends of number of inbred animals for five African breeds

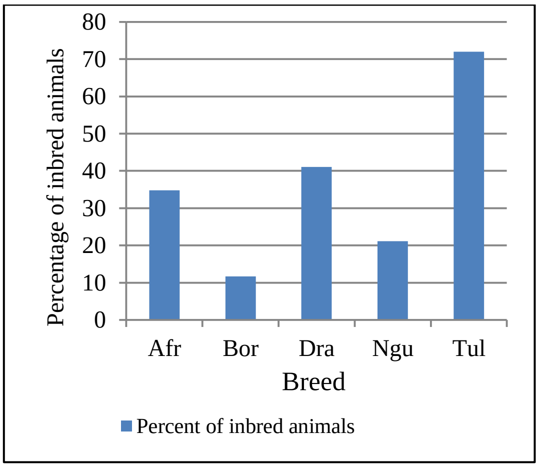

Figure 4.2.5.7: Percentage of inbred animals for five African breeds

Afr: Afrikaner; Bor: Boran; Dra: Drakensberger; Ngu: Nguni; Tul: Tuli

The trend of the proportion of inbred offspring has increased considerably in all five breeds (Figure 4.2.5.6). The proportion of inbred offspring for the Tuli, Afrikaner, Drakenberger and Nguni breeds have increased gradually and reached 87.9%, 76%, 72.7% and 39% in 2011 respectively in 2011. A greater increase in the proportion of inbred offspring started after 2000 in Boran breed, when its pedigree completeness improved and reached 35.2% in 2011. The increase in the proportion of inbred offspring of each breed has accounted to the total percentage of inbred offspring in the whole pedigree (Figure 4.2.5.7) of approximately 72% for Tuli breed. The second most inbred population was the Drakensberger with 41%, followed by the Afrikaner breed with 34.85%, Nguni breed with 21.1%. The rapid increased in inbreeding coefficient and ratio of inbred offspring in Tuli breed is of great concern as it may possibly lead to inbreeding depression and increase frequency of recessive homozygote for deleterious alleles. This situation could have been influenced by the small population size of the Tuli breed which minimizes the chance of getting new genes. Therefore, a study to investigate any possible effect of inbreeding in Tuli breed should be conducted.

It has been shown that continuous improvement in animal recording genetic evaluation and breeding methods contribute to successful selection and genetic improvement of the beef industry in many world beef producing countries (Johnston, 2007). Despite this success, the methods used have promoted an increase in the probability of relatedness and increased level of inbreeding that may compromise long term selection response and increase the risk of inbreeding depression (Weigel, 2001; Northcutt *et al.*, 2004; Carolino and Gama, 2008). It is therefore important to obtained insight on the genetic structure of a population to maintain within breed genetic diversity and sustainable improvement program (Malhado *et al.*, 2008).
The change in the average rate of inbreeding per year and generation outweighed the actual level of inbreeding coefficient. The level of inbreeding coefficient relatively depends on the base population, which is assumed to be unrelated while the average rate of inbreeding measures the rate of loss of genetic variation within a population (FAO, 1998b; Bijma and Woolliams, 2000; Groeneveld e*t al.*, 2009). The FAO guidelines (FAO, 1998) and Bijma (2000) have recommended a limit of 0.5-1% for the rate of inbreeding per generation to maintain fitness in a breed.

Several studies have reported unfavourable long-term effects of high rate of inbreeding on the efficiency of reproductive and production traits in cattle breeds. Burrow, (1998) has reported a decrease in the pregnancy rate and increased days to calving with increasing inbreeding coefficient in the tropical beef cattle breeds. Carolino and Gama, (2008) have reported significant effects of inbreeding on some reproductive efficiency traits, with a decline of nearly 0.02 calves produced through life and a reduction in longevity of about 0.2 months per 1% increase in individual breeding. Sewalem *et al.,* (2006), have also reported an increased trend toward risk of culling among more inbred animals in Canadian Dairy Cattle. Inbreeding unfavourably influences the status of dystocia and stillbirths in cattle breeds (Adamec *et al.*, 2006; Mc Parland *et al.*, 2008). In respect to male reproductive traits, a decrease in scrotal circumference was reported with increasing rate of inbreeding coefficient

(Burrow, 1998; Mc Parland *et al.*, 2008; Santana *et al.*, 2010; Santana *et al.*, 2012). With regard to growth traits, a significant decrease in birth weight of about -0.154kg was reported for the Bonsmara breed (Santana *et al.*, 2012), -5.8g for closed population of Herefords (Pariacote *et al.*, 1998) per 1% increase in individual breeding coefficient respectively. A reduction in weaning weight of about -0.44kg in several beef cattle breeds (Burrow, 1993) and −0.51kg in Brown Swiss cattle (Falcão *et al.*, 2001) per 1% increase in individual breeding were reported respectively. Similarly Pariacote *et al.*, (1998) has reported a decrease in weaning weight and daily weight gain due to individual and maternal inbreeding in a closed herd of Hereford cattle; Queiroz *et al.*, (2000) reported a decrease in weaning and yearling weights with increasing individual inbreeding in Gyr cattle, while Carolino and Gama, (2008) have reported an unfavourable effect of individual and maternal inbreeding on weight at 7 months of age and mean daily weight gain in Alentejana cattle. Moreover, increase in the level of inbreeding has also been reported to have negative impact on carcass yield and quality (Burrow, 1998; Mc Parland *et al.*, 2008; Santana *et al.*, 2010) as well as milk yield and composition (Mc Parland *et al.*, 2007b; Maiwashe *et al.*, 2008).

The average rate of change in inbreeding per year for all five breeds in this study are within the range of reported studies such as 0.02% for American Red Angus cattle (Márquez *et al.*, 2010), 0.06% for Brangus cattle (Steyn *et al.*, 2012), 0.07 to 0.59 for eight Spanish beef cattle breeds (Gutiérrez *et al.*, 2003), 0.12% for American Herefords (Cleveland *et al.*, 2005) and 0.06 to 0.13% for Irish beef cattle (Mc Parland *et al.*, 2007a). The estimated average rate of inbreeding coefficients per generation for all these breeds are lower than the reported average rate of 0.6% in American Herefords (Cleveland *et al.*, 2005) and within 0.4 to 2.2% in eight Spanish beef cattle breeds (Gutiérrez *et al.*, 2003) and 0.54 to 2.19% in Irish beef cattle (McParland *et al.*, 2007a) and 0.07 to 1.05% in Slovak beef cattle (Kadlečík and Pavlík, 2012). The estimated average rate of inbreeding coefficients per generation for Afrikaner (0.38%), Boran (0.18%) and Nguni (0.23%) are within the acceptable limit recommended by FAO, (1998b) and Bijma, (2000), which should be less than 0.5 – 1.0% per generation. The Tuli (0.52%) and Drakensberger (0.44%) breeds have however approached the minimum recommended limit for the rate of inbreeding. As a result caution should be taken to avoid further increase that would risk within breed genetic diversity and compromise future genetic gain.

The additive genetic relationship coefficient which is the degree of an individual's relatedness in a population influences the effectiveness of a selection program. It is the probability that alleles taken randomly from individuals in the pedigree of a population are identical by descent (Toro *et al.,* 2011). The coefficient of additive genetic relationship is therefore another additional tool useful for designing a mating program (Goyache *et al.,* 2003) and prediction of inbreeding in the subsequent generations (Márquez *et al.,* 2010). The result of the average rate of additive genetic relationships (Table 4.2.5.1) combined with its trends (Figures 4.2.5.1 to 4.2.5.5), reflected a continuous increase in additive genetic relationships in all studied breeds though with different rate of change. This increase in additive genetic relationships couple with high proportion of inbred animals (Figures 4.2.5.6 to 4.2.5.7) would ultimately increase the rate of inbreeding in the future. Therefore, breeders should be aware of this and continue applying proper selection and avoid mating of closely related individuals.

The degree of inbreeding and relatedness varies according to the status of recording and selection policies applied in the breeding program as observed in figures 4.2.5.1 to 4.2.5.5 and table 4.2.5.1. The average inbreeding coefficients are relatively higher than the average additive genetic relationship in all five breeds. The average inbreeding coefficients and the percentage of inbred offspring have increased concurrently, while the average inbreeding coefficient of inbred offspring has declined across the five breeds. The lowest average inbreeding coefficients and the percentage of inbred offspring observed for Boran breed have been under estimated due to aforementioned reason. Regular monitoring of inbreeding and its related factors within these breeds is however imperative, to ensure their sustainability especially in the challenging production environments of Africa.

4.3 Genetic trends

The ultimate objective of most modern beef cattle production systems is to improve the efficiency of production in order to be competitive and economically viable. Several activities including animal recording; genetic evaluation and selection are involved to accomplish this objective. The current performance recording systems along with the advances in the genetic evaluation to derive EBVs have influenced most of the economically important traits in beef cattle. The genetic trend is an important indicator of selection direction and success (Intaratham *et al.*, 2008; Bosso *et al.*, 2009). It also aids in planning for future breeding schemes. The number of animals with EBVs of traits measured between 1986 and 2012 for five indigenous African beef cattle breeds are presented table 4.3.1.

Table 4.3.1 Number of animals with EBVs of traits measured between 1986 and 2012 for five indigenous African beef cattle breeds

Trait (EBV)	Number of animals				
	Afrikaner	Boran	Drakensberger	Nguni	Tuli
Birth weight direct (kg)	136 947	47 673	103 245	47 154	43 413
Birth weight maternal (kg)	137 542	67 892	103 279	47 985	44 470
Weaning weight direct (kg)	143 566	42 170	103 521	48 058	42 436
Weaning weight maternal (kg)	134 722	41 615	103 520	48 055	37 400
Yearling weight direct (kg)	138 063	35 653	103 160	46 699	40 839
Final weight direct (kg)	135 045	31 119	102 636	46 011	39 459
Mature weight direct (kg)	84 533	24 804	93 077	44 901	35 298
Kleiber ratio (kg)	132 174	-	101 062	43 053	30 829
Scrotal circumference (mm)	134 108	-	101 433	42 892	35 960

The genetic trends for these economically important traits were estimated by averaging the predicted breeding values on birth year for each trait and each breed between 1986 and 2012. The most important point in these trends is the slope of the lines (Figures 4.3.1 to 4.3.19) and the rate of genetic change per year (Table 4.3.2), as they will indicate the direction of selection and trait (s) of priority for the breeders of each breed.

Table 4.3.2 Estimated annual rate of genetic trends of EBVs of traits measured between 1986 and 2012 for for five indigenous African beef cattle breeds

Trait (EBV)	Breed				
	Afrikaner	Boran	Drakensber	Nguni	Tuli
Birth weight direct kg/yr	+0.051	+0.018	+0.008	-0.003	+0.025
Birth weight maternal kg/yr	+0.007	-0.007	-0.006	-0.001	+0.008
Weaning weight direct kg/yr	+0.540	+0.104	+0.277	+0.062	+0.185
Weaning weight maternal kg/yr	+0.129	+0.021	+0.010	+0.021	+0.041
Yearling weight kg/yr	+0.759	+0.133	+0.406	+0.069	+0.327
Final weight kg/yr	+1.013	+0.157	+0.521	+0.093	+0.393
Mature weight kg/yr	+0.807	+0.410	+0.188	+0.108	+0.445
Kleiber ratio kg/yr	+2.922	_	+1.252	+0.613	+0.359
Scrotal circumference mm/yr	+0.472	_	+0.298	+0.183	+0.183

yr: year

The rate of change in birth weight direct per year was higher in Afrikaner followed by Tuli, Boran, Drakensberger and Nguni breed respectively. Limited change was revealed in both birth weight and weaning weight maternal in all five breeds. The estimates of annual rates of genetic change for all the growth traits were positive. Most genetic improvement in growth traits was in Afrikaner breed followed by Drakensberger and Tuli breed. The Boran breed has also shown improvement in the years since breed society was founded. Almost no improvement in growth traits was revealed in Nguni breed. Kleiber ratio has changed with more genetic improvement in Afrikaner breed followed by Drakensberger breed. The lowest improvement in Kleiber ratio was in Tuli breed. Similarly most genetic improvement in scrotal circumference was in Afrikaner followed by Drakensberger breed. Nguni and Tuli breeds have the least rate of genetic improvement in scrotal circumference.

Figures 4.3.1 to 4.3.5 present the genetic trends of Birth weight direct and maternal for Afrikaner, Boran, Drakensberger, Nguni and Tuli breeds over 25 years respectively.

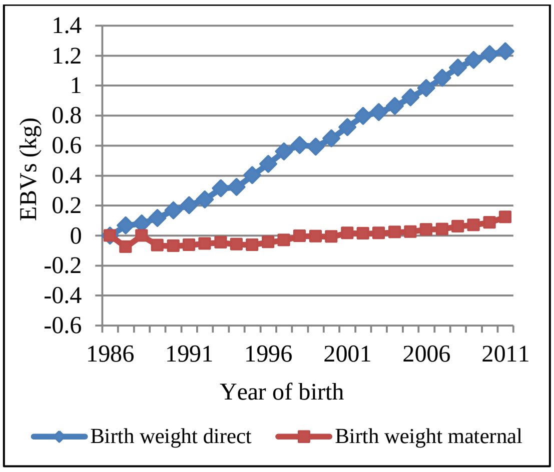

Figure 4.3.1: Trends of birth weight direct and birth weight maternal EBVs for the Afrikaner breed

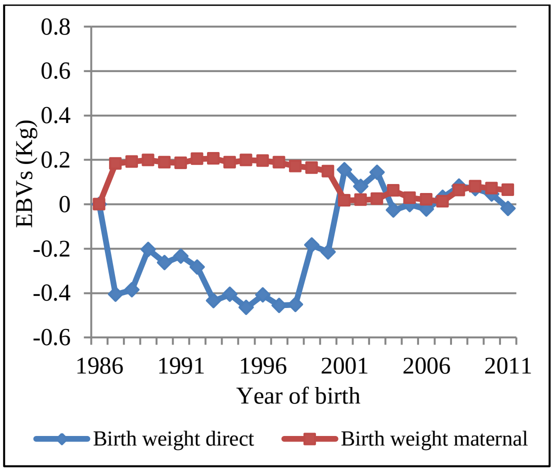

Figure 4.3.2: Trends of birth weight direct and birth weight maternal EBVs for the Boran breed

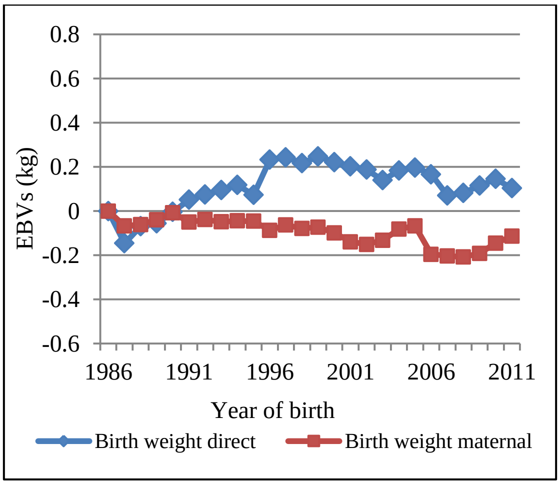

Figure 4.3.3: Trends of birth weight direct and birth weight maternal EBVs for the Drakensberger breed

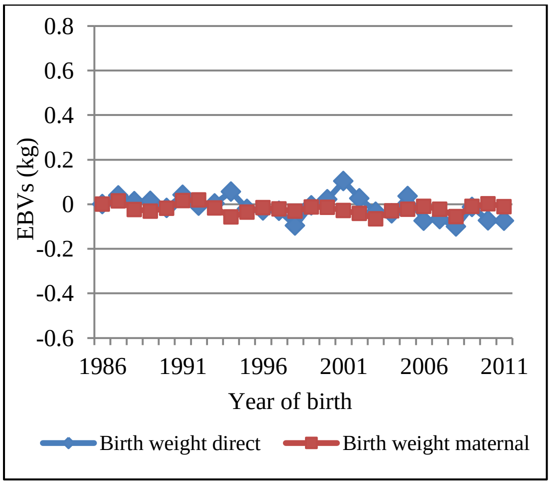

Figure 4.3.4: Trends of birth weight direct and birth weight maternal EBVs for the Nguni breed

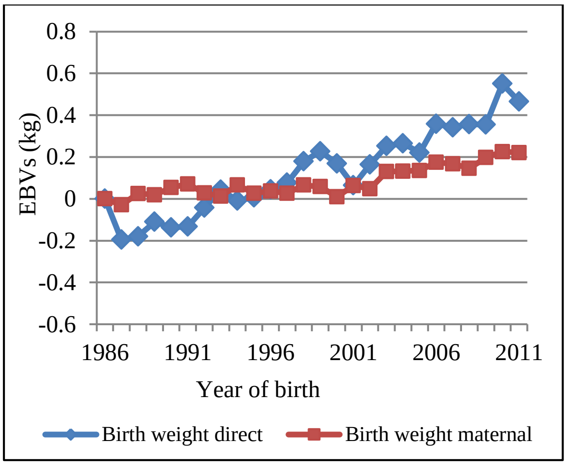

Figure 4.3.5: Trends of birth weight direct and birth weight maternal EBVs for the Tuli breed

For the Afrikaner there was a slight increase in average EBVs for birth weight and maternal direct (Figure 4.3.1), while in the Boran direct on year of birth has slightly increased, while birth weight maternal has remained almost constant especially from 2000 onward (Figure 4.3.2). The trend for birth weight direct resulted in small increase in the Drakensberger and Tuli (Figure 4.3.3). For the Nguni breed; trends of average EBVs of both birth weights direct and maternal have remained nearly constant (Figure 4.3.4). Consistent increase in birth direct is risky, because high trends for birth weight could lead to dystocia (Hickson *et al.*, 2006).

Figures 4.3.6 to 4.3.10 present the genetic trends of weaning weight direct and maternal for Afrikaner, Boran, Drakensberger, Nguni and Tuli breeds over 25 years respectively

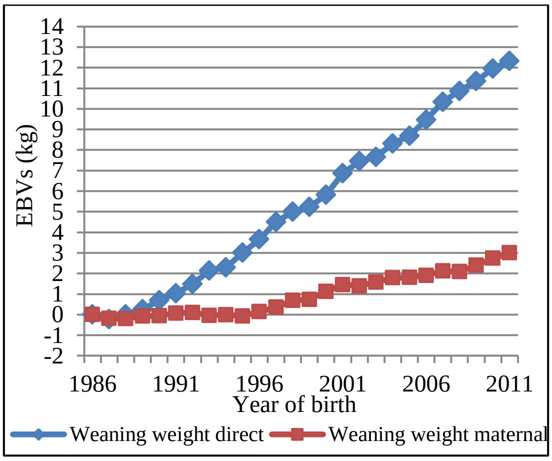

Figure 4.3.6: Trends of weaning weight direct and weaning weight maternal EBVs for the Afrikaner breed

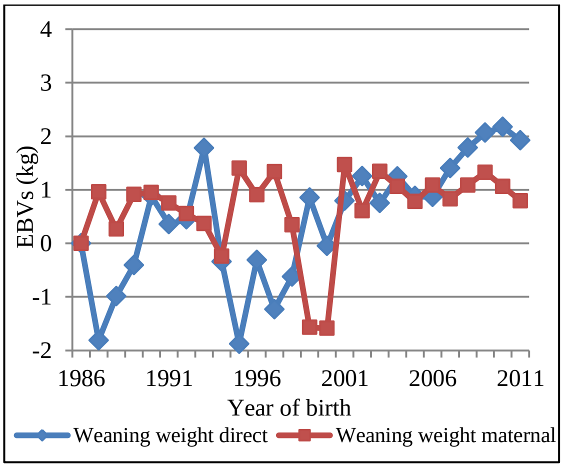

Figure 4.3.7: Trends of weaning weight direct and weaning weight maternal EBVs for the Boran breed

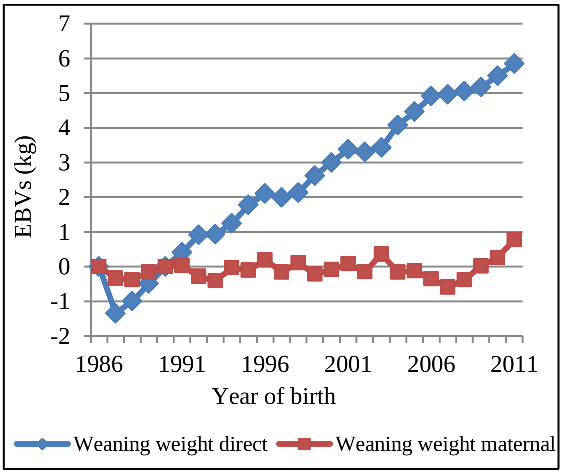

Figure 4.3.8: Trends of weaning weight direct and weaning weight maternal EBVs for the Drakensberger breed

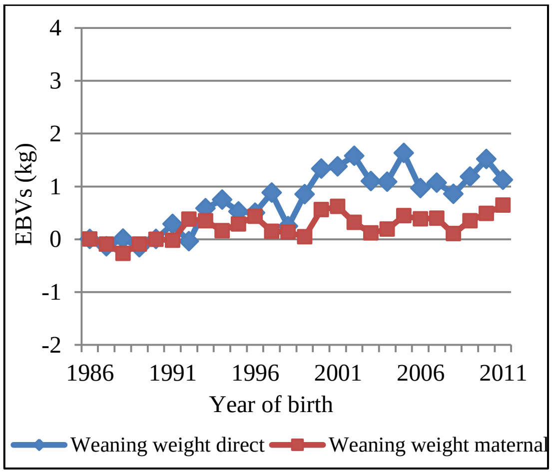

Figure 4.3.9: Trends of weaning weight direct and weaning weight maternal EBVs for the Nguni breed

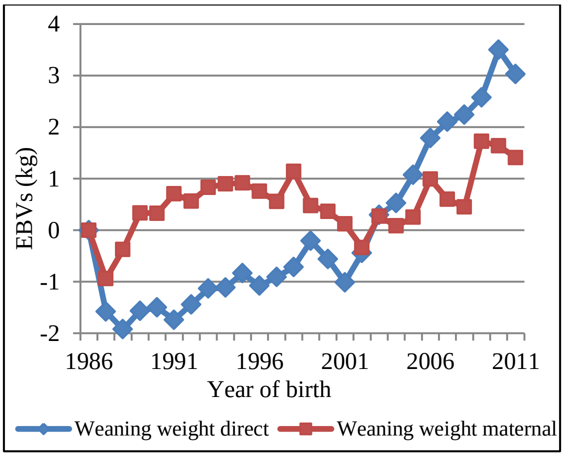

Figure 4.3.10: Trends of weaning weight direct and weaning weight maternal EBVs for the Tuli breed

The trends of average EBVs for weaning weight direct and maternal have variably increased in all the five breeds with minimum increased observed in weaning weight maternal (Figure 4.3.6 to Figure 4.3.10). However, the increase in weaning weight direct and maternal for the Nguni breed is only minor (Figure 4.3.9).

Figures 4.3.11 to 4.3.15 present the genetic trends of yearling, final and mature weights plus kleiber ratio (exept Boran) for Afrikaner, Boran, Drakensberger, Nguni and Tuli breeds over 25 years respectively.

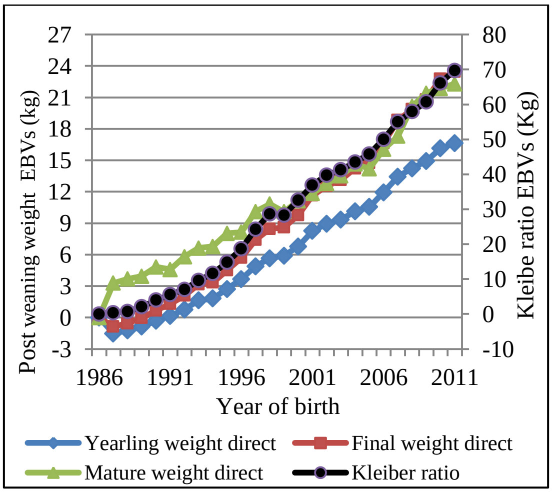

Figure 4.3.11: Trends of post weaning weights and kleiber ratio EBVs for the Afrikaner breed

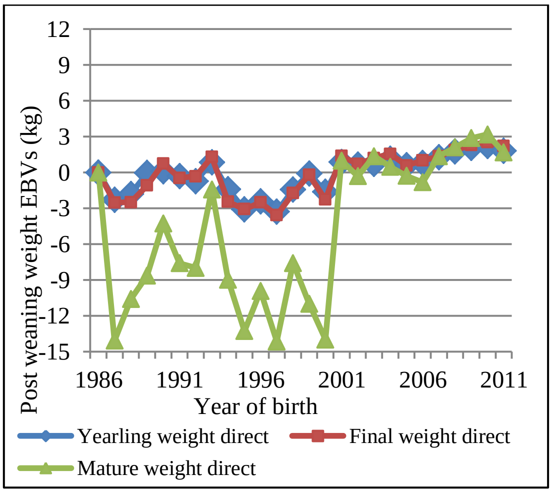

Figure 4.3.12: Trends of post weaning weights EBVs for the Boran breed

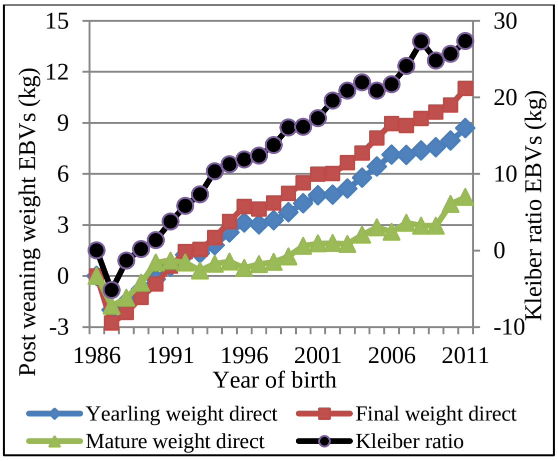

Figure 4.3.13: Trends of post weaning weights and kleiber ratio EBVs for the Drakensberger breed

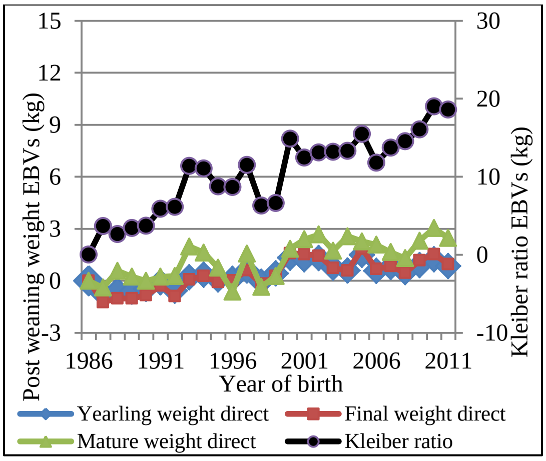

Figure 4.3.14: Trends of post weaning weights and kleiber ratio EBVs for the Nguni breed

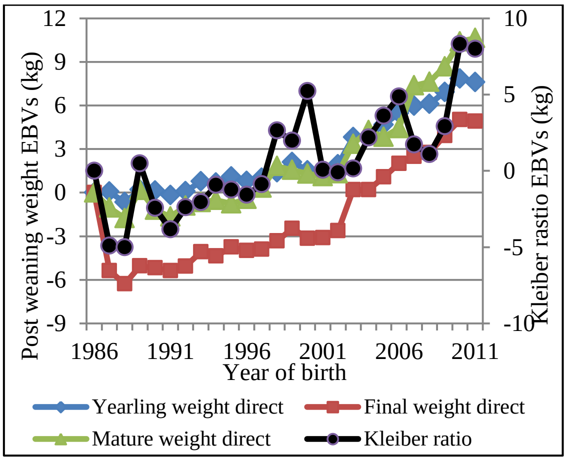

Figure 4. 4.3.15: Trends of post weaning weights and kleiber ratio EBVs for the Tuli breed

The trends of the average EBVs for all the post weaning weights have variably increased in all five breeds with very little increase observed in Nguni breed (4.3.11 to 4.3.15). The results of trends and their rate of change for growth traits have proved that progress has been made in weaning and post weaning weights in the breeds studied though with limited progress in the Nguni breed.

The trends of the average of EBV for kleiber ratio in Afrikaner, Drakensberger, Nguni and Tuli breeds have variably and considerably increased. This positive trend of kleiber ratio reflects improvements were made for feed efficiency and average daily gain in all the four breeds. As kleiber ratio is the ratio of average daily gain to metabolic weight (Kleiber, 1947; Scholtz *et al.*, 1990; Köster *et al.*, 1994). Moreover, there is positive and strong correlation between kleiber ratio and feed conversion ratio in beef cattle (Arthur *et al*. 2001).

Figures 4.3.16 to 4.3.19 present the genetic trend of scrotal circumference for Afrikaner, Drakensberger, Nguni and Tuli breed over 25 years respectively.

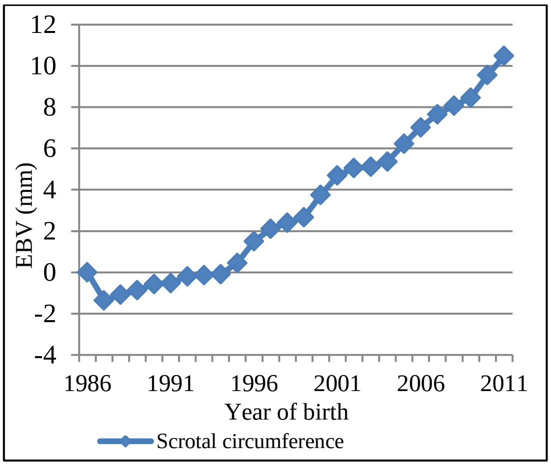

Figure 4.3.16: Trend of scrotal circumference EBV for the Afrikaner breed

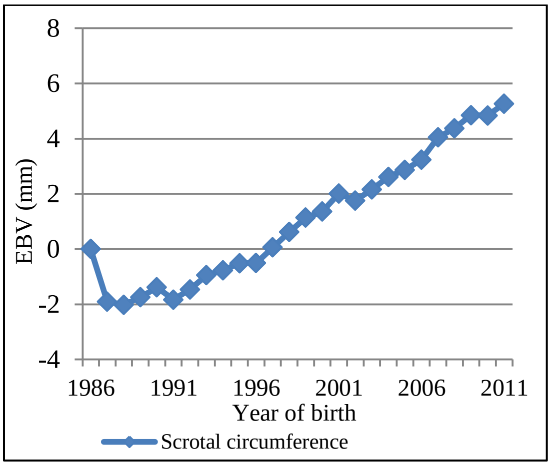

Figure 4.3.17: Trend of scrotal circumference EBV for the Drakensberger breed

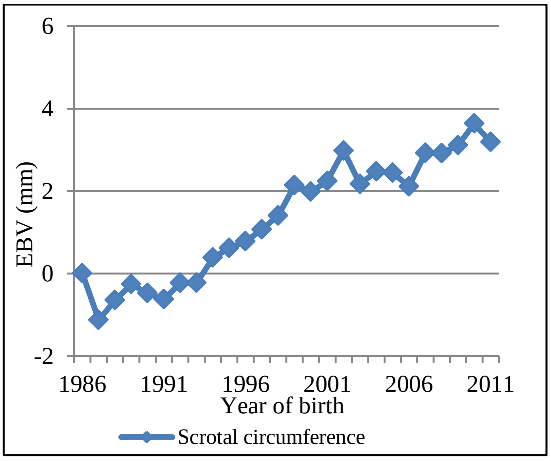

Figure 4.3.18: Trend of scrotal circumference EBV for the Nguni breed

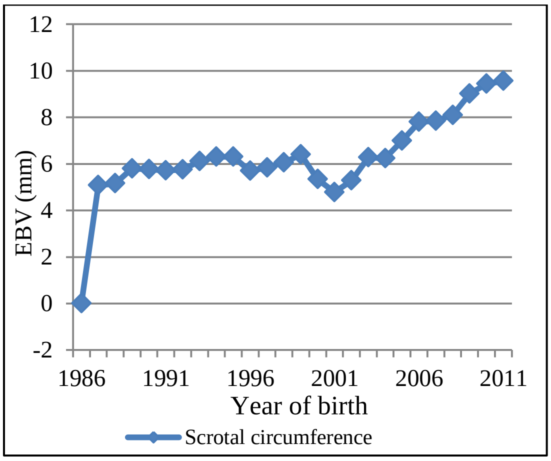

Figure 4.3.19: Trend of scrotal circumference EBV for the Tuli breed

Good progress has been made in scrotal circumference for all five breeds. The increased in the trend of scrotal circumference indicate a positive direction towards improvement in fertility traits. This is because scrotal circumference was found to have close relationships with spermatozoa quality and quantity in bull and age at puberty in bull's heifer (Brinks, 1994; Kealey *et al.*, 2006; Van Melis *et al.*, 2010).

Improvement in beef cattle production efficiency is not necessarily related to increase genetic trends for all the recorded traits. Some of these traits have been reported to have unfavourable genetic associations between them. For example, selection for rapid rate of gain in post-weaning weights usually increases both birth weight and mature size. Increases in birth weight (direct & maternal) are associated with dystocia (Bennett and Gregory, 2001; Hickson *et al.*, 2006), influences calf survival, increase culling and decrease fertility rates (Meijering, 1984; Rogers *et al.,* 2004). It will also increase the need for veterinary assistance as well as cost of medication. The increase in birth weight was the result of the correlated response of selecting for mature weight in bulls and maternal ability in cows (Plasse *et al.*, 2004). The selection for increased mature weight will be accompanied by an increase in the nutrient requirements for maintenance of the cow herd (Hersom, 2009; Luna-Nevarez *et al.*, 2010). Selection criteria to obtain moderate birth weights and mature weights while maintaining rapid growth rate is complex and needs a comprehensive selection decision. However, the Afrikaner and Drakensberger and lately Tuli breed have successfully selected for increased growth.

It was reported that methane emissions are closely linked with feed conversion efficiency per unit product and selection to improve this trait in ruminant livestock will contribute in the reduction of methane emissions per unit product (Cowie and Fairweather, 2008; Scholtz *et al.*, 2012; Hayes, *et al*, 2013). The increased genetic ability for Kleiber ratio observed in the Afrikaner, Drakensberger, Nguni and Tuli breeds indicates efficient conversion of feed in to muscle and by extension to indirect reduction of methane emissions.

Comparable to the present study; Plasse *et al.,* (2004), has reported the estimates of the annual genetic changes in breeding values for birth weight direct and maternal of 0.080kg and -0.002kg respectively with the corresponding weaning weight direct, weaning weight maternal and yearling weight of about 0.0515kg, 0.418kg and 0.894kg, respectively. Enns and Nicoll, (2008) have reported the estimates of annual genetic change in breeding values for weaning weight direct and maternal of about

0.43 and 0.03kg, respectively with corresponding annual genetic changes for yearling weight, 18 months (Harvest) weight, and mature of 0.72, 1.7 and 0.13kg, respectively. Pereira *et al.*, (2008) have reported the estimates of the annual genetic trend of breeding values of about 0.98kg for yearling weight and 0.27kg for 18 months weight respectively.

The genetic trend and its rate of change observed in the recorded traits for the five breeds under the present study have shown that improvement have been made though with some unfavourable changes. It was observed that enhanced genetic improvement in a breeding program will not only be achieved by consistent implementation of accurate measurement of traits in the breeding objective but also through efficient utilization of the information derived from them. With the exception of Nguni breed, the rest of the breeding programs are in continuous efforts to improve growth rate by targeting different stage of growth weights (weaning, yearling and mature weights) as presented by the change in their genetic trends. The Nguni breeders do not emphasize selection aimed at improving growth traits as demonstrated by changes in its genetic trends. Selection of individual animals based on the EBVs derived from accurate performance data will aid towards optimum genetic progress in a desirable direction.
The variation in the rate of genetic change in the studied breeds is probably due to the differences among the breeds in commencement of recording of trait (s) and application of modern performance evaluation (BLUP). Moreover the delayed in the rate of genetic improvement in some of these breeds might be attributed to selection emphasis on non-measured traits.

The above results and deliberations have proven the importance of animal recording system for genetic management of beef cattle breeds. It offers the opportunity for monitoring livestock genetic diversity and ensures sustainable improvement program. For this purpose, animal recording system could be recommended for management of beef cattle breeds in Africa.

Chapter 5
Conclusions and recommendations

The aim of this study was to investigate different African indigenous beef cattle breeds of larger and smaller population numbers that have been subjected to animal recording and assess the potential of animal recording in genetic management with the objectives of: monitoring within breed genetic diversity, exploring the genetic trends in the selected breeds using EBVs. The results obtained have given insight about the genetic structure of all five breeds and the trends of their genetic improvement.

The Afrikaner breed: Although the genetic diversity of this breed is not at risk, continued implementation of the current mating policies that promote the use of individuals with low additive genetic relationship is recommended. It is also advised that the increase in the trend for birth weight EBVs should be averted by selection of bulls with lower birth weight. This will help prevent the negative consequence of high birth weight during delivery.

The Boran breed: Although the Boran breed has shown an improvement in both pedigree and performance records in the last ten years of this study, animal recording should be improved in order to achieve better genealogy knowledge and increased production efficiency in the future. Improved pedigree recording will eventually lead to true estimates of inbreeding and effective population size.
The Drakensbereger breed: The current mating systems should be modified to reduce the rate in inbreeding and maintain genetic diversity, while obtaining the genetic gains which are well compatible with the current breeding objective.

The Nguni breed: The current mating strategies used in this breed could be continued as it appeared to control the rate of inbreeding and reduce the loss of genetic diversity. However, intensification of an awareness campaign to sensitise Nguni breeders to developed clear breeding objectives and improve recording is important.
The Tuli breed: Due to the high rate of inbreeding and small effective population size, the use of breeding animals with low additive genetic relationships in reproduction is strongly recommended to increase effective population size and maintain the genetic

diversity of this breed. Future studies to quantify the effect of the increased in the rate of inbreeding on economically important traits in this breed would be pertinent at this early stage. Moreover, birth weight EBVs in Tuli breed is increasing and this could lead to dystocia in the future. As such it could be advised that, the breeders should concentrate on moderate birth weight EBVs and above average EBVs for later growth in their selection decision to avoid any negative effect from heavy birth weight in the future.

The known genealogical information in the pedigree of all five inclined to be shallow in deeper generations. It is therefore, advised that the breeders should continue recording accurate pedigree records and encourages increase participation in performance recording. Improved pedigree records with deeper ancestral knowledge will enable continued monitoring of the rate of inbreeding, effective population size and genetic diversity in the future offspring. Increased participation in performance recording will enhance the accuracy of EBVs and selection decision and thereby increase genetic progress. From the results of the current study, animal recording has proved effective in maintenance of genetic diversity and sustainable genetic improvement of indigenous beef cattle breeds in Africa.

References

Adamec, V., Cassell, B.G., Smith, E.P., and Pearson, R.E. 2006. Effects of inbreeding in the dam on dystocia and stillbirths in US Holsteins. J. Dairy sci. 89: 307-314.

Alderson, L. 2010. Breeds at risk: criteria and classification. Report from a seminar Held in London. http://lawrencealderson.com/index.htm.

Anderson, P., and Lewis, M. 1990. The role of Angus Cattle in Commercial Beef Production. Beef Cattle Management Update, University of Minnesota Extension Service. Prepared for Wisconsin Angus Field Day, Sept. 22, 1990.

Arthur, P.F, Renand, G., and Krauss, D. 2001. Genetic and phenotypic relationships among different measures of growth and feed efficiency in young Charolais bulls. Livest. Prod. Sci 68: 131-139.

Assan, N., and Nyoni, K. 2009. Systematic environmental influences and variances due to direct and maternal effects and trends for yearling weight in cattle. Anim. Res Int. 20096: 1086-1092.

Aynalem, H., 2006. Genetic and economic analysis of Ethiopian Boran cattle and their crosses with Holstein Friesian in Central Ethiopia. PhD. Thesis Division of Dairy Cattle Breeding National Dairy Research Institute. Kamel-132001, Haryana, India.

Banga, C.B., Besbes, B., Balvay, B., Chazo, L., Jamaa, O.M., Rozstalynyy, A., Rovere, G., Toto, A., and Trivedi, K.R. 2010. Current situation of animal identification and recording systems in developing countries and countries with economies in transition. In: E. Skujina, E.G., O. Leray and C. Mosconi (eds.), ICAR Techn. Series No. 14. Farm animal breeding, identification, production recording and management, ICAR, Rome, Italy.

Banga, C.B. 2002. Performance testing for the smallholder sector in South Africa. Animal Genetic Training resource, Version, 2, 2006.

Barker, J.S.F. 2009. Defining fitness in natural and domesticated populations. In: Van der Werf, J., Graser, H.U. and Frankham, R. (eds.), Adaptation and fitness in animal populations: Evolutionary and breeding perspectives on genetic resource management. Springer, New York.

Barwick, S.A., Tier, B., Swan, A.A., and Henzell, A.L. 2013. Estimation of accuracies and expected genetic change from selection for selection indexes that use multiple-trait predictions of breeding values. J. Anim. Breed. Genet. 130: 341-348.

BCBS (Boran Cattle Breeders Society). 2007-2013. www.boran.org.za.

Beffa, L.M., van Wyk, J.B., and Erasmus, G.J. 2009. Genetic parameters and genotype x environment interaction for calf growth traits: long-term selection experiment with Afrikaner cattle. S. Afr. J. Anim. SCI. 39: 88-105.

Beffa, L.M. 2005. Genotype x environment interaction in Afrikaner cattle (Doctoral dissertation, University of the Free State).

Bennett, G.L., and Gregory, K.E. 2001. Genetic (co)variances for calving difficulty score in composite and parental populations of beef cattle: I. Calving difficulty score, birth weight, weaning weight, and postweaning gain. J. Anim. Sci. 79: 45-51.

Bergh, L. 2008a. Management and recording guidelines for accurate and reliable breeding values. Appl. Anim. Husb. Rural Dev. 1: 10-15.

Bergh, L. 2008b. Breeding objective: How to understand and use it. Retrievd from; http://www.beefpro.net.

Besbes, B., and Hoffmann, I. 2011. Animal identification for traceability and performance recording: FAO's multipurpose and integrated approach. FAO-ICAR-FEPALE Workshop on animal identification and recording systems for traceability and livestock development in LAC region, December 2011, Santiago, Chile.

Biedermann, G., Hecht, W., Fandrey, E., Rudolph, H., and Froelich, K. 2009. Population genetic analysis of White Park Cattle in Germany. Arch Tierz. 52: 561-573.

BIF (Beef Improvement Federation). 2010. Guidelines for uniform beef improvement programs. 9th edition. Beef Improvement Federation, North Carolina State University, Raleigh, NC, United States.

Bijma, P. 2000. Long-term genetic contributions. Prediction of rates of inbreeding and genetic gain in selected populations. Ph.D. Thesis, Wageningen University, The Netherlands.

Bijma, P., and Woolliams, J.A. 2000. Prediction of rates of inbreeding in populations selected on best linear unbiased prediction of breeding value. Genet. 156: 361-373.

Bill, H., 2007. Beef cattle breeding systems. PRIMEFACT 624.

Bisschoff, C., and Lotriet, R. 2013. The Drakensberger as competitive breed of cattle in the South African beef industry. 19th International Farm Management Congress. SGGW, Warsaw, Poland.

Blench, R.M. 1993. Ethnographic and linguistic evidence for the prehistory of African ruminant livestock, horses and ponies. In: Shaw, T., Sinclair, P., Andah, B. and Okpoko (eds); the Archaeology of Africa. Food, Metals and Towns. 71-103 London: Routledge.

Bodo, I. 1989. Methods and experiences with in situ preservation of farm animals. FAO Anim Prod Hlth Pp. 80: 85-103.

Boichard, D. 2002. PEDIG: a fortran package for pedigree analysis suited for large populations. In Proceedings of the 7th world congress on genetics applied to livestock production, Montpellier.

Boichard, D., Maignel, L., and Verrier, E. 1997. The value of using probabilities of gene origin to measure genetic variability in a population. Genet. Sel. Evol. 29: 5-23.

Bondoc, O.L., and Smith, C. 1993. Deterministic genetic analysis of open nucleus breeding schemes for dairy cattle in developing countries. J. Anim. Breed. and Genet. 110: 194-208.

Bosso, N.A., Van der Waaij, E.H., Agyemang, K., and Van Arendok, J.A.M. 2009. Genetic parameters for growth traits in N'Dama cattle under tsetse challenge in Gambia. Liv. Res. Rural Dev. 21(3), www.lrrd.org/lrrd21/3/boss21033.htm.

Bourdon, R.M. 2000. Understanding Animal Breeding. 2nd edition. Prentice Hall, New Jersey.

Bowman, B, Golden, B., Gould, L., Hough, R, Ponder, K., and Williams, R.E. 2010. Breeding Herd Evaluation. In Cundiff L.V., Van Vleck, L.D. and Hohenboken, W.D. (eds). Guidelines for uniform beef improvement programs, 9th edition. Raleigh, North Carolina, USA.

Bozzi, R., Franci, O., Forabosco, F., Pugliese, C., Crovetti, A., and Filippini, F. 2006. Genetic variability in three Italian beef cattle breeds derived from pedigree information. Ital. J. Anim. Sci. 5: 129-137.

Bredahl, M.E., Northen, J.R., Boecker, A., and Normile, M.A. 2001. Consumer demand sparks the growth of quality assurance schemes in the European food sector. Changing Structure of the Global Food Consumption and Trade.

Market and Trade Economics Division, Economic Research Service, US Department of Agriculture, Agriculture and Trade Report. WRS-01-1: 90-102.

Brinks, J.S. 1994. Relationships of Scrotal Circumference to Puberty and Subsequent Reproductive Performance in Male and Female Offspring. In Fields, M.J. and Sand, R.S., (eds.). Factors Affecting Calf Crop. CRC Press.

Budeli, M.A. 2010. Genetics evaluation of tick resistance in South African Bonsmara cattle (Doctoral dissertation, University of Limpopo (Turfloop Campus)).

Bullock, K.D., Pollak, E.J., Bertrand, J.K., Garrick, D., Enns, M., Weaber, B., and Wilson, D.E. 2003. International Beef Cattle Evaluation in the United States and the Role of the National Beef Cattle Evaluation Consortium. Proceedings of the 2003. Interbull Meeting. Rome, Italy.

Burrow, H.M. 2012. Importance of adaptation and genotype × environment interactions in tropical beef breeding systems. Anim. 6: 729-740.

Burrow, H.M. 1998. The effects of inbreeding on productive and adaptive traits and temperament of tropical beef cattle. Livest. Prod. Sci. 55: 227-243.

Burrow, H.M., 1993. The effects of inbreeding in beef cattle. Anim. Breed. Abstr. 61: 737-751.

Caballero, A., and Toro, M.A. 2000. Interrelations between effective population size and other pedigree tools for the management of conserved populations. Genet. Res. 75: 331-343.

Caja, G., Ghirardi, J., Hernández-Jover, M., and Garí, D. 2004. Diversity of animal identification techniques: from fire-age to electronic-age. In: Pauw, R., Mack, S. and Maki-Hokkonen, J. (eds). Development of Animal Identification and Recording Systems for Developing Countries. ICAR Tech. Series No. 9. Rome, Italy.

Campêlo, J.E.G., Lopes, P.S., Torres, R.D.A., Silva, L.O.C.D., Euclydes, R.F., Araújo, C.V.D., and Pereira, C.S. 2004. Maternal effects on the genetic evaluation of Tabapuã beef cattle. Gen Mol Bio. 27: 517-521.

Cañon, J., Gutie´rrez, J.P., Dunner, S., Goyache, F., and Vallejo, M. 1994. Herdbook analyses of the Asturiana beef cattle breeds. Genet. Sel. Evol. 26: 65-75.

Cardellino, R.A., and Boyazoglu, J. 2009. Research opportunities in the field of animal genetic resources. Livest. Sci. 120: 166-173.

Carolino, N., and Gama, L.T., 2008. Inbreeding depression on beef cattle traits: estimates, linearity of effects and heterogeneity among sire-families. Genet. Sel. Evol. 40: 511-527.

Carpenter, B.B., Forrest, D.W., Sprott, L.R., Rocha, A., Hawkins, D.E., Beverly, J.R., Hawkins, H.E., and Parish, N.R. 1992. Performance of Bos indicus-influenced bulls in serving capacity tests and multiple-sire breeding groups. J. Anim. Sci. 70: 1795-1800.

Carstens, G.E., and Tedeschi, L.O. 2006. Defining feed efficiency in beef cattle. In Proceeding. BIF 38th Annual Resources. Symposium Annual Meeting, Choctaw, MS, USA.

Chambaz, A., Scheeder, M.R.L., Kreuzer, M., and Dufey, P.A. 2003. Meat quality of Angus, Simmental, Charolais and Limousin steers compared at the same intramuscular fat content. Meat Sci. 63: 491-500.

Chase, C.C., Bastidas, P., Ruttle, J.L., Long, C.R., and Randel, R.D. 1994. Growth and reproductive development in Brahman bulls fed diets containing gossypol. J.Anim. Sci. 72: 445-452.

Cleveland, M.A., Blackburn, H.D., Enns, R.M., and Garrick, D.J. 2005. Changes in inbreeding of U.S. Herefords during the twentieth century. J. Anim. Sci. 83: 992-1001.

Comstock, C., Golden, B., and Bourdon, R. 1998. Exploring the RAAA's pedigree. Who are the most influential sires in the Red Angus breed. Amer. Red Angus Magaz. 34: 34-39.

Corbet, N.J., Shepherd, R.K., Burrow, H.M., Prayaga, K.C., Van der Westhuizen, J., and Bosman, D.J. 2006. Evaluation of Bonsmara and Belmont Red cattle breeds in South Africa. 2. Genetic parameters for growth and fertility. Anim. Prod. Sci. 46: 213-223.

Cowie, A., and Fairweather, H. 2008. Climate change research priorities for NSW Primary Industries. In: Hatcher, S., and Richards, J.S., (eds). Coping with a changing environment: environmental, technological, social and economic. NSW DPI Sheep and Beef Conference, Orange Agricultural Institute, Orange, Australia.

Crews, D.M., Dikeman, S.L., Dolezal, T.W., Marston, L.W., Olson, J.C., Paschal, Weaber, B., Williams, R.E., and Wilson, D.E. 2010. Animal evaluation. In

Cundiff L.V., Van Vleck, L.D., and Hohenboken W.D., (eds). Guidelines for uniform beef improvement programs, 9th edition. Raleigh, North Carolina, USA.

Cunningham, E.P. 1980. Methods for recording, evaluation and selection in adverse environments. FAO/UNEP Technical Consultation on Animal Genetic Resources, Conservation and Management. FAO (Food and Agriculture Organization of the United Nations), Rome, Italy.

DAGRIS, (Domestic Animal Genetic Resources Information System). 2007. In: Rege J.E.O., Hanotte, O., Mamo, Y. Asrat, B., and Dessie, T. (eds.). ILRI, Addis Ababa, Ethiopia.

Davis, G.P. 1993. Genetic parameters for tropical beef cattle in Northern Australia: a review. Crop and Past. Sci. 44: 179-198.

Day, M.L., and Nogueira, G.P. 2013. Management of age at puberty in beef heifers to optimize efficiency of beef production. Anim. Front. 3: 6-11.

de Araujo, J.W., Borgwardt, R.E., Sween, M.L., Yelich, J.V., and Price, E.O. 2003. Incidence of repeat-breeding among Angus bulls (Bos taurus) differing in sexual performance. Appl. Anim. Behav. Sci. 81: 89-98.

Delgado, C.L. 2003. Rising consumption of meat and milk in developing countries has created a new food revolution. J. of Nutr. 133: 3907S-3910S.

Demeke, S., Neser, F.W.C., and Schoeman, S.J. 2004. Estimates of genetic parameters for Boran, Friesian, and ncrosses of Friesian and Jersey with Boran cattle in the tropical highlands of Ethiopia: milk production traits and cow weight, J. Anim. Breed. Gen. 121: 163-175.

Dempfle, L., and Jaitner, J. 2000. Case Study about the N'Dama breeding programme at the International Trypanotolerance Centre (ITC) in The Gambia. In Galal, S., Boyazoglu, J., and Hammond, K. (eds.); Proceedings of the Workshop on Developing Breeding Strategies for Lower Input Animal Production Environments. ICAR Techn. Series, No. 3. Bella, Italy.

Djemali, M. 2004. Animal recording for low to medium input production systems. In Guellouz, M. Dimitriadou, A., and Mosconi, C. (eds), 2004. Performance recording of animals: State of the art, 2004. EAAP Publication No. 113. Wageningen, the Netherlands, Wageningen Academic Publishers.

Dodds, K.G., Tate, M.L., and Sise, J.A. 2005. Genetic evaluation using parentage information from genetic markers. J. Anim. Sci. 83: 2271-2279.

Drakensberger Handbook, 2011. www.drakensbergers.co.za.

Du Plessis, I., Hoffman, L.C., and Calitz, F.J. 2006. Influence of reproduction traits and pre-weaning growth rate on herd efficiency of different beef breed types in an arid sub-tropical environment. S. Afr. J. Anim. Sci. 36: 89-98.

Eler, J.P., Ferraz, J B.S., Balieiro, J.C.C., and Mattos, E.C. 2008. Genetic analysis of average annual productivity of Nellore breeding cows (COWPROD). Genet. Mol. Res. 7: 234-242.

Eler, J.P., Silva, J.A.I.I.V., Ferraz, J.B.S., Dias, F., Oliveira, H.N., Evans, J.L., and Golden, B.L. 2002. Genetic evaluation of the probability of pregnancy at 14 months for Nellore heifers. J. Anim. Sci. 80: 951-954.

Engen, S., Lande, R., and Saether, B.E. 2005. Effective size of a fluctuating age structured population. Genet. 170: 941-954.

Enns, R.M., and Nicoll, G.B. 2008. Genetic change results from selection on an economic breeding objective in beef cattle. J. Anim. Sci. 86: 3348-3357.

FABRE (Farm Animal Breeding and Reproduction) Technology Platform. 2006. Sustainable Farm Animal Breeding and Reproduction-A Vision for 2025.

Falcão, A.J.S., Filho, R.M., Magnabosco, C.U., Bozzi, R., and Lima, F.A.M., 2001. Effects of inbreeding on reproductive and growth traits, and breeding values in a closed Brown Swiss herd. Braz. J. Anim. Sci. 30: 83-92.

Falconer, D.S., and Mackay, T.F.C. 1996. Introduction to Quantitative Genetics. 4th edition Longman, Essex, England.

FAO (Food and Agricultural Organization). 2011. Status and Trends Report on Animal Genetic Resources-10. Commission on Genetic Resources for Food and Agriculture. 13th Regular Session. Rome, Italy.

FAO (Food and Agricultural Organization). 2010. Breeding Strategies for Sustainable Management of Animal Genetic Resources. Animal Production and Heallth Guidelines No. 3. Rome, Italy.

FAO (Food and Agricultural Organization). 2007a. Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration. Commission on Genetic Resources for Food and Agriculture. Rome, Italy.

FAO (Food and Agricultural Organization). 2007b. The state of the world's animal genetic resources for food and agriculture. In: Rischkowsky, B., and Pilling, D. (eds). Rome, Italy.

FAO (Food and Agriculture Organization of the United Nations). 1999. The global strategy for the management of farm animal genetic resources: Executive Brief. FAO–iDAD, Rome, Italy.

FAO (Food and Agricultural Organization). 1998a. Secondary guidelines for development of national farm animal genetic resources management plans; Animal Recording for Medium Input Production Environment. Rome, Italy.

FAO (Food and Agricultural Organization). 1998b. Secondary Guidelines for Development of National Farm Animal Genetic Resources Management Plans. Management of Small Populations at Risk. Initiative for Domestic Animal Diversity (IDAD). Geneva.

Flamant, J.C. 1998. The impact of socio-economic aspects on the development and outcome of animal recording systems. In Trivedi K.R. 1998, (ed). Workshop on animal recording for smallholders in developing countries. ICAR Techn. Series No.1. Anand, India.

Foote, R.H. 2003. Fertility estimation: A review of past experience and future prospects. Anim. Reprod. Sci. 75: 119.

Fuerst-Waltl, B., and Fuerst, C. 2010. Mortality in Austrian dual purpose Fleckvieh calves and heifers. Livest Sci. 132: 80-86.

Gandini, G.C., Ollivier, L., Danell, B., Distl, O., Georgoudis, A., Groeneveld, E., Martyniuk, E., Van Arendonk, J.A.M., and Woolliams, J.A. 2004. Criteria to assess the degree of endangerment of livestock breeds in Europe. Livest. Prod. Sci. 91: 173-82.

Garrick, D.J., and Saatchi, M. 2011. Opportunities and challenges for genomic selection of beef cattle. R. Bras. Zootec. 40: 310-316. (supl. Especial).

Garrick, D.J., and Golden, B.L. 2009. Producing and using genetic evaluations in the United States beef industry of today. J Anim Sci. 87: E11-18.

Geerlings, E., Mathias, E., and Köhler-Rollefson, I., 2002. Securing tomorrow's food-promoting the sustainable use of farm animal genetic resources. League for Pastoral People, Ober-Ramstadt, Germany.

Gibson, J., Gamage, S., Hanotte, O., Iniguez, L., Maillard, J.C., Risch-Kowsky, B., Semambo, D., and Toll, J. 2006. Option and Strategies for the Conservation of Farm Animal Genetic Resources: Report of an International Workshop (7-10 November 2005, France). CGIAR System-wide Genetic Resources Programme (SGRO)/Biodiversity International, Rome, Italy.

Goddard, M.E. 1998. Consensus and debate in the definition of breeding objectives. J. Dairy Sci. 81: 6-18.

Godfrey, R.W., and Lunstra, D.D. 1989. Influence of single or multiple sires and serving capacity on mating behavior of beef bulls. J. Anim. Sci. 67: 2897-2903.

Goyache, F., Gutierrez, J.P., Alvarez, I., Fernández, I., Royo, L.J., and Gomez, E. 2003. Genetic analysis of calf survival at different preweaning ages in beef cattle. Livest. Prod. Sci. 83: 13-20.

Groen, A.F., 2000. Breeding goal definition. In Gala S., Boyazoglu J., and Hammond K. (eds.); Proceedings of the Workshop on Developing Breeding Strategies for Lower Input Animal Production Environments. ICAR Tech. Series, No. 3. Bella, Italy.

Groeneveld, L.F., Lenstra, J.A., Eding, H., Toro, M.A., Scherf, B., Pilling, D., Negrini, R., Finlay, E.K., Jianlin, H., Groeneveld, E., and Weigend, S., The GLOBALDIV Consortium, 2010. Genetic diversity in farm animals - a review. Anim. Genet. 41: 6-31.

Groeneveld, E., Van der Westhuizen, B., Maiwashe, A., Voordewind, F., and Ferraz, J.B.S. 2009. POPREP: A generic report for population management. Genet. Mol. Res. 8: 1158-1178.

Guellouz, M., Dimitriadou, A., and Masconi, C. 2004. Technology and Engineering-2004. Performance recording of animals: state of the art, 2004 : proceedings of the 34th Biennial Session of ICAR, Sousse, Tunisia.

Gutiérrez, J.P., Altarriba, J., Díaz, C., Quintanilla, R., Cañón, J., and Piedrafita, J. 2003. Pedigree analysis of eight Spanish beef cattle breeds. Gen. Sel. Evol. 35: 43-64.

Haile, A., Ayalew, W., Kebede, N., Dessie, T., and Tegegne, A. 2011. Breeding strategy to improve Ethiopian Boran cattle for meat and milk production. IPMS (Improving Productivity and Market Success) of Ethiopian Farmers Project Working Paper 26. ILRI, Nairobi, Kenya.

Hanotte, O., Bradley, D.G., Ochieng, J.W., Verjee, Y., Hill, E.W., and Rege, J.E.O. 2002. African pastoralism: genetic imprints of origins and migrations. Sci. 296: 336-339.

Hanotte, O., Tawah, C.L., Bradley, D.G., Okomo, M., Verjee, Y., Ochieng, J., and Rege, J.E.O. 2000. Geographic distribution and frequency of a taurine Bos *taurus* and an indicine Bos *indicus* Y specific allele amongst sub-Saharan African cattle breeds. Mol. Ecol. 9: 387-396.

Harmon, L.J., and Braude, S. 2009. Conservation of Small Populations: Effective Population Sizes, Inbreeding, and the 50/500 Rule.

Hayes, B.J., Lewin, H.A., and Goddard, M.E. 2013. The future of livestock breeding: genomic selection for efficiency, reduced emissions intensity, and adaptation. Trends in Genetics, 29: 206-214.

Herath, H.M.S.P., and Mohammad, S. 2009. The current status of cattle breeding programmes in Asia. In: Boettcher, P., and Perera, B.M.A.O. (eds). Selection and breeding of cattle in Asia: strategies and criteria for improved breeding. IAEA, Vienna, Austria.

Herlocker, D., 1999. Rangeland Resources in Eastern Africa: Their Ecology and Development. GTZ, Germany Technical Co-operation, Nairobi.

Hersom, M. 2009. Relationship of Cow Size to Nutrient Requirements and Production Management Issues. http://edis.ifas.ufl.edu/an226.

Hetzel, D.J.S., and Seifert, G.W. 1986. Breeding objectives and selection traits for extensive beef cattle production in the tropics. Proc. 3rd Wrld. Cong. Genet. Appl. Livest. Prod, Lincoln, Nebraska, USA.

Hickson, R.E., Morris, S.T., Kenyon, P R., and Lopez-Villalobos, N. 2006. Dystocia in beef heifers: a review of genetic and nutritional influences. New Zealand Vet. J. 54: 256-264.

Hiemstra, S.J., de Haas, Y., Mäki-Tanila, A., and Gandini, G. 2010. Local cattle breeds in Europe. Development of policies and strategies for self-sustaining breeds. Wageningen Academic Publ., Wageningen, The Netherlands.

Hoffmann, I. 2010. Climate change and the characterization, breeding and conservation of animal genetic resources. Anim genet. 41: 32-46.

Hohenboken, W., Jenkins, T., Pollak, J., Bullock, D., and Radakovich, S. 2005. Genetic improvement of beef cattle adaptation in America. In Proceedings of the beef improvement federation's 37th Annual Research Symposium. 37: 115-120.

Holloway, L. 2005. Aesthetics, genetics, and evaluating animal bodies: locating and displacing cattle on show and in figures. Environment and Planning D: Societ and Space 23: 883-902.

Hui, Y.H. 2012. Handbook of Meat and Meat Processing. 2nd edition. CRC Press.

ICAR (International Committee for Animal Recording). 2012. International Agreement of Recording Practices. Guidelines approved by the General Assembly held in Cork, Ireland.

ICAR (International Committee for Animal Recording). 2004a. Development of animal identification and recording systems for developing countries, Proceedings of the ICAR/FAO Seminar held in Sousse, Tunisia, 29 May 2004, jointly organized with FAO, ICAR Techn. Series No. 9. ICAR, Rome, Italy.

ICAR (International Committee for Animal Recording). 2004b. Current status of genetic resources, recording and production systems in African, Asian and American Camelids. Proceedings of the ICAR/FAO Seminar held in Sousse, Tunisia, 30 May 2004, ICAR Techn. Series No. 11. ICAR, Rome, Italy.

ICAR (International Committee for Animal Recording). 2001. Beef recording guidelines: A synthesis of an ICAR survey. In: Simianer, H., Täubert, H. and Küttner, K. (eds). ICAR Techn. Series No. 6. Rome, Italy.

Intaratham, W., Koonawootrittriron S., Sopannarath P., Graser H-U., and Tumwasorn S. 2008. Genetic Parameters and Annual Trends for Birth and Weaning Weights of a Northeastern Thai Indigenous Cattle Line, Asian-Aust. J. Anim. Sci., 21: 478-483.

Intaratham, W., 2002: The Thai Indigenous Cattle Breeding Improvement Project. In: Allen, J., and Na-Chiangmai, A. (eds.). Development Strategies for Genetic Evalution for Beef Production in Developing Countries. ACIAR Proceeding, No. 108, Wastson Ferguson and Co., Brisbane, Australia.

Johnston, D.J., Corbet, N.J., Barwick, S.A., Wolcott, M.L., and Holroyd, R.G. 2013. Genetic correlations of young bull reproductive traits and heifer puberty Traits with female reproductive performance in two tropical beef genotypes in northern Australia. Anim Prod. Sci. 54: 74-84.

Johnston, D.J. 2007. Genetic trends in Australian beef cattle making real progress. In Genetic improvement: making it happen. Proceedings of the Seventeenth Conference of the Association for the Advancement of Animal Breeding and Genetics, Armidale, New South Wales, Australia.

Johnston, D.J., Graser, H.U., and Tier, B. 2007. New developments in beef cattle genetic evaluation in Austral. Interbull Bullet. 37: 8-11.

Journaux, L., Wickham, B., Venot, E., and Pabiou, T. 2006. Development of routine international genetic evaluation services for beef cattle as an extension of Interbull's services. Interbull Bulletin. 35: 146-152.

Kadlečík, O., and Pavlík, I. 2012. Genealogical analysis in small populations: the case of four Slovak beef cattle breeds. Slov. J. Anim. Sci. 45: 111-117.

Kahi, A.K., Rewe, T.O., and Kosgey, I.S. 2005. Sustainable community-based organizations for the genetic improvement of livestock in developing countries. Outlook on Agric. 34: 261-270.

Kealey, C.G., MacNeil, M.D., Tess, M.W., Geary, T.W., and Bellows, R.A. 2006. Genetic parameter estimates for scrotal circumference and semen characteristics of Line 1 Hereford bulls. J. Anim. Sci. 84: 283-290.

Keane, M.G., and O'Ferrall, G.J. 1992. Comparison of Friesian, Canadian Hereford x Friesian and Simmental x Friesian steers for growth and carcass composition. Anim. Prod. 55: 377- 387.

King, J.M., Parsons, D.J., Turnpenny, J.R., Nyangaga, J., Bakara, P., and Wathes, C.M. 2006. Modelling energy metabolism of Friesians in Kenya smallholdings shows how heat stress and energy deficit constrain milk yield and cow replacement rate. Anim. Sci. 82: 705-716.

Kios, D., Van Marle-Köster, E., and Visser, C. 2012. Application of DNA markers in parentage verification of Boran cattle in Kenya.Trop. Anim. Hlth. Prod. 44: 471-476.

Kleiber, M. 1947. Body size and metabolic rate. Physiol. Rev. 27: 511-541.

Kluyts, J.F, Neser F.W.C., and Bradfield, M.J. 2003. Development of breeding objectives for beef cattle breeding: derivation of economic values: Review: S. Afri. J. Anim. Sci. 33: 142-158.

Köhler-Rollefson, I., 2004. Farm animal genetic resources.Safeguarding national assets for food security and trade. Summary Publication about four workshops on animal genetic resources held in the SADC Region. FAO/GTZ/CTA.

Köhler-Rollefson, I. 1997. Indigenous practices of animal genetic resource management and their relevance for the conservation of domestic animal diversity in developing countries. J. Anim. Breed. Gen.114: 231-238.

Koots, K.R., Gibson, J.P., and Wilton, J.W. 1994b. Analyses of published genetic parameter estimates for beef production traits; 2. Phenotypic and genetic correlations. Anim. Breed. Abstr. 62: 825-853.

Koots, K.R., Gibson, J.P., Smith, C., and Wilton, J.W. 1994a. Analysis of published genetic parameter estimates for beef production traits: 1 Heritability. Anim. Breed. Abstr. 62: 309-338.

Kosgey, I.S., Mbuku, S.M., Okeyo, A.M., Amimo, J., Philipsson, J., and Ojango, J.M. 2011. Institutional and organizational frameworks for dairy and beef cattle recording in Kenya: a review and opportunities for improvement. FAO. Anim Genet Res. 48: 1-11.

Kosgey, I.S., and Okeyo, A.M. 2007. Genetic improvement of small ruminants in low-input, smallholder production systems: technical and infrastructural issues. Small Rumin. Res. 70: 76-88.

Köster, E., Van der Westhuizen, J., and Erasmus, G.J. 1994. Heritability estimates for different Kleiber ratios obtained from growth performance data in a Hereford herd. S. Afr. J. Anim. Sci. 24: 71-72.

Kugonza, D.R., Nabasirye, M., Hanotte, O., Mpairwe, D., and Okeyo, A.M. 2012. Pastoralists' indigenous selection criteria and other breeding practices of the long-horned Ankole cattle in Uganda. Trop. Anim. Hlth. prod. 44: 557-565.

Leroy, G., Mary-Huard, T., Verrier, E., Danvy, S., Charvolin, E., and Danchin-Burge, C. 2013. Methods to estimate effective population size using pedigree data: Examples in dog, sheep, cattle and horse. Gen. Sel. Evol. 45: 1-10.

Luna-Nevarez, P., Bailey, D.W., Bailey, C.C., VanLeeuwen, D.M., Enns, R.M., Silver, G.A., DeAtley, K.L., and Thomas, M.G. 2010. Growth characteristics, reproductive performance, and evaluation of their associative relationships in Brangus cattle managed in a Chihuahuan Desert production system1. J. Anim. Sci. 88: 1891-1904.

MacCluer, J.W., Boyce, A.J., Dyke, B., Weitkamp, L.R., Pfenning, D.W., and Parsons, C.J. 1983. Inbreeding and pedigree structure in Standardbred horses. J. Hered. 74: 394-399.

MacHugh, D.E., Shriver, M.D., Loftus, R.T., Cunningham, P., and Bradley, D.G. 1997. Microsatellite DNA variation and the evolution, domestication and phylogeography of taurine and Zebu cattle (Bos *taurus* and Bos *indicus*). Genet. 146: 1071-1086.

MacNeil, M.D., and Northcutt, S.L. 2008. National cattle evaluation system for combined analysis of carcass characteristics and indicator traits recorded using ultrasound in Angus cattle. J. Anim. Sci. 86: 2518-2524.

Maiwashe, A., Nephawe, K.A., and Theron, H.E. 2008. Estimates of genetic parameters and effect of inbreeding on milk yield and composition in South African Jersey cows. S. Afr. J. Anim. Sci. 38: 119-125.

Maiwashe, A.N., Bradfield, M.J., Theron, H.E., and Van Wyk, J.B. 2002. Genetic parameter estimates for body measurements and growth traits in South African Bonsmara cattle. Livest. Prod. Sci. 75: 293-300.

Malhado, C.H.M., Carneiro, P.L.S., Malhado, A.C.M., Martins, J.A.M., Martins Filho, R., and Bozzi, R. 2010. History of registered Gyr breed in Brazilian Northeast: population structure and genetic improvement of growth traits. Ciencia Rural. 40: 1385‑1391.

Malhado, C.H.M., Carneiro, P.L.S., Pereira, D.G., and Martins Filho, R. 2008. Genetic progress and population structure in Nellore cattle in Bahia State, Brazil. Bra. Agric. Res. 43: 1163-1169.

Márquez, G.C., Speidel, S.E., Enns, R.M., and Garrick, D.J. 2010. Genetic diversity and population structure of American Red Angus cattle. J. Anim. Sci. 88: 59-68.

Márquez, G.C., and Garrick, D.J. 2007. Selection intensities, generation intervals and population structure of Red Angus cattle. In: Proceedings of the Western Section American Society of Anim. Sci. 58: 55-58.

Marshall, D.M. 1994. Breed differences and genetic parameters for body composition traits in beef cattle. J. Anim. Sci. 72: 2745-2755.

Martínez, R.A., García, D., Gallego, J.L., Onofre, G., Pérez, J., and Cañón, J. 2008. Genetic variability in Colombian Creole cattle populations estimated by pedigree information. J. Anim. Sci. 86: 545‑552.

Martojo, H. 2003. Indigenous Bali cattle, the best suited cattle breed for sustainable small farming in Indonesia. In: Chang H.L, Huang, Y.C (eds), The Relationship between Indigenous Animals and Humans in Apec Region. Chin. Soc. Anim. Sci., Taiwan.

Mason, I.L., and Buvanendran, V. 1982. Breeding plans for ruminant livestock in the tropics. FAO Anim Prod Hlth Pp. 34.

Matjuda, L.E., 1997. The possibility of a major gene for fertility in Afrikaner cattle. MSc Agric treatise, University of the Free State, Bloemfontein.

McDermott, J.J., Staal, S.J., Freeman, H.A., Herrero, M., and Van de Steeg, J.A. 2010. Sustaining intensification of smallholder livestock systems in the tropics. Livest. Sci. 130: 95-109.

Mc Parland, S., Kearney, J F., MacHugh, D.E., and Berry, D.P. 2008. Inbreeding effects on post weaning production traits, conformation, and calving performance in Irish beef cattle. J. Anim. Sci. 86: 3338-3347.

Mc Parland, S., Kearney, J.F., Rath, M., and Berry, D.P. 2007a. Inbreeding trends and pedigree analysis of Irish dairy and beef cattle populations. J. Anim. Sci. 85: 322-331.

Mc Parland, S., Kearney, J.F., Rath, M., and Berry, D.P. 2007b. Inbreeding effects on milk production, calving performance, fertility, and conformation in Irish Holstein–Friesians. J. Dairy Sci. 90: 4411-4419.

Meijering, A. 1984. Dystocia and stillbirth in cattle: A review of causes, relations and implications. Livest. Prod. Sci. 11: 143-177.

Melton, B.E. 1995. Conception to consumption: the economics of genetic improvement. In: Proceedings of the 27th Research Symposium and Annual Meeting of the Beef Improvement Ferderation, Sheridan, WY.

Mendelsohn, R. 2003. The challenge of conserving indigenous domesticated animals. Ecol. Econ. 45: 501-510.

Meuwissen, T.H.E. 1999. Operation of conservation schemes. In: Oldenbroek, J.K. (ed). Genebanks and the Conservation of Farm Animal Genetic Resources. DLO Inst. for Anim. Sci. Hlth., Lelystad, The Netherlands.

Meyer, E.H.H. 1984. Chromosomal and biochemical genetic markers of cattle breed in Southern Africa. In Proceedings of the 2nd World Congress on Sheep and Beef Cattle Breeding. Pretoria, South Africa.

Meyer, K. 1992. Variance components due to direct and maternal effects for growth traits of Australian beef cattle. Livest. Prod. Sci. 31: 179-204.

Meyer, K., Hammond, K., Parnell, P.F., Mackinnon, M.J., and Sivarajasingam, S. 1990. Estimates of heritability and repeatability for reproductive traits in Australian beef cattle. cattle. Livest. Prod. Sci. 25: 15-30.

Miller, S. 2010. Genetic improvement of beef cattle through opportunities in genomics. Revista Brasileira de Zootec. 39: 247-255.

Miller, S.P. 2002. Beef cattle breeding programmes: progress and prospects. In Proceeding of the 7th World Congress of Genetics Applied to Livestock Production, Montpellier, France.

Moll, H. 2005. Costs and Benefits of Livestock Systems and the Role of Market and Non Market Relationships. Agric Econ. 32: 181-93.

Montaldo, H.H., Casas, E., Sterman Ferraz, J.B., Vega-Murillo, V.E., and Román-Ponce, S.I. 2012. Opportunities and challenges from the use of genomic selection for beef cattle breeding in Latin America. Anim Front. 2: 23-29.

Moreki, J.C., Ndubo, N.S., Ditshupo, T., and Ntesang, J.B. 2012. Cattle Identification and Traceability in Botswana. J. Anim. Sci. Advan. 2: 925-933.

Morris, C.A., Wilson, J.A., Bennett, G.L., Cullen, N.G., Hickey, S.M., and Hunter, J.C. 2000. Genetic parameters for growth, puberty, and beef cow reproductive traits in a puberty selection experiment. N. Zealand J.Agric Res. 43: 83-91.

Mpofu, N. 2002. The multiplication of Africa's indigenous cattle breeds internationally: the story of the Tuli and Boran breeds. AGTR Case Study. ILRI, Nairobi, Kenya.

Mwandoto B.A.J., Carles, A.B., and Cartwright, T.C., 1988. Weaning and 18 month weights of Boran, East African Shorthorn Zebu and Sahiwal breeds or crosses in Kenya. Trop. Agric. 65: 257-264.

Mwansa, P.B., Crews, D.H., Wilton, J.W., and Kemp, R.A. 2002. Multiple trait selection for maternal productivity in beef cattle. J. Anim. Sci., Breed. Genet. 119: 391-399.

Ndofor-Foleng, H.M., Ebangi, A.L., Agu, C.I., and Okenyi, N. 2012. Estimation of genetic parameters for preweaning and postweaning growth traits in the Gudali beef cattle using multiple trait derivatives free restricted maximum likelihood. Afri. J. Biotec. 11: 14410-14416.

Nephawe, K.A., Maiwashe, A., and Theron, H.E. 2006. The effect of herd of origin by year on post-weaning traits of young beef bulls at centralized testing centres in South Africa. S. Afr. J. Anim. Sci. 36: 33-39.

Nephawe, K.A. 2004. Application of random regression models to the genetic evaluation of cow weight in Bonsmara cattle of South Africa. S. Afr. J. Anim. Sci. 34: 166- 173.

Neser, F.W.C., Van Wyk, J.B., Fair, M.D., and Lubout, P. 2012. Genetic evaluation of growth traits in beef cattle using random regression models. S. Afr. J. Anim. Sci. 42: 474-477.

Newman, S. 2011. The Role of genetic evaluation technology in enhancing global competitiveness. In: Proceedings of the 43ed Research Symposium and Annual Meeting of the Beef Improvement Federation. Montana State University Bozeman, Montana.

Newman, S., and Coffey, S.G. 1999. Genetic Aspects of Cattle Adaptation in the Tropics. In: Fries, R., and Ruvinsky, A. (eds.). The Genetics of Cattle. CAB International, Wallingford, UK.

Nicolas, F.W., 2003. Introduction to veterinary genetics. 2nd edition. Blackwell Publishing. Oxford UK.

Nino-Soto, M., and King, W.A. 2004. Genetic factors that affect normal reproduction and fertility in domestic cattle. Med. Vet. Du Quebec Can. 34: 71-72.

Nomura, T., Honda, T., and Mukai, F. 2001. Inbreeding and effective population size of Japanese Black cattle. J. Anim. Sci. 79: 366-370.

Norris, D., Banga, C., Benyi, K., and Sithole, B.C., 2004. Estimation of genetic parameters and variance components for growth traits of Nguni cattle in Limpopo province, South Africa. Trop. Anim. Hlth. Prod. 36: 801- 806.

Northcutt, S.L., Buchanan, D.S., and Clutter, A.C. 2004. Inbreeding in Cattle. Division of Agricultural Sciences and Natural Resources, Oklahoma State University.

Notter, D.R., 1999. The importance of genetic diversity in livestock populations of the future. J. Anim. Sci. 77: 61-69.

Nuñez-Dominguez, R., Cundiff, L.V., Dickerson, G.E., Gregory, K.E., and Koch, R. M. 1991. Lifetime production of beef heifers calving first at two vs. three years of age. J. Anim. Sci. 69:3467- 3479.

Nwakalor, L.N., Brinks, J.S., and Richardson, G.V. 1986. Selection in Hereford cattle. I. Selection intensity, generation interval and indexes in retrospect. J. Anim. Sci. 62: 927-936.

Ojango, J.M., Panandam, J.M., Bhuiyan, A.K.F.H., Khan, M.S., Kahi, A.K., Imbayarwo-Chikosi, V.E., Halimani, T. E., Kosgey, S. I., and Okeyo, A. M. 2010. Higher education in animal breeding in developing countries: challenges and opportunities. In 9th World Congress on Genetics Applied to Livestock Production, Lepizig, Germany.

Okeyo, A.M., Persley, G., and Kemp, S.J. 2010. Livestock and Biodiversity; the Case of Cattle in Africa. Paper prepared for presentation at the "Biodiversity and World Food Security": Nourishing The Planet And Its People" conference conducted by the Crawford Fund for International Agricultural Research, Parliament House, Canberra, Australia.

Olesen, I., Groen, A.F., and Gjerde, B., 2000. Definition of animal breeding goals for sustainable production systems. J. Anim. Sci. 78: 570-582.

Olori, V.E. 2012. Data recording and profitability in livestock breeding: Lessons from poultry breeding. www.icar.org.

Oltenacu, P.A., and Broom, D.M. 2010. The impact of genetic selection for increased milk yield on the welfare of dairy cows. Anim. welfare, (Supplement 1). 19: 39-49.

Pariacote, F., van Vleck, L.D., and Hunsley, R.E. 1998. Genetic and phenotypic parameters for carcass traits of American Shorthorn beef cattle. J Anim. Sci. 76: 2584-2588.

Parkinson, T.J. 2004. Evaluation of fertility and infertility in natural service bulls. Vet. J. 168: 215-229.

Parnell, P.F., Herd, R.M., Perry, D., and Bootle, B. 1994. The Trangie experiment- Response in growth rate, size, maternal ability, reproductive performance, carcase composition, feed requirements and herd profitability. Proc. Aust. Soc. Anim. Prod. 20: 17-26.

Pentz, E. 2009. Marketing perceptions of the Drakensberger breed of cattle/E. Pentz (Doctoral dissertation).

Pereira, M.C., Mercadante, M.E.Z., Razook, A.G., Figueiredo, L A., and Albuquerque, L.G. 2008. Results of 23 years of selection for post-weaning weight in a Caracu beef herd. S. Afi. J. Anim Sci. 38: 136-144.

Philipsson J., Rege, J.E.O., and Okeyo, A.M. 2006. Sustainable breeding programs for tropical farming systems. In: Ojango, J.M., Malmfors, B. and Okeyo, A.M. (eds). Animal Genetics Training Resources. International Livestock Research Institute, Nairobi Kenya and Swedish University of Agricultural Sciences, Uppsala, Sweden.

Philipsson, J., and Lindhe, B. 2003. Experiences of including reproduction and health traits in Scandinavian dairy cattle breeding programmes. Livest. Prod. Sci. 83: 99-112.

Phocas, F., and Laloe, D. 2004. Genetic parameters for birth and weaning traits in French specialized beef cattle breeds. Livest. Prod. Sci. 89: 121-128.

Pico, B.A., Neser, F.W.C., and Van Wyk, J.B. 2004. Genetic parameters for growth traits in South African Brahman cattle. S. Afr. J. Anim. Sci. 34 (suppl 2): 44-46.

Plasse, D., Arango, J., Fossi, H., Camaripano, L., Llamozas, G., Pierre, A., and Romero, R. 2004: Genetic and non-genetic trends for calf weights in a Bos indicus herd upgraded to pedigree Brahman. Livest. Res. Rur. Dev. 16: 142-159.

Pollak, E.J., Bennett, G.L., Snelling, W.M., Thallman, R.M., and Kuehn, L.A. 2012. Genomics and the global beef cattle industry. Anim. Prod. Sci. 52: 92-99.

Pollak, E.J. 2005. Application and impact of new genetic technologies on beef cattle breeding: a real world perspective. Aust. J Exptl Agric 45: 739-748.

Pollott, G.E. 1998. Goal-led livestock recording systems for low to medium input production systems. In: Trivedi, K.R. (ed.) International Workshop on Animal Recording for Smallholders in Developing Countries. ICAR Techn. Series No.1. Anand, India.

Prayaga, K.C., Henshall, J.M., Swain, D.L., and Gilmour, A.R. 2008. Estimation of maternal variance components considering cow-calf contacts under extensive pastoral systems. J. Anim. Sci. 86: 1081-1088.

Prayaga, K.C. 2004. Evaluation of beef cattle genotypes and estimation of direct and maternal genetic effects in a tropical environment. 3. Fertility and calf survival traits. Crop and Past. Sci. 55: 811-824.

Prayaga, K.C. 2003. Evaluation of beef cattle genotypes and estimation of direct and maternal genetic effects in a tropical environment. 1. Growth traits. Crop and Past. Sci. 54: 1013-1025.

Queiroz, S.A., Albuquerque, L.G., and Lanzoni, L.A. 2000. Inbreeding effects on growth traits of Gyr cattle in Brazil. Braz. J. Anim. Sci. 4: 1014-1019.

Rauw, W.M., Kanis, E., Noordhuizen-Stassen, E.N., and Grommers, F.J. 1998. Undesirable side effects of selection for high production efficiency in farm animals: a review. Livest. Prod. Sci. 56: 15-33.

Rege, J.E.O., Marshall, K., Notenbaert, A., Ojango, J.M.K., and Okeyo, A. M. 2011. Pro-poor animal improvement and breeding: What can science do?. Livest. Sci. 136: 15-28.

Rege, J.E.O., and Gibson, J.P. 2003. Animal genetic resources and economic development: issues in relation to economic valuation. Ecol Econ. 45: 319-330.

Rege, J.E.O., Kahi, A.K., Okomo-Adhiambo, M., Mwacharo, J., and Hannotte, O. 2001. Zebu cattle of Keneya: Uses, performance, farmer preference, measures of genetic diversity and options forimproved use. Animal Genetic Resources Research 1. ILRI, Nairobi, Kenya.

Rege, J.E.O., and Tawah, C.L., 1999. The state of African cattle genetic resources II. Geographic distribution, characteristics and uses of present-day breeds and strains. Anim. Genet. Res. Info. 26: 1-25.

Rege, J.E.O., 1999. The state of African cattle genetic resources I. Classification framework and identification of threatened and extinct breeds. Anim. Genet. Res. Info. 25: 1-25.

Reist-Marti, S.B., Simianer, H., Gibson, J., Hanotte, O., and Rege, J.E.O. 2003. Weizman's approach and conservation of breed diversity: an application to African cattle breeds. Cons. Bio. 17: 1299-1311.

Reverter, A., Johnston, D.J., and Graser, H.U. 2002. First experiences with an across country genetic evaluation system for beef cattle. In: Crettenand, J., Moll, J., Mosconi, C., and Wegmann, S. (eds). Performance recording of animals: state of the art 2002. In: Proceedings of the 33rd Biennial Session of ICAR, Interlaken, Switzerland.

Rewe, T.O., Herold, P., Kahi, A.K., and Valle Zarate, A. 2009. Breeding indigenous cattle genetic resources for beef production in Sub-Saharan Africa. Outlook on Agriculture. 38: 317-326.

Rewe, T., 2009. Breeding objectives and selection schemes for Boran cattle in Kenya (Doctoral dissertation). Universitat Hohenheim.

Rewe, T., Herold, P., Piepho, H.P., Kahi, A.K., and Zárate, A.V. 2008. Institutional framework and farm types characterising the Kenya Boran cattle breeding programme. Deutsche Deutsche Tropentag, Universität Hohenheim, Germany.

Rios Utrera, A., and Van Vleck, L.D. 2004. Heritability estimates for carcass traits of cattle: a review. Genet. Mol. Res. 3: 380-394.

Rogers, P.L., Gaskins, C.T., Johnson, K.A., and MacNeil, M.D. 2004. Evaluating longevity of composite beef females using survival analysis techniques. J. Anim. Sci. 82: 860-866.

Rust, T., Theron, H.E., Schultz, M.M., and Berg, L. 2010. The practical use of breeding values in beef cattle breeding. In: Scholtz (ed); Beef breeding in South Africa. 2nd edition. Pretoria, South Africa.

Rust, T., and Groeneveld, E. 2002. Variance component estimation of female fertility traits in two indigenous and two European beef cattle breeds of South Africa. S. Afr. J. Anim. Sci. 32: 23-29.

Rust, T., and Groeneveld, E., 2001. Variance component on female fertility traits in beef cattle. S. Afr. J. Anim.Sci. 31: 131-141.

Rust, T., and Kanfer, F.H.J., 1998. Variance component and breeding value estimation for age at first calving of Afrikaner and Drakensberger beef cattle. Proc. 36th Nat. Congr. S.A. Soc. Anim. Sci., Stellenbosch, South Africa.

Santana, M.L., Oliveira, P.S., Eler, J.P., Gutiérrez, J.P., and Ferraz, J.B.S. 2012. Pedigree analysis and inbreeding depression on growth traits in Brazilian Marchigiana and Bonsmara breeds. J. Anim. Sci. 90: 99-108.

Santana, M.L., Oliveira, P.S., Pedrosa, V.B., Eler, J.P., Groeneveld, E., and Ferraz, J.B.S. 2010. Effect of inbreeding on growth and reproductive traits of Nellore cattle in Brazil. Livest. Sci. 131: 212-217.

SAS Institute Inc. 2010. Administering SAS® Enterprise Guide® 4.3. Cary, NC: SAS Institute Inc.

Schoeman, S.J. 1989. Recent research into production potential of indigenous cattle with special reference to Sanga (Review). S. Afr. J. Anim. Sci. 19: 55 - 61.

Scholtz, M.M., Steyn, Y., Van Marle-Köster, E. and Theron, H.E., 2012. Improved production efficiency in cattle to reduce their carbon footprint for beef production. S. Afr. J. Anim. Sci. 42: 450-453.

Scholtz, M.M., McManus, C., Okeyo, A.M., Seixas, L., and Louvandini, H. 2010. Challenges and opportunities for beef production in developing countries of the southern hemisphere. Proceedings of International Committee on Animal Recording (ICAR) 37th Annual Meeting. Riga, Latvia.

Scholtz, M.M., 2010. Beef breeding in South Africa. 2nd edition. Pretoria, South Africa.

Scholtz, M.M., Roux, C.Z., DE Bruin D.S., and Schoeman, S.J. 1990. Medium Term responses and changes in fitness with selection for parameters of the allometric autoregressive model. S. Afr. J. Anim. Sci. 20: 65-70.

Seroba, M.M., Maiwashe, A., Nephawe, K.A., and Norris, D. 2011. Genetic parameter estimates for live animal ultrasound measures of carcass traits in South African Angus cattle. S. Afr. J. Anim. Sci. 41: 243-249.

Sewalem, A., Kistemaker, G.J., Miglior, F., and Van Doormaal, B.J. 2006. Analysis of inbreeding and its relationship with functional longevity in Canadian dairy cattle. J. Dairy sci. 89: 2210-2216.

Simianer, H. 2005. Decision making in livestock conservation. Ecol. Econ. 53: 559-572.

Simm, G., Bünger, L., Villanueva, B., and Hill, W.G. 2004. Limits to yield of farm species: genetic improvement of livestock. In Sylvester-Bradley, R., and Wiseman, J. (eds). Yields of farmed species: constraints and opportunities in the 21st century. Nottingham, UK: Nottingham University Press.

Smith, B.A., Brinks, J.S., and Richardson, G.V. 1989. Relationships of sire scrotal circumference to offspring reproduction and growth. J. Anim. Sci. 67: 2881-2885.

Smith, C. 1988. Genetic improvement of livestock using nucleus-breeding units. W. Anim. Rev. 65: 2-10.

Snelling, W.M., Golden, B.L., and Bourdon R.M. 1995. Within-herd genetic analyses of stayability of beef females. J. Anim. Sci. 73: 993-1001.

Sørensen, M.K., Sorensen, A.C., Baumung, R., Borchersen, S., and Berg, P. 2008. Optimal genetic contribution selection in Danish Holstein depends on pedigree quality. Livest. Sci. 118: 212-222.

Sørensen, A.C., and Norberg, E. 2008. Inbreeding in the Danish populations of five Nordic sheep breeds. Acta Agriculturae Scand Section A. 58: 1-4.

Sørensen, A.C., Sørensen, M.K., and Berg, P. 2005. Inbreeding in Danish dairy cattle breeds. J. Dairy Sci. 88:1865-1872.

Steyn, J.W., Neser, F.W.C., Hunlun, C., and Lubout, P.C. 2012. Preliminary report: Pedigree analysis of the Brangus cattle in South Africa. S. Afr. J. Anim. Sci. 42: 511-514.

Steyn, J., Ayalew, W., Rege, J.E.O., Mulatu, W., Malmfors, B., Dessie, T., and Philipsson, J. 2009. Livestock keeper perceptions of four indigenous cattle breeds in tsetse infested areas of Ethiopia. Trop. Anim Hlth. Prod. 41: 1335-1346.

Strydom, P.E., Naudé, R.T., Smith, M.F., Kotzé, A., Scholtz, M.M., and van Wyk, J.B. 2001 Relationships between production and product traits in subpopulations of Bonsmara and Nguni cattle. S. Afr. J. Anim. Sci. 31: 181-194.

Syrstad, O. 1992. Utilisation of indigenous animal genetic resources. In: Rege, J E.O., and Lipner, M.E. (eds.). African Animal Genetic Resources: Their Characterisation, Conservation, and Utilisation: Proceedings of the Research Planning Workshop Held at ILCA, Addis Ababa, Ethiopia. ILRI (aka ILCA and ILRAD).

Tada, O., Muchenje, V., and Dzama, K. 2013. Preferential traits for breeding Nguni cattle in low-input in-situ conservation production systems. SpringerPlus. 2: 1-7.

Thornton, P.K. 2010. Livestock production: recent trends, future prospects. Philosophical Transactions of the Royal Society B: Biological Sciences, 365: 2853-2867.

Toelle, V.D., and Robison, O.W. 1985. Estimates of genetic correlations between testicular measurements and female reproductive traits in cattle. J.Anim. Sci. 60: 89-100.

Toro, M.Á., García-Cortés, L.A., and Legarra, A. 2011. A note on the rationale for estimating genealogical coancestry from molecular markers. Genet Sel Evol. 43: 27.

Toro, M., and Lopez-Fanjul, C. 1998. Recent advances in animal breeding theory and its possible application in aquaculture. In: Proceedings of the TECAM Seminar on Genetics and Breeding of Mediterranean Aquaculture Species. CIHEAM/FAO.

Trivedi, T.R., 1998. A case study of buffalo recording systems under the Dairy Co-operative Organisation in India. In: Proceedings of the International Workshop on Animal Recording for Smallholders in Developing Countries.ICAR Techn. Series No 1. Anand, India.

Van der Werf, J., 2000. Livestock straight-breeding system structures for the sustainable intensification of extensive grazing systems. In: Gala S., Boyazoglu, J., and Hammond, K. (eds.). Proceedings of the Workshop on

Developing Breeding Strategies for Lower Input Animal Production Environments. ICAR Techn. Series, No 3. Bella, Italy.

Van der Werf, J. 1999. An overview of animal breeding programs. Animal Breeding Use of New Technologies (This is a Post Graduate Foundation Publication).

Van der Westhuizen, R.R., Van der Westhuizen, J., and Schoeman, S.J. 2009. A genetic analysis of post-weaning feedlot performance and profitability in Bonsmara cattle. Gen. Mol. Res. 8: 179-196.

Van der Westhuizen, R.R., Van der Westhuizen, J., and Schoeman, S.J. 2004. Genetic relationship between feed efficiency and profitability traits in beef cattle. S. Afr. J. Anim. Sci. 34: 50-52.

Van der Westhuizen, R.R., and Groeneveld, E. 2004. Population and pedigree analysis of indigenous South African beef breeds. In Van Der Honing Y., (ed): Book of Abstracts of the 55th Annual Meeting of the European Association for Animal Production. Bled, Slovenia.

Van der Westhuizen, R.R., Schoeman, S.J., Jordaan, G.F., and Van Wyk, J.B. 2001. Genetic parameters for reproductive traits in a beef cattle herd estimated using multitrait analysis. S. Afr. J. Anim. Sci. 31: 4-48.

Van der Westhuizen, R.R., Schoeman, S.J., Jordaan, G.F., and Van Wyk, J.B. 2000. Heritabilities of reproductive traits in a beef cattle herd using multitrait analysis. S. Afr. J. Anim. Sci. 30: 140-141.

Van Doormaal, B.J., Miglior, F., Kistemaker, G., and Brand, P. 2005. Genetic diversification of the Holstein breed in Canada and internationally. Interbull Bullet. 33: 93-97.

Van Eenennaam, A.L. 2012. How might DNA- based information generate value in the beef cattle sector? Proceedings of the 38th International Committee for Animal Recording (ICAR) Biennial Conference, Cork, Ireland.

Van Eenennaam, A.L., Thallman, R.M., Quaas, R.L., Hanford, K., and Pollak, E.J. 2009. Validation and estimation of additive genetic variation associated with DNA tests for quantitative beef cattle traits. In Proceedings of the Association for Advancement of Animal Breeding and Genetics. 18: 129-132.

Van Marle-Koster, E., Mostert, B.E., and van der Westhuizen, J.A.P.I.E. 2000. Body measurements as selection criteria for growth in South African Hereford cattle. ARCHIV FUR TIERZUCHT, 43: 5-16.

Van Melis, M.H., Eler, J.P., Rosa, G.J.M., Ferraz, J.B.S., Figueiredo, L.G.G., Mattos, E.C., and Oliveira, H.N. 2010. Additive genetic relationships between scrotal circumference, heifer pregnancy, and stayability in Nellore cattle. J. Anim. Sci. 88: 3809-3813.

Van Niekerk, M., Neser, F.W.C., and Van Wyk, J.B., 2004. (Co)variance components for growth traits in the Nguni cattle breed. S. Afr. J. Anim. Sci. 34 (Sppl. 2): 113-115.

Wasike, C.B., Magothe, T.M., Kahi, A.K., and Peters, K.J. 2011. Factors that influence the efficiency of beef and dairy cattle recording system in Kenya: A SWOT-AHP analysis. Trop. Anim. Hlth Prod. 43: 141-152.

Wasike, C.B., Indetie, D., Ojango, J.M.K., and Kahi, A.K. 2009. Direct and maternal (co) variance components and genetic parameters for growth and reproductive traits in the Boran cattle in Kenya. Trop Anim Health Prod. 41: 741-748.

Weber, K.L, Thallman, R.M, Keele, J.W, Snelling, W.M, Bennett, G.L, Smith, T.P, McDaneld, T.G, Allan, M.F, Van Eenennaam, A.L, and Kuehn, L.A. 2012a. Accuracy of genomic breeding values in multibreed beef cattle populations derived from deregressed breeding values and phenotypes. J Anim Sci. 90: 4177-4190.

Weber, K.L., Drake, D.J., Taylor, J.F., Garrick, D.J., Kuehn, L.A., Thallman, R.M., Schnabel, R.D, Snelling, W.M, Pollak, E.J., and Van Eenennaam, A.L. 2012b. The accuracies of DNA-based estimates of genetic merit derived from Angus or multibreed beef cattle training populations. J. Anim. Sci. 90: 4191-4202.

Weigel, K.A. 2001. Controlling inbreeding in modern breeding programs. J. D. Sci. 84: E177-E184.

Wendorf, F., and Schild, R. 1994. Are the early Holecene cattle in the Eastern Sahara domestic or wild? Evol. Anthro. 3: 118-128.

Wickham, B.W., and Dürr, J.W. 2011. A new international infrastructure for beef cattle breeding. Anim. Front. 1: 53-59.

Williams, R. 2012. US genetic trends, production numbers and discussion on how Breed Associations may need to adapt. Retrived from; www.icar.org.

Woolliams, J.A., Matika, O., and Pattison, J. 2008. Conservation of animal genetic resources: approaches and technologies for in situ and ex situ conservation. Anim. Genet. Res. Info. 42: 71-89.

Worede, G.M., Forabosco, F., Zumbach, B., Palucci, V., and Jorjani, H. 2013. Evaluation of genetic variation in the international Brown Swiss population. Int. J. Anim. Biosci. 7: 1060-1066.

Wright, S. 1923. Mendelian analysis of the pure breeds of livestock. I. The measurement of inbreeding and relationship. J. Hered. 14: 339-348.

Wurzinger, M., Ndumu, D., Baumung, R., Drucker, A.G., Okeyo, A.M., Semambo, D.K., and Sölkner, J. 2006. Assessing stated preferences through the use of choice experiments: valuing (re) production versus aesthetics in the breeding goals of Ugandan Ankole cattle breeders. In Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Minas Gerais, Brazil, Instituto Prociência.