Genetic diversity and estimation of genetic parameters for economically important traits in Zambian cattle

by

Ellison Musimuko
(*BAgricSc, DipAgricSc*)

A Thesis Submitted for the Degree of Master of Philosophy at the

University of Adelaide, School of Animal and Veterinary Sciences

February 2014

Contents

Tables

Figures

Abbreviations

AFLP	Amplified Fragment Length Polymorphism
AI	Artificial Insemination
AMOVA	Analysis of Molecular Variance
AnGR	Animal Genetic Resources for Food and Agriculture
BLUP	Best Linear Unbiased Prediction
bp	base pair
CBPP	Contagious Bovine Pleuro pneumonia
CGIAR	Consultative Group on International Agricultural Research
DAD-IS	Domestic Animal Diversity Information System
DAGRIS	Domestic Animal Genetic Resources Information System
DNA	Deoxyribonucleic Acid
DS	Nei's Standard Genetic Distance
EAAP	European Association for Animal Production (http://www.eaap.org)
EBV	Estimated Breeding Value
FAO	Food and Agriculture Organization of the United Nations
FAOSTAT	Food and Agriculture Organization of the United Nations Statisitcal
FMD	Foot-and-Mouth Disease
Ho	Observed Homozygosity
IAEA	International Atomic Energy Agency
IICA	Inter-American Institute for Cooperation on Agriculture
ILRI	International Livestock Research Institute (http://www.ilri.org)
ISAG	International Society of Animal Genetics (http://www.isag.org.uk)
LD	Linkage Disequilibrium
LU	Livestock Units
MACO	Ministry of Agriculture and Cooperative
mtDNA	Mitochondrial Deoxyribonucleic Acid

Ne	Effective Population Size
NIAH	National Institute of Animal Husbandry
PCR	Polymerase Chain Reaction
REML	Restricted Maximum Likelihood
RFLP	Restriction Fragment Length Polymorphism
SADC	Southern African Development Community
SNP	Single Nucleotide Polymorphism

Dedication

This thesis work is dedicated to my family and friends. A special feeling of appreciation goes to my loving wife, Rosemary Mhango Msimuko, for her tireless encouragement and pushy towards my successfully completion of this process. My children Phaskani, Fiskani and Luskani Taonga who continued performing well at school and you are exceptional. My warm and tender gratitude goes to my mother for her spiritual support throughout my entire program.

Further dedication goes to my special friends who have supported me throughout the process, especially Wido Nugroho for helping with technology skills in GIS. Finally the team in the picture below, I say, you are special.

The University of Adelaide Intercollegiate Meat Judging Team 2013:At far back are Nick van den Berg and Logan Dennis; (middle row) David Wooley, Kat Vallance, Julia Huser, Bonnie Chapman, Tracey Fischer (coach) and Reece Mason; (front) Megan Jaeschke, Emily Buddle, Cathy Dodd (coach), Ellison Musimuko and Sam Walkom (head coach).
Source: Sam Walkom

Abstract

Current genetic erosion of indigenous breeds is common. Globally, this has become a major concern. In Zambia, genetic improvement programs rely upon traditional selection and breed substitution, and do not utilise local animal genetic resources. The aim of this work was to provide information for genetic improvement strategies, including the preferred traits of cattle breeders, estimating genetic diversity and genetic parameters, to improve and conserve local well-adapted indigenous cattle.

This study used quantitative survey data, collected between September 2012 and December 2012. Both parametric and non-parametric tests were conducted to test if there were significant differences in preferences for traits between three regions of Zambia, namely Namwala, Chipata and Lundazi. The tests revealed that there were no significance differences for the traits preferred between the regions. However, large-scale farmers preferred larger sized animals and emerging small-scale cattle farmers preferred fertility traits.

Genetic data from 274 alleles generated using 32 microsatellite markers from 72 individuals representing three indigenous Zambian cattle breeds (Angoni, Tonga and Barotse) was used to assess genetic diversity and population structure. Although, Zambian indigenous cattle breeds did not exhibit a high and unique breed's purity, cattle exhibited a higher level of genetic diversity within breeds than between breeds. Despite the evidence of a close gene flow between the three populations, inbreeding was largely insignificant going by the Bayesian cluster at K=2. It may be further evidence of existing divergent and multi-loci genetic admixtures between and within breeds. If accurate, the uniqueness of the population

clustering offers valuable information on the gene pool available for selection within breeds for utilisation, genetic improvement and conservation. However, Tonga and Barotse breeds appeared to exhibit lower genetic diversity than Angoni.

To measure the genetic parameters for growth, data for 266 Angoni and 606 Boran weaning weights for 15 years were used in linear mixed models to estimate variances and heritabilities. The change in the log-likelihood was used to test for improvements when comparing models. Fixed effects of sex, breed, and age were determined on weaning weight. Random effects included breed by animal and breed by dam. Separate breed variances were not significant and so the overall direct heritability and maternal heritability was moderate (20% and 19%, respectively) using the best model (6). Thus, these heritability estimates of direct and maternal effects on weaning weight indicate it should be possible to make good genetic progress for this trait.

Zambian indigenous cattle provide rich genetic resources, exhibiting moderately heritability, and therefore, have the potential to be improved by using appropriate planning and flexible breeding programs. This is important because the current trends show a substantial increase in demand for meat worldwide and if farmers in Zambia wish to develop an export market, beef production must be improved. However, Zambia will require separate breeding objectives and genetic parameter estimates for large-scale farmers and emerging small-scale farmers in order to exploit the wide range of diversity through genetic selection. This could be through focusing on different breed for each group.

Declaration

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission in my name, for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree.

I give consent to this copy of my thesis, when deposited in the University Library, being made available for loan and photocopying, subject to the provisions of the Copyright Act 1968.

I also give permission for the digital version of my thesis to be made available on the web, via the University's digital research repository, the Library Search and through web search engines, unless permission has been granted by the University of Adelaide to restrict access for period.

Ellison Musimuko
February 2014

Acknowledgements

This task was huge and required a team effort. Therefore, I am indebted to numerous people and organisations that contributed significant time and resources to enable me complete this research.

I would like to acknowledge and thank the providers of the Scholarship, Australia Awards Scholarships for Africa (AusAID), for the considerable financial support I received to undertake this study and the government of Zambia for granting me paid study leave.

In recognition of my principal supervisor Associate Professor Wayne Pitchford, thank you very for your guidance that is exceptional and ever valuable in imparting research knowledge and skills. Your dedication to work has indeed motivated me to take any future challenges without fear or favour. Out of your busy schedule, you always found time for me without that I would not have completed my work as scheduled. You are truly my living example across numerous domains of my life ranging from professional development, teaching to general outlook.

A significant appreciation goes to my co supervisor Associate Professor Cynthia DK Bottema (Animal Genetic Technologies, South Australia), for her swift and tremendous feedback on written and oral work that was provided during the course of my study. In particular many thanks for your assistance in addressing genotyping requirements and providing all necessary laboratory facilities for the DNA extraction. Your input really was tremendous special to me. Thank you 'Cindy.'

To Dr Dana Thomsen, my social science advisor and editor, thank you for showing the strong commitment to this work for supporting and comments provided to chapter two of this

thesis. Your advice on the outline, structure, methods and results has been particularly valuable. Social science is too bulky and can easily wear someone out, but you quickly helped and your time provided important advice on how to integrate both social and the core science in my project Above all for being my editor that which you highlighted spelt checks, citations and clarity of ambiguity. Many thanks to you.

Most sincerely, acknowledgement goes to Professor Emily Piper from The University of Queensland (Science Leader, Animal Genetics Laboratory Group) for providing the genotyping services for this work in Chapter 3. At a short notice, you and your group were able to provide the real services required at a reasonable cost. Thank you.

Rugang Tian, I am in awe of the laboratory skills you provided to me. Your patient and nature inspires me. I am grateful.

This project has drawn on numerous data sources and I am very grateful to have had access to such a wide array of data. In particular, thanks to Mr Alan Miller, Boran and Angoni breeder, for kindly allowing me access the animal performance records on his Lilayi farm. In addition, I appreciate the farm manager, Mrs Charity Monga for her guidance on the records formatting. Without her, the data would meaningless.

To scientists within the Genetic Characterisation of Indigenous Cattle Breeds in Zambia Project, thank you very much for all your help in blood sample collection and other laboratory facilities provided. Special thanks to Mr Bwalya Katati for the entire help given to me while working in his laboratory in Zambia.

I would like to acknowledge the cattle farmers interviewed in this study. The success of this research depended on cattle farmers in Namwala, Chipata and Lundazi who willingly

accepted to be interviewed and respond to the questionnaires. I am indebted to all farmers and each interview was enjoyable.

To the research group, I say thanks for all the comments during my presentations and the research day organisers for awarding me with a second best poster in 2013.

Special thanks to Dr. Stephen Lee, Cathy Dodd and Dr. Sam Walkom for their contributions to data analysis and approach.

Finally, I acknowledge several individuals whom I may not include in the lists including from other universities I had contacted for assistance in data analysis and allowing me to use their bioinformatics tools.

Chapter 1

1.0 General introduction and Literature Review

1.1 Human population growth and livestock demand trends

Globally, consumption of meat and milk has been increasing over the past thirty years. The total meat and milk consumption in the developing world grew from approximately at 4% to 6% per year during the same period (FAO 2011). However, current population demographic data from the United Nations Food and Agriculture Organization (FAO) strongly indicates that world demand for livestock and livestock products is likely to continue increasing into the near future as the human population is projected to rise to 9.2 billion in 2050 (Gill 1999; UN Population Division 2007 ; FAO 2011). This faster human population growth, rising in the standard of living of most people and changes in human dietary preferences, will substantially increase the demand of livestock products (Delgado et al., 1999).

In Sub-Sahara Africa, dietary pattern changes is likely to occur quickly for both qualitative and quantitative individual food preferences, moving away from low quality towards high-quality foods, such as meat and milk (Steinfeld et al., 2006; World Bank 2007). For example, in Zambia, individual dietary preferences, household shared capacity and the high pace at which Zambia is becoming highly urbanized in Sub-Sahara Africa has largely influenced food choices and consumption patterns (Mason et al., 2011). As countries become more urbanized, better socio-economic and environmental interactions occur within the populations that consequently increase global food choices and result in increased demand (Delgado et al., 1999; Thornton, 2010).

The growth in demand for meat, milk and other livestock products is presumed to take two separate characteristics. In developed countries, the demand for livestock and livestock products is likely to be slow and predicted to exhibit a relative stagnant growth towards 2050, while in developing countries, the demand for meat and milk is highly expected to be high and possibly triple within the same period (Figure 1.1) (Thornton et al., 2002; FAO 2006b; Ruto et al., 2008).

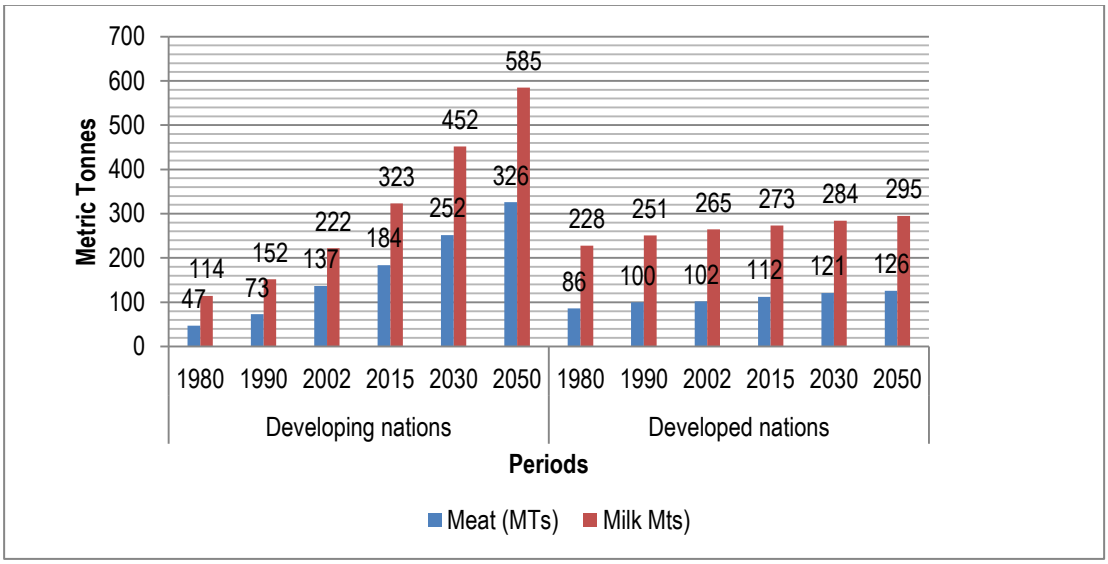


Figure 1 1: World projected data of milk and meat consumption.
Source: (Thornton, 2010)

Data in (Figure 1.1), indicates that the total meat and milk production in some developing nations has doubled and even tripled in some countries between the years 1990 and 2010 (FAO 2011). For example, in East Africa, milk consumption trends increased from approximately 1.5 million metric tonnes in 1975 to 3.2 million metric tonnes in 1995, while meat consumption rose from 0.5 million metric tons to 0.9 million metric tons in the same period (Thornton et al., 2004; Ruto et al., 2008). Further projections indicate that the total

consumption of meat and milk in East Africa will more than double between 1997 and 2020 to reach 1.9 and 7.3 million metric tonnes, respectively, by 2020 (Thornton, 2010).

The trend of Zambia's production and consumption of beef and dairy products is slightly different from other developing nations. Total production and demand for livestock was still small and expected to grow at a slower rate than in most other developing nations, such as Brazil (Chilonda et al., 1999). In the year 2008, Zambia produced 58,400 tonnes of beef at a value of approximately US$194 million and 65,000 tonnes of raw milk at a value of US$39 million (CSO 2010). Even though the country produced such quantities of beef and milk, consumption per capita was still low ranging from 4kg to 11kg depending on income and life styles of individuals (Mason and Maule, 1960; Mulemba 2009)

Overall beef and milk consumption per capita is also lower in Sub-Saharan Africa than elsewhere in the developing world (World Bank 2011), and meat consumption per capita of about 11kg is below two-thirds of the population according to World Health Organization's (WHO) recommended guidelines (FAO 2010). However, records indicate that generally, beef production and consumption increased from 28.1 thousand metric tonnes in 1990 to 40.8 thousand metric tonnes in 2002 and milk production and consumption also increased from 58.8 to 64.2 thousands metric tonnes during the same period in relationship to population growth (Mulemba, 2009; Conway and Shah, 2010). In value terms, Zambian livestock accounts for about 39% of national agricultural output and is one of the major contributors to the Zambian economy (Table 1.1), making agriculture the fastest growing economic sector in Zambia. Approximately, 80% of agricultural production comes from small-scale farmers whose livelihoods depend on agriculture. Given the high growth of

agriculture and its localised nature, measures to improve livestock management will have a positive effect on reducing poverty in rural communities in general.

Table 1.1: Structure of the Zambian economy

Sector	1991	2001	2011
Agriculture	4.3	3.0	7.7
Industry	-3.7	8.4	4.9
Manufacturing	1.2	4.0	5.0
Services	1.2	4.0	5.0

Zambia, on average, imports more beef than it does exports, with 2004 seeing a significant variation in favour of beef exported as compared to beef imported (Figure 1.2). One of the main reasons for continuously import is low productivity and high demand (MACO 2008). However, early in 2002, the government launched a livestock-restocking program to restore breeding stock and increase productivity and animal draught power (Mulemba, 2009). The government also adopted an Animal Disease Control Programme and created disease free zones to preserve the current population of livestock. This subsequently resulted in more beef exports in the 2004. In 2006 and onwards, however, these introduced cattle did not adapt to local environments hence their population declined (Musialela et al., 2008; Muuka et al., 2013), while the human population was growing and becoming more urbanised increasing the demand for livestock products (Appendix I.2).

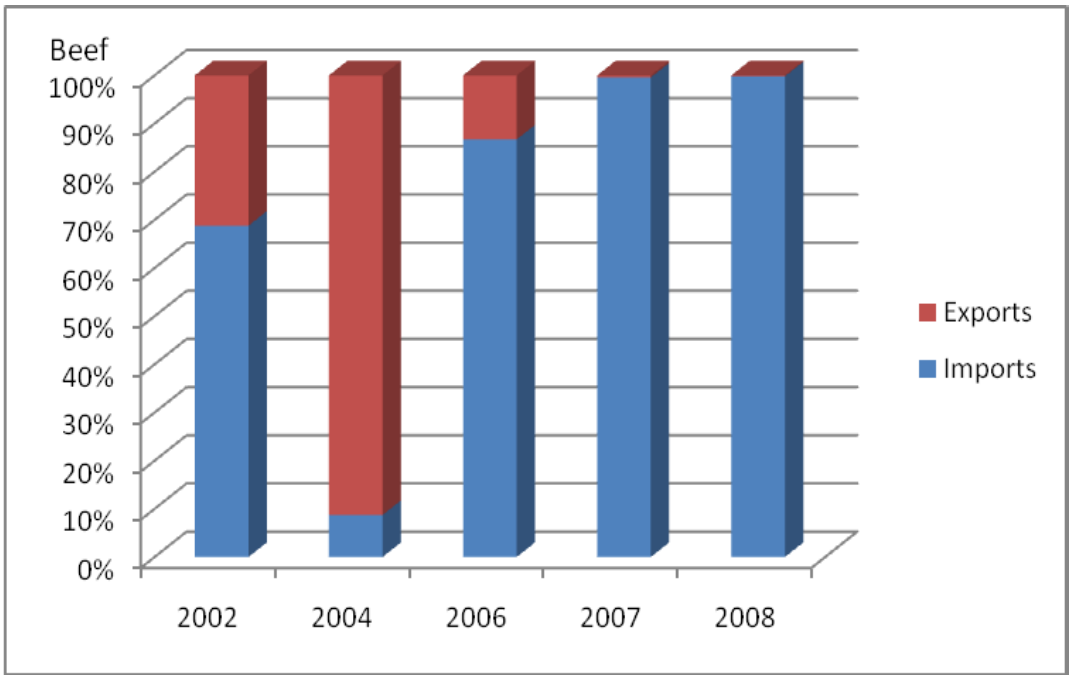


Figure 1 2: Trends of import and exports of beef in Zambia
Source: Adopted from Mulemba 2009, NALEIC statistical database of 2008

1.2 Land as a major factor of cattle production system

Livestock production, especially cattle, is usually robust in nature and requires enormous quantities of land. The cattle sector uses millions of hectares of land for grazing, fodder and crop production worldwide (Steinfeld et al., 2006). In most pastoral agricultural systems in Sub-Sahara Africa, cattle keepers depend on a large area of land for livestock production (Rege, 1999; Fynn et al., 2000; Pitchfold, 2007). The Illa pastoralists of Zambia are among the old established pastoral people whose livelihoods depend on cattle (Fielder et al., 1973; Steele et al., 1981). Under their system, a major increase in cattle productivity usually results from a seasonal progressive shift of the livestock population from the lowlands during rainy season to higher and drier potential areas. During the dry season, cattle are moved to the lowlands where there is fresh and succulent grass. Along with this benefit of pasture availability acquired from progressively inter-annual movement of cattle from lowland to

highlands, there is a stable and economic use of land resources (Amer et al., 1998; Fisher et al., 2012). Even though, there is economic use of land under this system, overall production levels remain very low as compared to commercial production systems with no animal re-location (Bebe et al., 2003; Bishop and Woolliams, 2004).

In the commercial sector, cattle are bred to improve quantity and quality of livestock products. Breeding goals are directed towards achieving high productivity and efficiency (Phacos et al., 2003; Rewe et al., 2006; Pitchford 2007), including increased fertility, improved growth rates and higher milk yield per cow with calf (Dekkers and Hospital 2002; Bobe et al., 1999). In contrast, there are no definite breeding strategies developed for Zambian pastoral systems. With an understanding of the characteristics of pastoral production system and cattle, traits preferences of pastoral/subsistence livestock producers, their breeding strategies can be meaningfully translated into useful programs for Zambian livestock production systems (Scoones, 1992; Baker and Rege 1994;). This should, in turn, increase the value of total cattle head per hectare of land use.

1.3 Economic and non-economic value of cattle

Livestock, especially cattle, play multi-purpose roles worldwide. Literature from the FAO and other organisations have described the importance of livestock to human livelihoods and its relationship to other agriculture production systems (Steele, 1981; Anderson 2003; Ruto et al., 2008; Rewe et al., 2009; Assan, 2012). Livestock play an important and integral role in the occupations of most rural populations, and agricultural development is particularly important to the majority Zambian communities (Lungu, 2003; Mulemba, 2009).

1.3.1 Value of cattle traction as a trait

One of the most important uses of cattle in Zambia relates to crop production and transport of agricultural produce and inputs. For the majority of Zambians living in rural communities cannot afford to purchase or hire farm tractors. Small-scale farmers use cattle to cultivate agriculture lands for crop production to produce staple foods and cash crops. Studies have shown that a pair of oxen can produce crops valued between $3500- $4500 per year in Zambia (Figure 1.3a) (Haggblade and Tembo, 2003; Mulemba, 2009). After harvest, the pair of oxen may be also used to transport farm produce either to the homestead or to market places. In some instances, cattle are the only means to transport critical patients to a nearest clinic (Figure 1.3b). A review of several studies in Southern Africa region, 64% of people preferred keeping cattle mostly as source of traction (Scoones, 1992; Team and Team, 2003; Mapiye et al., 2007). It is common to use mature cows and oxen for various traction activities, such as ploughing and weeding croplands in Africa.

Figure1.3a: Cattle Ploughing

Figure 1.3b: Cattle as Transport 1

Figure 1 3: Use of cattle as source of traction

1.3.2 Value in supplying plant nutrients in agriculture systems

Manure collected from cattle yards act as source of plant nutrients for crop production. Cattle manure contains several plant nutrients such as nitrogen and phosphorus (Brady and Weil, 2010; Hartemink et al., 2008). The opportunity cost of manure is significant in vegetable production. Manure, as a source of plant nutrients, contains a high level of stable organic nitrogen compounds that is released slowly into the soil solution for plant uptake, providing a steady supply of nutrients available to the crop throughout the growing season (Brady and Weil, 2010). Depending on the type or stage of pasture growth, cattle manure may contain large amounts of weed seeds. In addition, dry cattle manure acts as a source of fuel for domestic use, more frequently in regions where firewood is scare.

1.3.3 Value in investments, savings and supply of high quality dietary foods

At a domestic level, home economics of agriculture are heterogeneous in character. Cattle have multiple economic functions that include, boosting household finances, providing long-term savings and sound investments (Thorpe et al., 1980; Rege et al., 1999; Tano et al., 2003). Cattle assume both financial and insurance roles due to the lack of adequate banking institutions in most parts of Zambia. For example, in Namwala, there is only one bank and most of the time it is non-functioning. Thus, farmers prefer investing money in cattle rather than saving money in the bank and a general-purpose currency in traditional communities (Fielder, 1973; Barrett, 1992; Singogo et al., 1996; Moll et al., 2007).

1.3.4 Non-economic value of cattle in traditional cultures

In most parts of Sub-Sahara Africa, cattle ownership is multifaceted. This complex character of African cattle ownership was developed at very early stage in the history of Africa, as described by Herkovists (1926) '*The Bantu Cattle Complex myth'* cited by Mtetwa, 1978. Several members of a particular family may own cattle jointly and decisions regarding cattle are usually made collectively (Barrett, 1992). Significantly, this presents a strong form of social security for unemployed rural and elderly people who may have a limited source of income and strength to perform physical duties (Steele, 1981).

In other communities, cattle are important as an agency of bridging the socio-economic gap between the wealthy and the poor. This occurs when the cattle herd size increases to a point that extra animals are leased out to less fortunate people through a processing called '*herding out'* (Mtetwa, 1978). The process allows cattle to be shared among the richer and the less privileged societies.

For the majority of traditional Bantu speaking people, cattle are used as a dowry (*Lobola*) transaction that usually creates a strong bond between participating families (Steele, 1981). In Zambia, the number of cattle required may range from 8 to 15 depending on the local culture. Furthermore, cattle may be used to settle torts for offences committed within traditional communities in local courts. Most traditional ceremonies in Zambia involve cattle, such as *Shimunenga ceremony* in Namwala districts and *Ncwala* ceremony in Eastern Province of Zambia that celebrated creasing spiritual ancestral

1.4 Cattle distribution and production systems in Zambia

1.4.1 Cattle distribution

Like most countries in world, Zambia has a range of cattle production systems. These include commercial production system that has cow-calf, seedstock and feedlot segments characterised by a well-defined management and breeding goals. The commercial sector accounts for approximately 15% of the total beef output (Chilonda et al., 1999). The traditional cattle production system accounts for approximately 80% of total Zambian output distributed throughout the country (Mwenya, 1993; Chilonda et al., 1999). The cattle density varies from one region to another (Figure 1.4). A high density of cattle greater than 250 livestock units per km^2 is found in Southern Province, where beef commercial farming is predominant. Northern and North-West Provinces of Zambia have less than 1 livestock per km^2 because of the high prevalence of tsetse flies and mining activities.

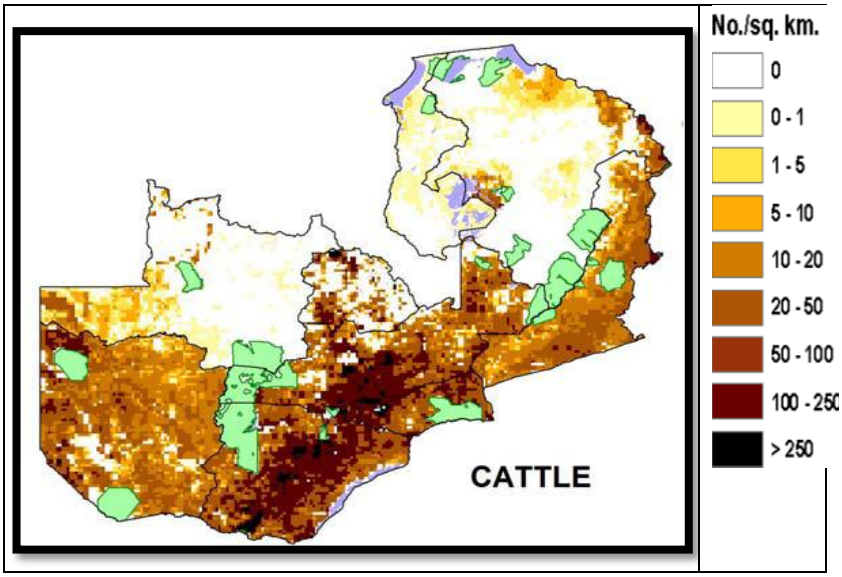


Figure 1 4: Cattle density and distribution in Zambia
Source: FAO 2001

1.4.2 Cattle production systems in Zambia

The two main cattle production systems in Zambia rely mostly on the use of extensive grasslands. Commercial beef production is based on tropical and exotic breeds such as Boran, Brahman Hereford, Sussex, South Devon, and Bosmara. General management includes restricted breeding seasons, which could either be summer from mid-December to late March or/and the winter breeding season from July to October. Within the commercial sector, seed stock breeders in Zambia keep herds of purebred animals and breed bulls for sale to other farmers.

Cattle genetic improvement in commercial farms is through selecting breeding stock within the same population based on phenotype and pedigree data. Animals selected for breeding either for commercial production or replacement for seedstock breeding are from isolated small and elite breeding populations that were introduced in Zambian history (Mtetwa et al., 1978; Thorpe et al., 1980). Such practice is likely to encourage genetic similarities in animals that possibly may results in inbreeding depression. General herd structure in the commercial sector is well defined and normally made up of 0.075 bull, 0.08 calf, 0.15 replacements, 0.2-culled cow and 0.7 yearling sales per cow, for most large commercial farms. The main expenses are those associated with purchase of acaricides, rentals, taxes and labour.

In the traditional sector, cattle rearing vary significantly from one geographic region to another, but are confined to southern, western, eastern and central provinces (Mwenya, 1993). Communal grazing is largely practiced in environments with high incidences of disease outbreaks and low quality grass. Even though cows run with bulls all year round, the

majority of cows conceive during the summer season and calves are born from September to November when climate is hot and dry, with lesser incidences of parasites.

To improve productivity in the traditional sector, several organisations and government agencies have employed various measures. Non-government organisations (NGOs), such as Heifer International, O'land Lakes and World Vision, are involved in acquisition and introduction of improved cattle breeds to local communities in Zambia (Conway and Shah, 2010). The main common objective is to reduce of poverty for the majority of Zambians who depend on livestock for their livelihood in order for Zambia to reduce extreme poverty and hunger (FAO 2011). The use of introduced breeds to local environments is failing because the introduced breeds are not adaptable to local environments. Local cattle breeds, such as the Angoni, are highly fertile and well adapted to environments with a high prevalence of tick borne diseases and droughts (Walker, 1957; Thorpe et al., 1989; Muuka et al., 2013). Thus, farmers may still prefer traditional breeds compared to the introduced breeds and their crosses. Therefore, there is a need to design specific breeding plans for small-scale farmers.

1.5. Cattle breeds in Zambia

The main Zambian indigenous cattle breeds found in the traditional sector are Angoni, Tonga and Barotse. There are also other breeds, such as Brahman and Boran, reared under this sector. In the commercial sector, temperate breeds reared included Sussex, Hereford, Santa Getrudis and Simmental and tropical breeds (Afrikander, Red Sindi) and a composite breed Bosmara. A few commercial beef cattle farmers keep a local Angoni breed (e.g Lilayi Farm).

1.5.1 Angoni

The Angona group of cattle breeds found in central Africa are known as, Angoni in Zambia while Malawi Zebu in Malawi and Angone in Mozambique, (Walker, 1957; Rege and Tawah, 1999). In Zambia, Angoni cattle are distributed between 9° to 14°S and e 30° to 31°E (Thorpe et al., 1979; Chilonda et al., 1999) and adjoining areas of Malawi between the west and Lake Malawi in the east, spreading southwards reaching north-western Mozambique (Figure 1.5)

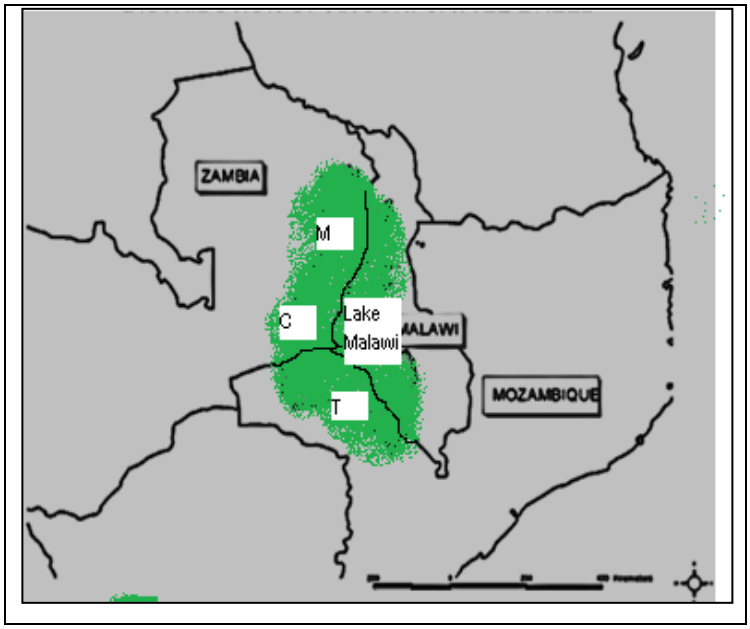


Figure 1 5: Distribution of Angoni cattle in central Africa
M=Mpolokoso, C=Chipata, T=Tete
Source: Adapted and modified from ILRI 2007

In Mozambique, the Angone cattle are distributed in the plateau of Tete and along the coast between Lake Malawi (Butterworth and McNitt, 1983; Hanotte et al., 2000).

The Angoni (Figure 1.7) is the largest Zebu breed among those found in Malawi and Mozambique (Thorpe et al., 1980c; Butterworth and McNitt, 1983). The most distinctive

features of the Angoni cattle are high fertility, resilience to a wide range of diseases and drought with good response to improved management conditions in selecting for beef qualities (Thorpe et al., 1980b). Genetic analysis in east Africa indicates that the frequency of *taurine* alleles is high in Angoni relative to other Zebu breeds (Hanotte et al., 2002). The coat colour of Angoni zebu varies significantly from mainly black with white spots to red, white, and pigmented. Their size varies from medium to large, with heavy bulls weighing up to 730 kg (Thorpe et al., 1980a; Wiener, 1994)

Figure 1.6a. Source: AGTR 2007

Figure 1.6b. Source: AGTR 2007

Figure 1.6c. Boran Cattle. Photo by E. Musimuko

Figure 1.7d: Brahman Cattle. Photoby E. Musimuko

Figure 1 6: Zambian main beef cattle breeds (*Bos taurus indicus*)

1.5.2 Barotse

Barotse cattle (Figure 1.6b) are Sanga type and have been in existence in Zambia since the 1800s (Mason and Maule 1960; Payne and Williamson, 1990). The Barotse breed is distributed in the flood plains of Bulozi and Caprivi in western provinces of Zambia. The Barotse is well adapted to produce beef under the wet conditions of the flood pains. They are large framed with heavy bones and large spreading horns typically lyre shaped. The coat colours are black and brown, but range from fawn to grey and sometimes are mixed with white. Mature bulls and cows can reach on average 630kg and 450kg respectively (Thorpe et al., 1979; Wiener, 1994). These cattle are well adapted to flood plains environments characterised with deep sandy soils and endemic diseases such as contagious bovine pleural pneumonia.

1.5.3 Tonga

The Tonga cattle are short horned Sanga, largely found in the southern region of Zambia between the Kafue and Zambezi rivers near Zimbabwe (Kebede, 1985; Chilonda et al., 1999). The breed resembles the black Mashona breed of Zimbabwe. Their numbers have greatly declined in the last three decades due to indiscriminate crossbreeding that has taken place between the Tonga and the exotic breeds in Zambia. Currently, it is very difficult to find pure Tonga cattle. In the Tonga breed, cattle horns are shorter than the Barotse but longer than in the Angoni cattle. Mature bulls weigh approximately 560kg and cows weigh average 360kg (Walker, 1964; Thorpe et al., 1981)

1.5.4 Boran

Boran zebu (Figure 1.6c) is the largest zebu breed and originated from Kenya. In east Africa, the Boran is mainly distributed in southern Ethiopia and adjacent areas of Kenya and Somalia (Rege et al., 2006; Kassie et al., 2009). These cattle are well adapted to high mountains and drought conditions of east Africa. Boran breed improvement started in the 1920s in Kenya through genetic selection that resulted in a well-adapted improved breed (Anderson, 1949; Mason and Maule 1960). The ranchers bred and selected these animals mainly for beef production in these regions (Lampkin and Lampkin 1960; Rewe et al., 2006). From Kenya, the Boran spread throughout eastern and central Africa including Tanzania, Uganda, the Democratic Republic of Congo and Zambia (Mason and Maule 1960; Mwenya, 1993; Ouma et al., 2007).

Zambia imported Boran cattle during the 1940s to 1950s through Zambia Agricultural Development Limited (Walker, 1964; Mpofu, 2002). Currently, this breed has the largest number of registered cattle according to the Herd Book Society of Zambia. Through an effective breeding program, Australia, the United States, Brazil and Mexico imported Zambian Boran embryos in 1989 (Chilonda et al., 1999; Mwenya, 1993). It has been a popular breed in Zambia.

Boran coat colour ranges from white to fawn and usually the skin is well pigmented. Mature body weight ranges from 255 to 395kg in males and from 250 to 355kg in females but in the improved Boran, mature body weight ranges from 550 to 850kg in males and from 400 to 550kg in females (Payne and Williamson 1990; Rege et al., 2006). The improved Kenyan Boran has similar morphological attributes to other Boran types, but it is typically

characterised by a straight top line and well-developed hindquarters. Usually, the coat colour is white with black spots, but coat colours commonly range from brown to red. Boran cattle are very versatile, and adapt well to various environments.

1.5.5 Brahman

The Brahman (*Bos taurus indicus*) cattle (Figure 1.7d) originated in India, but was improved in USA. In India, Brahman cattle evolved in extreme tropical weather conditions, characterised by high ambient temperatures, shortages of feeds, high incidences of parasites and diseases (Payne and Williamson 1990; Kim et al., 2003). Consequently, Brahman cattle developed outstanding adaptive features, such as short, thick hair coat, black pigmented skin and plenty of loose skin folds with more sweat glands.

In Zambia, Brahman cattle have been useful in crossbreeding with either temperate or tropical breeds, fulfilling unique functions in cattle production systems. Brahman cattle and their crosses have been extremely useful in Zambia where they have demonstrated the ability to withstand hot and adverse weather and tolerate parasites and diseases. In the recent past, Brahman cattle have spread considerably from commercial farms and are widely now found throughout traditional pastoral farms of the Namwala area (Kafue floodplains) in Zambia. Pastoral farmers have preferred Brahman cattle for their growth, size and ability to produce a very satisfactory milk flow in adverse conditions (FAO/EAEA 2011).

1.6 Origin and spread of cattle in Africa

This historical origin and spread of different cattle breeds in Africa is very evident in most in genetic studies. Different cattle breeds act as storehouses of genetic variation that form the basis for genetic improvement through selection, and can be conserves as reserves of genetic

material for future use (Rege and Gibson, 2003). The broad collection of breeds and species that have evolved in various environments, nutritional regimes and management systems certainly represent idiosyncratic sets of genetic diversity (Machado et al., 2010; Rege, 1999). Among the broad collection of these breeds, zebu breeds are the largest single type made up of approximately 75 breeds distributed mainly in eastern, central and southern Africa (Epstein, 1971; Rege, 1999).

Arab traders introduced numerous cattle breeds into the African continent, more notably through the eastern part of Africa (Figure 1.7) (Hanotte et al., 2000; Hanotte et al., 2002). The Borana group are the most recent zebu cattle to be introduced in Africa from Asia and descended from the secondary cattle domestication of *Bos primigenius namadiucus,* approximately 5000 years ago (Mason and Maule 1960; Payne and Williamson 1990). Several studies indicate that zebu cattle evolved from three cattle breeds of Indian Guzera, Nelore and Gir (Hanotte et al., 2006; Rege et al., 1999) and later spread to the east coast of Africa. Genetic evidence strongly supports this theory because of the amount of *zebuline* genes found in cattle along the east coast of Africa and on the island of Madagascar (Hanotte et al., 2002; Dessie, 2011).

The major principal dispersion of zebu cattle perhaps followed the movements of Fulani pastoralists about 2000 years ago (FAO 2007). During their movement, the Fulani pastoralists herded zebu cattle from the east coast towards the central and southern parts of Africa. In the process, zebu cattle were crossbred with the local Sanga breed and ultimately, zebu cattle became the most dominant cattle within the area between latitudes 20°N and 15°S (Epstein and Mason 1984; Hanotte et al., 2002). European farmers settled in southern Africa

and influenced the Fulani pastoralists by crossbreeding their cattle with other *Bos indicus* including Brahman and Afrikander, resulting in composite breeds (Hanotte et al., 2006).

1.6.1 Historical cattle disasters in Africa

Two main cattle disasters occurred in the early 1890s, these were disease outbreaks and cattle seizures. During that period, it is reported that some organisation, together with other foreigners, seized large numbers of cattle from the natives and a few years later, most of the cattle died from rinderpest disease that is characterised by heavy salivation and small blisters (Van Onselen, 1972). The outbreak of rinderpest disease in 1896 killed approximately 95% of African cattle leaving approximately 55 155 cattle in Africa (Barrett and Rossiter, 1999), severely affecting the lives of people and consequently, influencing loss of genetic diversity for certain cattle. Rinderpest disease persisted for almost 45 years in Africa (Plowright 1982). Therefore, the population reduced heavily and severely influenced the cattle current genetic diversity that exists now.

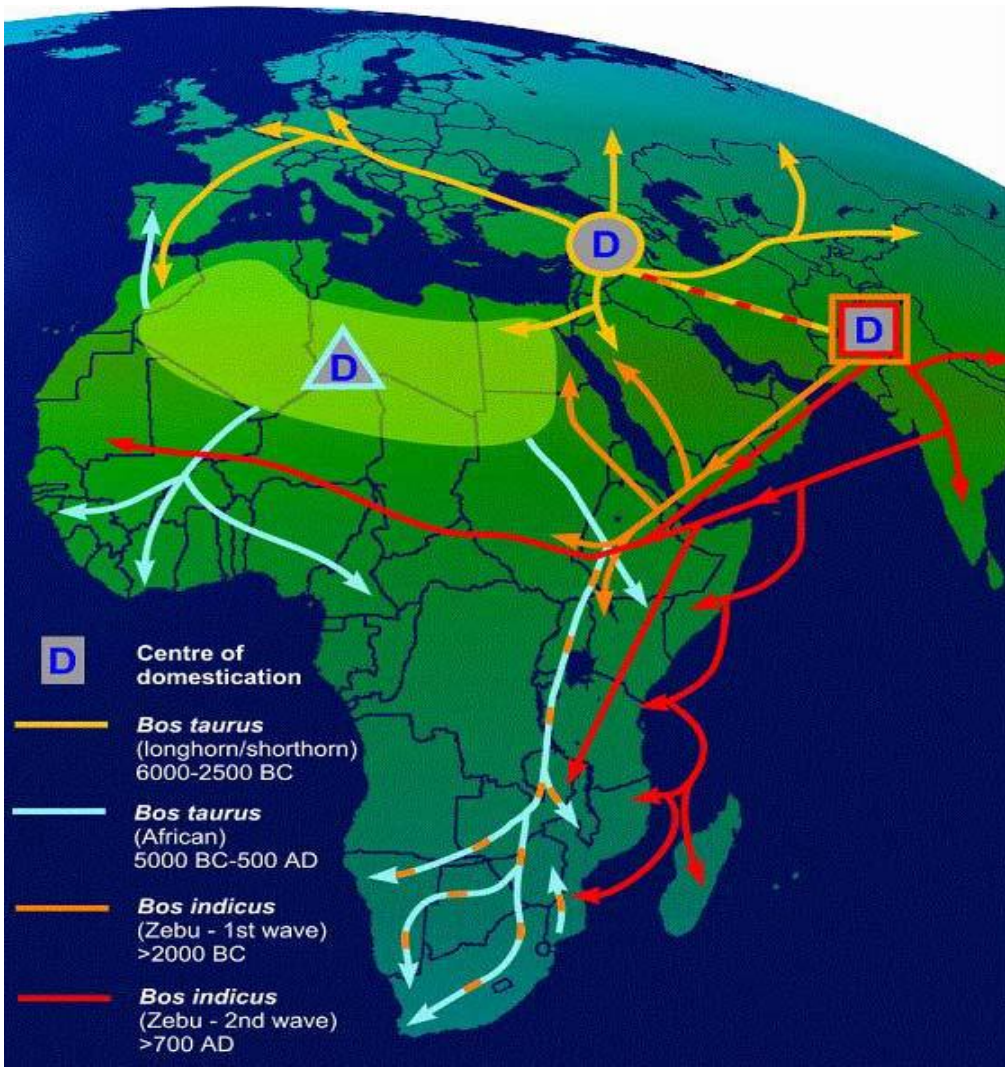


Figure 1 7: Original and migration routes of cattle in Africa
Source: ILRI (2007)

1.6.2 Description of Zebu Cattle

The *Bos taurus indicus* subspecies is differentiated from *Bos taurus taurus* both phenotypically and genetically. Phenotypically, *Bos taurus inidicus* subspecies have a well-defined large thoracic hump and lyre-shaped horns which are absent from *Bos taurus taurus* (Epstein, 1971). Naik (1978) presented an interesting finding in haematological studies, *Bos taurus indicus (*zebu*)* have hemoglobin variants that was not encountered in any of the *Bos taurus taurus* cattle breeds. In addition, the mitochondrial DNA (mtDNA) shows a distinct

genetic difference between *Bos indicus* and *Bos taurus taurus*. *Bos indicus* bulls possess an acrocentric Y-chromosome while the *Bos taurus taurus* bulls have a sub-metacentric Y-chromosome (Hiendleder et al., 2005). This study on chromosomal difference in bulls helps to clarify the controversy surrounding the evolution of cattle, and supports the evolution theory of their independent origin.

Bos taurus indicus (zebu) cattle seem essentially to be one of the cattle types that have positively prospered under these tropical hash environments. These cattle have evolved so that their physiology, behaviour and genetic constitutions have modified that make them more adaptable to environments characterised with high incidences of drought, disease and parasites (Franklin, 1986; Baker and Rege, 1994; Bishop, 2012). They have well adapted body temperature regulating mechanisms both at the physiological and cellular level, such as having more sweat glands and hair follicles (Bradley et al., 1997; Cardellino and Boyazoglu, 2009). Hence, these animals may require less body water for their metabolism (Rege, 1999, Nicholas, 2005). They are hardy and capable of moving long distances in search of food and water because they possess hard hooves, lighter bones and short hair that allow them to tolerate long journeys (Loftus et al., 1994). Because of these unique adaptive attributes in zebu cattle, pastoralists have spread zebu cattle to other drier agro-ecological counties of east and central Africa.

Adaption is a process brought about by the development of various genotypes over many years. For example, the N'Dama cattle and Red Massai sheep in Kenya have almost developed resistance to nematode parasites (Bishop and Woolliams, 2004; Bishop, 2012). Angoni and Boran breeds of cattle have also adapted to local environments over time by

developing small mature body sizes possibly in response to different environmental conditions of various regions and management systems (Epstein, 1971; Thorpe et al., 1979; Hall and Bradley, 1995). In Zambia, the Angoni is larger than Mozambique Angoni (Epstein 1971; Thorpe et al., 1980) and Boran cows from Kenya are capable of reaching over 500kg mature weight, compared to about 350 kg for the Boran cow in Somalia (Payne and Williamson 1990), regardless of their similar evolutionary origins (Rege and Tawah, 1999) (Table 1.3)

Table 1. 2: Different body weight and sizes for African zebu cattle

Group or breed	Birth weight (kg)		Mature body weight (kg)		Wither height at maturity (cm)	
	Male	Female	Male	Female	Male	Female
Ethiopian/Kenya Boran	25	23	300–385	300–350	118–147	115–127
Karamajong	–	–	320–490	300–410	–	–
Abyssinian Shorthorned Zebu	–	–	250–350	200–280	113–117	107–113
Kenana	24	22	400–610	300–435	132–148	123–139
Nkedi	19	18	240–450	270–325	102–121	99–107
Tanganyika Shorthorn	–	–	200–350	180–250	109–119	104–114
Angoni	154	112	270-450	270-350	122-127	112-120
Ethiopian/Kenya Boran	25	23	300–385	300–350	118–147	115–127

Sources: Adopted and modified from Rege and Tawah (1999) and Zulu 2008

1 7 Designing breeding objectives for Zambian cattle farmers

Management and maintenance of genetically improved cattle genotypes requires complex decisions making processes. The complex decision making process would be easier to make if comprehensive information on the economic importance of cattle genotypes, preferred traits, specific utility and production systems is readily available and accessible (Ouma et al., 2007; Scholtz et al., 2011; Byrne et al., 2012). For example, in France (Phacos et al., 1998)

and Developing country animal breeding programs for specific economic traits in well-defined production systems with commonly recognised and clearly demarcated units of stable genetic improvement is easier (Ponzoni and Newman, 1989; Smith, 1988; Ouma et al., 2007). However, in the Sub-Sahara regions, cattle have multiple important functions in the livelihood of rural people where value is rooted in traits that are not economically valued per dollar (Drucker et al., 2001; Rege and Gibson, 2003; Pitchford, 2007). Consequently, this makes it difficult to define clear breeding objectives. For example, it is difficult to define a breeding objective for traditional traits in livestock as animals are considered as a breed and not as a trait (Moyo, 1996; Tano et al., 2003; Desta et al., 2011).

While, in most developing countries attempts have been made to improve cattle productivity through genetic improvement, this has been limited to concentrating on one trait that can easily be measured, such as carcase yield or milk production, in isolation from the broader systems for indigenous breeds (Pitchford 2007; Eggen 2012). Besides, adequate methodologies for determining the extent of contribution of cattle genetic resources to cattle value are almost completely lacking in most developing countries (Scarpa et al., 2007; Kosgey et al., 2008; Rewe et al., 2009). Subsequently, there is an urgent need to ascertain the tangible value of cattle genetic resources in developing nations in order to implement appropriate cattle genetic improvement and conservation programs.

To ascertain the actual value of cattle genetic resources, traits related to traction, manure, forms of investment, prestige, dowry payment and use in traditional ceremonies should be included (Steele, 1981; Anderson, 2003). Fundamentally, it is important to realise that in traditional cattle production systems, yield stability is viewed to be more vital than yield itself and attributes associated with disease resistance, drought tolerance and longevity,

which are key, are not normally considered. Therefore, attempts to manage and improve animal genetic resources should consider this combination of complex attributes of cattle and the diverse environments where cattle are likely to be raised to produce the yield itself.

Farmers with very low income can manage to maintain genetically improved livestock accompanied with improved husbandry practices. FARM Africa's Meru project in Kenya provides an example of an all-inclusive, flexible and sustainable crossbreeding program. Okeyo, (1997) and Ahuya et al., (2005) reported on the success of one community-based and all-inclusive dairy goat breeding program in a low-input smallholder system in Kenya. The successful breeding program involved crossbreeding between local goats breeds called Galla and East African goats with British goats breed (Toggenburg). Apparently, local communities were finding it difficult to maintain the local breeds on their small pieces of land and famers opted to shift from goat production to other sources of income. Based on previous introductions of goats in the east highlands of Kenya, the Toggenburg dairy goat breed has proved to have potential to adapt the local environment. Consequently, 62 male Toggenburg were imported and started crossbred with 68 selected local goat dams in Kenya. These exotic dairy goats were selected to improve milk production while the local goats provided traits that were more adaptable to bearing offspring.

Duguma et al., (2011) and Ahuya et al., (2005) demonstrate that implementation of the program adopted an all-inclusive approach, and was participatory in formulation of plans and all supporting mechanisms. This project also linked farmers in the production chain, government institutions, research stations and marketing institutions. To maintain and monitor genetic progress, mating was done at the breeder association station that helped to

register individual goats with the Kenyan herd book society (Ahuya et al., 2005; Okeyo, 1997). Therefore, by adopting such an approach, Zambian small-scale farmers may improve their cattle in selected regions.

1.8 Use of Molecular Markers in Genomic Studies

Historically, the practice of conventional phenotypic characterisation for breeding programs has been effective. However, improvement in some traits has been very slow because of limited records for measuring traits (Dekkers and Werf, 2007; Davis et al., 2009; Calus, 2010). Numerous molecular DNA markers together with bioinformatic tools have had a complementary effect to phenotypic characterisation of livestock (Lasley 1987; Lande and Thompson 1990; Young 1999). Molecular DNA markers are identifiable DNA sequences, found at specific sites of the genome presented as different detectable variants (Dekkers 2004; Toro et al., 2009). They rely on DNA assays to determine the genotype of the markers, and the assays vary because of different types of molecular markers exist (Malau-Aduli et al., 2000; Meuwissen and Goddard, 2000). Molecular DNA markers, however, are not genes, as they usually do not have any biological effect (Hayes and Goddard 2001; Pryce et al., 2010), but instead, they act as landmarks in the genome (Hayes et al., 2003; Olsen et al., 2010). These tools have potential to measure genetic diversity within populations and partition total genetic diversity into subpopulations as well as assess ancestral linkages and gene flow (Bradley et al., 1997; Cunningham et al., 2001; Falush et al., 2007).

1.8.1 Allozymes and Restriction Fragment Length Polymorphisms

Allozymes were the first markers used to analyse DNA sequencing in livestock (Cunningham et al., 2001; Grapes et al., 2004). Allozymes are gene-coding protein

polymorphisms that provide a low number of loci that can be assayed (Honda et al., 2009; Goddard and Hayes 2009). Restriction Fragment Length Polymorphisms (RFLPs), Random Amplified Polymorphic DNA (RAPDs) and Amplified Fragment Length Polymorphisms (AFLPs) were developed (Gwakisa et al., 1994; Hocquette et al., 2007). The AFLPs are dominant biallelic markers that are easy to use, but these types of markers may not be very informative in analysing between breeds variation. DNA markers, such as RAPDs and AFLPs are not frequently used unless their use is essential for answering a specific question. The RAPD-PCR method to estimate genetic diversity and relatedness has several problems. The results obtained usually have low reproducibility (Kios et al., 2012). Solberg et al., (2008) demonstrated that it is problematic to distinguish between heterozygotes from homozygote RAPD alleles, thus, marker genotypes can be ambiguous and their techniques require relatively large amounts of DNA also the protocols are technically challenging.

1.8.2 Single-Nucleotide Polymorphisms

Single-nucleotide polymorphisms (SNPs) are single base changes that occur abundantly within the genome of a specific species (Malau-Aduli et al., 2000; Fernandez and Toro 2006). SNPs usually occur throughout the genome but are less common within coding regions of genes and therefore, are usually neutral variants (VanRaden et al., 2009; Toro et al., 2011). There are various methods for assaying SNPs, and these include low-density and high-density genomic screens with bead or chip arrays to obtain the certain genotypes of that breed (Young 1999; Habier et al., 2010).

SNPs are comparatively preferred because datasets from other sources can be integrated without much ambiguity with a large of number of SNPs (Chen et al., 2007; Liu et al., 2009),

and there is unprecedented accuracy in the description of individual and breed relationships (Leland et al., 2008; Afolayan et al., 2009). These characteristics may allow the generated genomic information from SNPs to predict of breeding values within and possibly even across breeds in populations that lack adequate records. Some of the SNPs are monomorphic and species specific, but loci that are polymorphic only in one species are likely to be excluded from the panel. In addition, the SNPs in commercial panels have been selected to have high minor-allele frequency (MAF) and, consequently, greater variability in the international transboundary breeds, without considering variability in other breeds. As a consequence, diversity in the other breeds, including those located close to the domestication centres, can be underestimated and estimates of relationships among breeds can be distorted (FAO 2007). However, the current high cost of the high-density assays such as 50K and 800K SNP at US$100 and $300, respectively, usually prohibit the use of these type of markers in DNA analysis, and equipment for analysis high-throughput SNP panels is also quite expensive.

1.8.3 Microsatellite Markers

Microsatellite markers are simple sequence repeats (SSRs) or short tandem repeats (STRs), and have been a choice in most studies on genetic diversity (Freeman et al., 2006; MacHugh 1998; Marletta et al., 2006; Groeneveld et al., 2010). These repeats vary in length and tend to occur in non-coding DNA in the intragenic sequence or in the introns (Gomez-Ramano et al., 2013). The degree of polymorphism in microsatellites is high, because of high mutation rate and consequently, provides an important tool for studying genetic variation within and across breeds (Hocquette et al., 2005; FAO 2011).

In the past two decades, microsatellites quickly became important markers for most genome studies to evaluate evolutionary theories (Hiendleder et al., 2005; Maillard et al., 2008), degree of relatedness of individuals or groups (Pritchard et al., 2000; Mao et al., 2008), parentage identification and inbreeding levels (Meuwissen and Goddard 2001). Using bioinformatic tools, such as GenAIEx v 6.5 (Peakall and Smouse 2012) and Structure v 2.3 (Pritchard et al., 2000) microsatellite genotype data has proven to be valuable in estimating genetic diversity, allelic richness, genetic distances and population bottlenecks. The effective population size (Ne), directionality of gene flow (Nm) between and within populations can be determined in any population (Nei, 1972; Wright, 1978). Barendse et al., (1997) and Pritchard et al., (2000) have demonstrated the use of microsatellite data in phylogenetic studies that seek to explain the concordant biogeographic and genetic histories in many animal species. Despite the extensive use of microsatellite over the years, there are some considerations to take into account because of the high mutation rates:

- Primers for these markers are more specific to certain taxa meaning that primers suitable for *Bos taurus taurus* species may not be suitable for *Bos taurus indicus* species (FAO 2006) despite being sub-species.
- High rates of mutation also cause primers to exhibit homoplasy making it difficult to assume whether two alleles are identical in state or are identical by ancestry (Dekkers and Werf, 2007).
- In addition, allele calling has poor reliability across laboratories and integration of data can thus be problematic (FAO 2011).

Many existing datasets for animal genetic resources studies worldwide that have used microsatellite DNA markers particularly for cattle, sheep and goats are those recommended by ISAG–FAO Advisory Group on Animal Genetic Diversity.

1.8.4 Application of Microsatellites in Genomic Studies in Africa

The current analysis based on FAO's Global Databank for Animal Genetic Resources for Food and Agriculture shows Africa has 154 cattle breeds (FAO 2011). In Africa, few studies to assess the variation in the genotypes of these putative breeds have been conducted (Gwakisa et al., 1994; Mwacharo et al., 2006; Hassen et al., 2007). Most livestock breeds in Africa, including Zambia, are classified based on historical, anthropological and morphological evidence (Rege and Lipner, 1992; Zulu, 2008). However, most often, these methods do not give enough information for embarking on genetic conservation in livestock. In Kenya, evidence indicates that there is wide genetic variation within and between breeds in the east African Zebu (Rege, 1999; Gibson et al., 2006; Zerabruk et al., 2012). This is probably due to the development of new molecular techniques and bioinformatic platforms that have led to an increase focus on the genetic characterisation of domestic breeds using various types of genotyping markers (Hayes et al., 2003). These methods have widely been used to determine not only genetic diversity in cattle as well as other species, but to also help understand relationships between population structure, genotype background and environment using mixed model analyses.

Mao et al., (2008) demonstrated the use of 12 pairs of microsatellites in measuring genetic diversity in different indigenous cattle populations. Numerous parameters were obtained and results showed there was low heterozygosity in *Bos taurus* breeds. In European cattle, breeds

from France, Spain and Portugal have more genetic diversity (Canon et al., 2001) relative to cattle breeds from the British Isles (MacHugh et al., 1998). Studies assessing genetic diversity in Zebu cattle have been conducted in India (Sodhi et al., 2005) and Ethiopia (Ibeagha-Awemu and Erhardt, 2004: Zerabruk et al., 2011) demonstrate the reliability of ISAG-FAO recommended microsatellites DNA markers because results obtained were in agreement regardless of different areas where the study was conducted.

To date, studies carried out to evaluate genetic diversity within the 150 the African indigenous cattle breeds indicate that genetic diversity is reasonably high among livestock populations (FAO 2010). However, in the past decade there have been concerns about current breed status because of large use of exotic breeds. Approximately 35% are seemly classified as at risk of extiction and 22% became extinct 100 years ago (Rege and Tawah 1999) (see Figure 1.8) in Africa where there are approximately 200 million head of cattle (FAO 2007b).

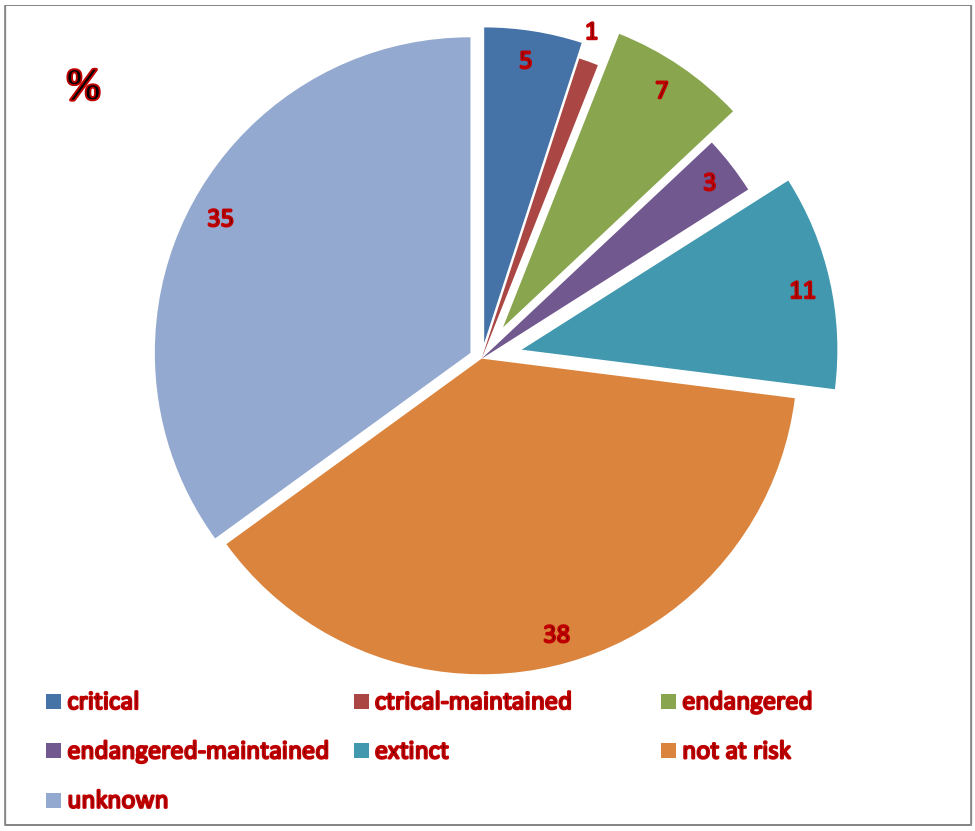


Figure 1 8: Status of world mammalian breeds
Source: FAO 2006b

1.8.5 Major Causes of Gene Erosion in Cattle

There are several drivers that persistently encourage loss of cattle genetic diversity in Sub-Sahara Africa and worldwide. There has been increasing evidence indicating that unsystematic crossbreeding between exotic breeds and indigenous breeds, breed substitution and poor management of animal genetic resources are among the significant causes of animal genetic erosion in African cattle (Hall and Ruane, 1993; Hanotte et al., 2002; Simianer et al., 2003). Misguided and uncontrolled introduction of new breeds occurs because uncoordinated breeding programs are designed without involving interested candidates in the cattle production chain and this usually results in loss of genetic diversity especially in developing countries (Reist-Marti et al., 2003; Caballero, 2009). The rapid changes in production

systems and consumer preferences usually exacerbate the introduction of exotic breeds to rapidly improve cattle productivity to meet the increased livestock demand because of the increased interactions between social and economic factors. The effects are devastating, especially in extreme scenarios, and can lead to some breeds becoming extinct (Cardellino, 2009). However, the most significant threat to animal genetic diversity in the developing world is likely the usual use of uncontrolled importation of high performing animals from developed countries through semen or embryos driven by well-developed communication and transportation systems (Moore and Hansen, 2003; Tisdell, 2003; Ibeagha-Awemu and Erhardt, 2004; Goddard et al., 2011).

In the recent past, greater economic globalisation has encouraged regional specialisation in a single product such as the production of genetic material (semen or embryos) at the farm level which may contribute of loss genetic diversity as companies promote government programs of transboundary breed improvement for t profit (Tisdell, 2003). Improved exotic germplasm have proven attractive to breeders as well as government policy makers and this encourages easy replacement of local breeds even though these local breeds have evolved within their environments (Bishop, 2012; Burrow, 2012). For example, in Zambia, government-breeding schemes adopted a restocking program that aimed at improving livelihood of small-scale farmers by replacing local breeds with an improved Friesian dairy breed (Jayne et al., 2007). However, this program has failed because the cattle breed was not adapted to local environments, characterised by incidences of parasites, disease, drought and poor nutrition (Rege and Gibson, 2003; Delgado et al., 2011).

The persistence of introducing exotic breeds that threatens the loss of genotype adapted to local environments has become a matter of urgency in developing countries to assess and

find ways of conserving the well-adapted local genotypes (Notter, 1999; Rege and Gibson, 2003; Araya et al., 2010). Steinfeld et al. (2006) and Thornton (2011) demonstrated that the conserved local genotypes could act as gene bank, a resource for original genes that can allow continued genetic improvement in cattle. These locally adapted cattle may be useful in the future because of ever-changing environments accelerated by climate change (Reist-Marti et al., 2003; Toro et al., 2006). It is due to this background that a great deal of research is being conducted to take stock of unique genotypes that can be conserved, especially in developing countries.

1.9 Estimation of genetic parameters for production traits

Livestock genetic improvement is a process of positive change that involves careful planning. The planning should take into account the socio-economic factors, markets, production environments and genetic response (breeding value) for the traits of interest so that improvement can bring positive benefits to the owners of the animals, community and the nation (Okeyo, 2007; Kosgey, 2010). There have been several methods of improving livestock and one is through the estimation of breeding values (EBVs) for production traits (Ponzoni and Newman, 1989). Henderson (1973) developed the first mixed model of methodology the best linear unbiased prediction (BLUP) based on an animal model to predict expected genetic progress production traits. Falconer, (1989) and Bijma, (2006) identified BLUP as a powerful statistical procedure that can separate additive genetic variance, maternal genetic variance, environmental effects and covariance components that provides means and fixed effects for breeding values. The weakness of BLUP procedure is that it requires initial knowledge of the heritability estimates of a particular trait (Henderson, 1975).

Numerous studies have used BLUP procedures to achieve enhanced productivity, usually achieved by measuring genetic parameters of economic traits such as growth (Meyer and Hill, 1997; Pico et al., 2004; Wasike et al., 2009; Praharani, 2009). However, choice of the appropriate genetic quantitative model to be used in assessing genetic parameters for both direct and maternal effects is critical and must be accurate and take into account other biological effects involved.

Several methods to estimate variance components and genetic parameters in beef cattle have been studied extensively (Willhan, 1972; Meyer et al., 1997; Karlsen et al., 2000; Roughsedge et al., 2005; Thompson, 2008). In any appropriate animal model used in determining genetic variance, analysis of livestock must split the completely phenotypic variance into separate components like direct genetic effect, maternal genetic effect and environmental effects (Meyer and Hill, 1997; de Albuquerque 2001; Gilmour et al., 2000; Wasike 2006). As a result, recently different animal models have been developed, such as individual animal model, animal maternal model or breed-animals used to predict the genetic parameters for production traits (Pico et al., 2004; Bijma, 2006; Wasike et al., 2006; Assani, 2012).

For a large and complicated data set, that is not only complicated, but time consuming and may require extended multiple trait analyses, computer programs have been developed to simplify the procedure. Henderson (1975) use restricted maximum likelihood (REML) to predict breeding values. One of the main advantages of this program is that it uses a multiple trait analysis matrix to obtain more than one observed genetic variance component for a trait and trait correlation factor between direct and maternal effects (Demeke et al., 2004, Wasike et al., 2009; Davison et al., 2009; Gilmour et al., 2009; Raphaka and Dzama, 2010).

Studies conducted using the REML program reported that multi-trait analyses are more accurate and can eliminate bias caused by culling animals based on weaning and yearling weight only (Ducrocq, 1994). Raphaka and Dzama (2010) estimated genetic parameters for production traits of indigenous breeds in Botswana and reported similar results to studies on Kenyan Boran cattle using similar animal models (Wasike et al., 2006). Gutiérrez et al., (2007) and Pico et al., (2004) used REML models also to measure genetic parameters for production traits cattle, and both generated appropriate models that estimated the genetic parameters for production traits to use in predicting the genetic response in selection programs. Since, most beef cattle producers prefer growth as an economical value trait in their selection programs in developing and developed countries (Kahi et al., 2006; Haile et al., 2009). Therefore, correct prediction of the genetic value of beef cattle at weaning will significantly optimise fast genetic progress and is essential for designing sound genetic livestock improvement programs.

1.10 Research Project Aims and Objectives

The aim of the research herein was to establish which cattle traits are preferred by Zambian small cattle farmers whose livelihoods depend on livestock. Using this information, the aim was to develop all-inclusive, flexible and sustainable breeding objectives for cattle genetic improvement and conservation. In designing appropriate genetic improvement and conservation programs, an in-depth knowledge of genetic variation that exists within cattle populations is required to effectively implement genetic selection. Therefore, the aim of this work was also to assess the genetic diversity, population structure and relatedness of Zambian local cattle breeds.

A feasible method of improving cattle productivity is by selection of production traits based on individual performance data and knowledge of genetic parameters for the specific traits of interest. It has been difficult to ascertain genetic response without this information. Hence, another research aim was to estimate the genetic parameters for production traits in beef cattle based on two cattle breeds reared under similar management systems.

The research outcomes will identify Zambian small-scale cattle farmers from different region the perceived preferred cattle traits, such as growth, size, adaptation, traction and fertility. Furthermore, the research will unveil genetic variation is present among Zambian local cattle breeds and also identify unique genetic diversity and bottlenecks that needs to considered in designing cattle genetic improvement and conservation programs in Zambia. The research will provide information on utilisation of current production performance data obtained from commercial beef cattle breeders to determine the rate of genetic gain in Zambian cattle

This research hypothesises that Zambian small-scale cattle farmers from different regions have specific preferences to cattle traits, such as growth, size, adaptation, traction and fertility because of the differences in agriculture systems that exists among the studied regions. Moreover, genetic diversity present among Zambian local cattle breeds is expected to vary because of genetic introductions, diseases and poor management of genetic resources in Zambia and high inbreeding levels. The final hypothesis is that information on the current production performance data obtained from commercial beef cattle breeders under similar production systems will provide adequate information to help assess genetic parameters for production traits in order to determine the rate of genetic gain in Zambian cattle

This project will help develop genetic selection strategies that take into account farmer's interest in cattle traits that will improve genetic gain in established breeding programs, assess

the cattle genetic diversity among and within the populations of Zambian cattle. This will help introduce cattle breeding programs that can increase local productivity and conserve well-adapted local cattle genotypes in Zambia. Finally, this study will guarantee processes towards the design of suitable, flexible and comprehensive demand driven cattle improvement programs that will benefit most cattle breeders, policy makers, cattle owners, researchers and non–governmental organisations in Zambia. This research is important also in adding to the existing body of knowledge and it is a stem for acquiring new animal breeding and genetic knowledge. Above all, it is a basis of founding and connecting to various animal breeding and genetic associations and professions (such as ISAG, AAABG, ICMJ, ASGGN).

Chapter 2

2.0 Understanding Diverse Preferences for Cattle Attributes.

2.1 Introduction

Breeding programs that lead to genetic improvement require an approach that is supported by producers if it is to increase cattle productivity in Zambia. However, current genetic improvement programs rely mostly upon introduced cattle breeds, which require expensive nutritional, disease and parasite management systems. The primary objective of livestock improvement in Zambia is to reduce poverty and increase productivity. This is not simple as introduced breeds with greater growth and muscle are less adapted to the harsh local environments, resulting in high mortality rates (Demplfle 1992; Mwenya, 1993; Burrow, 2012). Indigenous cattle breeds, such as the Angoni, have proved to be more reproductively reliable than exotic breeds despite been subjected to unfavourable conditions, characterised by a high prevalence of tick-borne diseases and long periods of drought (Walker, 1964; Thorpe et al.,1980a; Wiener, 1994). Therefore, local cattle farmers are reluctant to adopt exotic cattle breeds into their production systems.

Although, indigenous cattle breeds may be less productive than exotic breeds or cross breeds in terms of yield, local breeds have been shown to be superior where there is high incidence of disease and low quality pasture (Lwago et al., 2010) Cattle farmers preferred attributes are often those that guarantee multi-functionality, flexibility and resilience in order to deal with the variable environmental conditions (Okeyo, 1997; Rege et al., 2001; Byrne et al., 2012). Davis (1993) showed that Zebu breeds in the Australian Northern Territories where there are

high ambient temperatures, poor feed quality and high parasite and disease incidence were superior to *Bos taurus taurus* breeds, in terms of production and reproduction. Studies in Zimbabwe (Moyo 1996; Assan, 2012) and Zambia (Walker, 1964; Thorpe et al., 1980) have demonstrated indigenous cattle are more productive in terms of cow-calf unit than the exotic breeds and their crosses in local environment conditions.

Cattle, like any other goods and services, have different utilities. The stated preference analysis theory developed by Lancaster (1966) postulates that preferences for goods and services are a function of traits or characteristics possessed by the particular goods and services, rather than goods *per se* (Hensher, 1994; Hensher and Greene et al., 2003). For cattle farmers, their preference for cattle breeds are based on the utility they perceive to result from various cattle traits (Scarpa et al., 2003; Tano et al., 2003). In Zambia, studies to ascertain the importance of cattle for small-scale farmers and to identify the general constraints in cattle have been conducted (Mwenya, 1993; Moll et al., 2007; Zulu, 2008). However, no study has been conducted to determine the most preferred traits among small-scale cattle farmers and to understand the management constraints associated with disease control with the goal of developing appropriate breeding goals for the specific regions (Olesen et al., 2000).

Aims and Objectives of the Study

The aim of this research was to gather information that could guide development of breeding objectives for Zambian small-scale cattle farmers within the existing national livestock development plan. To achieve this aim, two objectives were set:

1) Evaluate the cattle traits that are perceived most important; and

2) To identify major production management practices amongst the small-scale cattle farmers in the agricultural diverse production areas.

2.2 Materials and Methods

Fieldwork included collection of qualitative data consisting of in-depth interviews with open-ended and neutral questions including general questions about farming and breeding practices in the various locations (Appendix 2.3). The sites of interviews were variable suiting the farmers (household or a group) and included participation in traditional ceremonies, homes, dipping sites and schools. The groups ranged from 5 to 10 individuals while at the family level was a wife and husband. Three main local languages were used Tonga, Nyanja and Tumbuka in addition to English, the Zambian official language, and notes were taken in English.

2.2.1 Study Areas

The study was conducted in three districts in Zambia, namely Namwala, Chipata and Lundazi, each with different cattle management systems (Figure 2.1). The history of livestock farming systems was a criterion used to select these districts. The indigenous people of these areas belong to the Bailla ethnic group in Namwala who are the pastoralists, and the Ngoni ethnic group (Chipata and Lundazi) who practice mixed agriculture. However, there is an increasing migration of people from other ethnic groups to these areas. Namwala district is located on the Kafue flood plains and has a permanent river water supply. This district receives between 600 to 800mm of annual rain and land is covered by shallow eroded sand soils and does not support much crop production. The Chipata and Lundazi districts are

located in the Eastern Province of Zambia and receive rainfall approximately between 800mm to 1000mm annually (Conway and Shah, 2010).

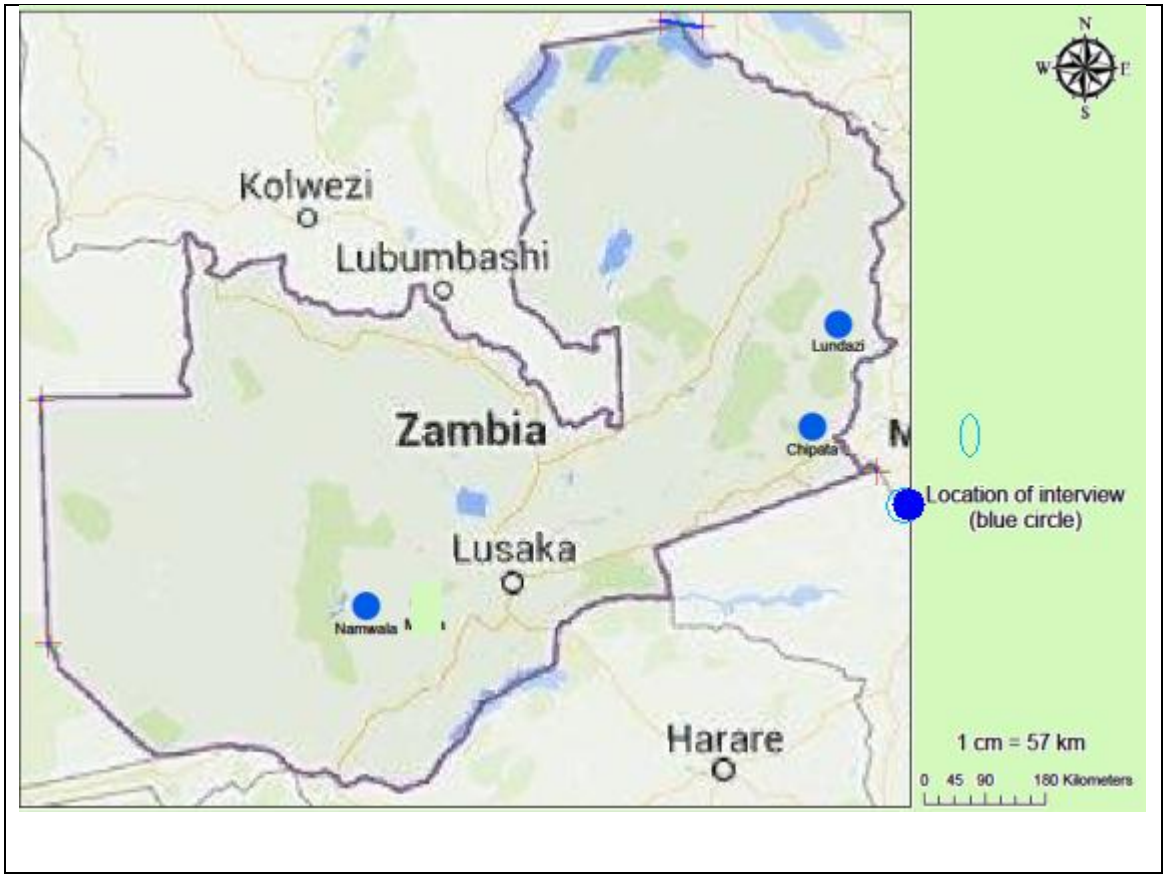


Figure 2.1 Map of study sites in Zambia where small-scale farmers were interviewed conducted.
Source: <https://maps.google.com.au>

2.2.2 Collection of Data

The data was collected between September 2012 and December 2013 in the surveyed areas using a modified SADC/UNDP/FAO questionnaire for management of farm animal genetic resources in the Southern Africa Development Coordinating (SADC) regions (Appendix 2.1). To ensure that ethical principles and values prevailed, an approval to conduct the research was obtained from The University of Adelaide Human Research Ethics Committee

(Project number 2012-121) and a statement of informed participation consent sheet (Appendix 2.2), was designed according to protocols of Walter (2006). The methods used followed the protocols described by Patton (1990), and studies conducted by Ruto (2005) and design of the questionnaires adopted the protocols of Barriball and While (1994).

All households in the study areas were purposefully chosen in consultation with livestock extension officers for the particular regions to address the research question, considering time, participant's willingness to be interviewed and the available resources (Patton 1990). Trust to acquire credible information necessary for validation of information was developed through engaging the participants in the research topic and appreciating their time and efforts. Despite the limitation of time and resources, the sampled groups provided valid and meaningful information that generated an insight into cattle husbandry. A total number of 270 questionnaires were distributed and 75 were returned (Table 2.1). The low number of questionnaires return was due to most farmers' failure to respond to required questions and some famers did not understand the questions due to low literature levels.

The interviews focused on cattle traits that small-scale farmers' deem as important in contributing to their social and economic value. Additional topics associated with the overall social and economic use of cattle in the three regions were also explored during the interviews including cattle management and persons in charge of cattle decision making, use of cattle, process of animal selection, animal health management, feeding and reproductive rate, breed choice and farmers future plans. The in-depth interviews combined audio recording and note taking. A total number of 11 households were interviewed in detail and their interview recorded in various districts. The low number selected was due to large similarities of farming activities and short period during the study period. However, this was

necessary to allow for capturing of data that may have been missed during note taking, and permitted systematic comparison of interviewee responses about particular traits perceived as important (Appendix 2.3).

Table 2.1: Number of questionnaires distributed in the study sites and category of farmers

	Number					
Regions	Questionnaires distributed	Qualitative[2] total	Quantitative[1] total	Rich*	Medium*	Emerging*
Namwala	100	4	29	15	12	2
Chipata	100	3	31	8	11	12
Lundazi	70	4	15	2	8	5
Total	**270**	**11**	**75**	25	31	19

Quantitative1 method focused on numbers and frequencies, Qualitative2 method collecting data concerned with describing meaning, rather than with drawing statistical inferences, Large having cattle more than 100 cattle, Medium having cattle between 50-100, Emerging having cattle between 0-50 in Namwala districts. * In Chipata and Lundazi, Large describing farmers who own cattle above 50, Medium 10- 50 and Emerging less than 10.

To increase the accuracy of data collection, eleven cattle farmers were interviewed with their interviews voice recorded; this provided detailed and rich information to help answer the research question. All participants received a participation sheet. The interviews took approximately 30-45 minutes per household. Some interviews were conducted as a group discussion or family conversation depending on how many farmers were willing to be surveyed. For example in Namwala a famer preferred in to be interviewed at his home (Figures 2.2a) and a group of farmers supported by World Vision Zambia preferred to be interviewed at cattle dipping facility (Figure 2.2b). In three instances during the interviews, it was difficult to have a full record of interviews because of malfunction of the tape caused by

wrong settings or low battery. However, on most occasions, it was helpful to capture some of the information that was not recorded by note taking.

2.2.3 Interview Transcription and Data Coding

The verbatim transcription of interviews was combined with written field notes taken during interviews and soon after to ensure accurate interpretation. Using a tape recorder, interviews were tape recorded and transcribed in full. Both transcripts and field notes obtained during interviews were kept in their primary form for analysis to avoid the risk of losing important information from the data. The data were analysed using a content analysis approach according to protocols of Patton (1990), and Barriball and While (1994).

Data for each interview was carefully checked for its consistency on a particular subject, finding common messages, or contrasting information coming out for a particular trait. Cattle farmers interviewed represented all the different farming systems in three regions classified depending on the number of cattle herd as large, medium and emerging farmers based on regions.

The primary quantitative data was grouped by ranking of the importance of five traits. The traits ranked were fertility (frequency of calving, age at first birth), adaptability (ability to resist weight loss during dry season, ability to walk long distances, ability to resist disease, frequency of treatment), size (body length, frame at slaughter), growth (time in years to reach maturity), and traction (ability to work, docility). The five traits were classified according to a scale with the most important trait being 5, and the least important trait being 1. The respondents were coded as (P01/01...33) for Namwala, (P02/01…34) for Chipata and (P03/01…..19) for Lundazi.

Figure 2.2a:

2.2b:

Figure 2.2: Some participants in the study from Namwala and Chipata. 2.2a= large farmer (P01/04) in Namwala district of Zambia and 2.2b= A group of emerging and medium cattle farmers in Chipata.

2.3 Data Analysis

Descriptive, frequency counts, frequencies and inferential statistics were analysed. The research hypothesis is that there are differences in the preferred most important traits between category of small-scale farmers and between regions. Both parametric and non-parametric test were used to determine if there were differences in most important traits between regions. A linear model containing fixed effects of region and category of famers large, medium and emerging were determined to predict differences in the preferences for the five important traits size, adaptability, growth, traction and fertility using ASREML (Gilmour et al., 2009).

2.4 Results and Discussion

2.4.1 Capturing information

The process of conducting interviews was challenging and required at times translation of questions from English to the local language while taking notes in English. while Patton (1990) described taking verbatim notes during the interview as a strategy for demonstrating credibility in qualitative research, the effectiveness of note taking decreases as the length of the interview increases. Consequently, Bryman (2007) acknowledged that audio recording is important for social surveys

On average, three interviews were conducted per day. More time was spent with Namwala farmers because one of the chiefs was very interested in the program and invited the author to attend the *Shimunenga* ceremony of the Ba-Illa people in which most cattle are displayed. The traditional ceremony is held on the Kafue Flats in Namwala district of Southern

Province. The ceremony expresses the people's devotion to their divine ancestors to pay respects to their ancestors at the shrine and culminates in the showing of cattle wealth (http://www.lusakatimes.com/2010/09/22). During the ceremony more information was captured and understood the important cultural value indigenous cattle play in the local community's livelihood. Based on this secondary source of information, data on the value of crops produced using traction were collected. This was important to quantify the approximate value of cattle traction as a trait in order to design appropriate breeding programs for each region.

2.4.2 General Management of Cattle

Source of Cattle and Primary Reasons for Keeping Cattle

In all three study areas, Namwala, Chipata and Lundazi districts, about 45% of farmers keep livestock and cattle are more important than any other livestock in Zambia (pigs, goats, chickens) because cattle is more associated with their livelihood (Mtewa, 1978; Thorpe et al., 1989; Chilonda et al., 1999; Mulemba, 2009). Sources of cattle are either through inheritance, purchased as investments in cattle business or sharing through traditional practices, such as dowry. In Namwala, a medium farmer **(P01/02)** explained why they preferred keeping cattle and how they acquired their cattle.

"We started keeping cattle when we were young. Our parents gave these animals to us when we used to go school, so that we can be supporting ourselves. Until now, we are able to look after ourselves. We have 42 cattle and few goats. These animals are kept as per our tradition. If you do not own cattle here, then you are considered nobody. We sometimes sell cattle to solve some problems at home like payment of school fees for our children and buy

other household goods, while ox are used for cultivating our croplands. We slaughter goats for home consumption and not cattle."

(P01/02)

The source of cattle for farmer **P01/02** suggests that most people in rural areas acquire cattle through inheritance as well as sharing. This view is inconsistent with some other reports (Chilonga et al., 1999; Musialela et al., 2008; FAO 2011). However, using the information from the discussion, it strongly suggests that individuals can own cattle at an early age in the pastoralists' communities. Consequently, the majority of people own a large number of cattle per household and are reluctant to sell cattle as was also reported in the findings in the study of Mtewa (1978, p26):

"As I have mentioned, the [1]Rhodesian African, like all his counterparts elsewhere on the continent looks on his cattle as an asset to be kept and increased and not as a revenue-earning commodity and we still read about thousands of head of cattle in the tribal lands being allowed to die of starvation in drought years because their owners refuse to sell them."

Not all farmers in Namwala acquire cattle through inheritance. In particular, other ethnic groups that migrated into this area had to purchase cattle as a business investment, as a former government worker and business person who is categorised as large farmer **(P01/03)**

explained:

[1]Rhodesian Africa refers to Zambia as Northern Rhodesia and Zimbabwe as Sothern Rhodesian until the federation of 1963.

"I have slightly over 500 animals and the numbers of calves are about 220 to 230. I started keeping these animals 11 years ago. I was just a worker and I am a business person. I hope I can also have more than 2000. Cattle is now a big business here."

(P01/03)

The initial source of cattle for most farmers in the Lundazi district is through purchase using money generated from various sources, such as retirement benefits after working in government or profits from investments or sale of agricultural produce. Cattle in this region are used mainly for agriculture activities, such as ploughing agricultural land. A medium scale farmer who is a retired teacher from Lundazi district and served as contact farmer in the area explained how he started owning cattle:

"I started keeping cattle in 1997 after retiring from government as head teacher from Nkhumba School and bought two oxen. These animals were for traction. We started producing crops and with money raised; I bought cows. The other [2]man sitting there, started selling diesel until he raised enough money to buy also two cattle. These two oxen are used for ploughing. Now the two cows have two calves in the kraal as you can see."

(P03/04)

Most farmers in this region had a similar experience in how they started owning cattle as enlightened by an emerging farmer **(P03/01):**

"Firstly, after producing and sale of maize crop, we bought two oxen. We used to them for ploughing, however, after some time these animals used to die and then needed to buy again. We then discovered that we were making losses by delayed ploughing. Thereafter, we

[2] One of the farmers in the group family member.

thought of buying one female, which started producing. The number reached 15, but now in that kraal as you saw, mine are only 7 and two calves, most have died because of lack of dipping facilities."

(P03/01)

The process of acquiring cattle has a bearing on overall cattle management skills (Steele, 1981). Individuals from long-standing cattle keeping households are more likely to learn various cattle management skills through informal learning. For example, the Maasai sheep pastoralists in Kenya are able to employ a range of management techniques from a young age, such as cattle feeding, castration and treating (Babe et al., 2003; Ayole et al., 2005). Similarly, in Zambia, the majority of people, regardless of their level of education are able to carry out crop management practices without acquiring any formal education, based on the knowledge learnt from their parents (Haggblade and Tembo, 2003). However, in all regions, the majority of famers reported that they did not have adequate cattle management skills and relied on government veterinary officers who require payments for service delivery. This need to pay for advice results in farmers employing 'trial and error methods. (P03/03) and his family an emerging cattle farmers explained some of the trial and error methods;

"We go to their [3]offices and tell them that our animals are sick, and then they will tell us what medicine to buy. It is a problem. Each one for himself, surprising we have not gone to school, how can we know these types of diseases? So, we just used chemicals we spray cotton called [4]Cypermethrin to dip cattle to control ticks."

(P03/03)

[3] Veterinary offices
[4] Poison herbicide used to control certain insect pests in crops which contains cypermethrin as active ingredient.

Cattle Grazing and Feeding Regime

The lack of basic livestock knowledge is a constraint to livestock management for small-scale cattle farmers in Zambia and elsewhere in Sub-Sahara Africa (Ahuya et al., 2005). Farmers may be willing to acquire cattle in order to improve their living standard, but they are unable to manage animals properly resulting in high mortality. Therefore, training cattle farmers in basic management skills will equip farmers with knowledge to improve their livelihood.

The other major constraint in livestock improvement is lack of adequate nutrition during dry the season (Owens et al., 1993; Okeyo, 1997). Cattle in the traditional sector are raised on pasture without any feed supplementation during the dry season. All interviewed farmers showed a lack of knowledge on how to supplement cattle with maize bran during dry season, despite some having the capacity to buy feed. In Chipata, farmers could not feed their cattle with maize bran even though it was available from local millers. Farmers said they did not know whether cattle could feed on maize bran and most farmers expressed an interest to in understanding cattle supplementation feeding program to improve their cattle welfare as explained by an emerging cattle farmer (Figure 2.3):

"We feed pigs with maize bran, but can cattle eat maize bran? The main problem is lack of grazing during dry season. So if we can be trained on how to make these feeds, we can be feeding our animals during this time. We also need to know how to make this feed."

(P02/02)

Figure 2.3: Female medium cattle (P02/02) farmer feeding her cattle.
Photo by J Msimuko

Housing

Kraals[5] made of wood and barbed wire are commonly used as housing for cattle, mostly to protect cattle at night (Figure 2.3). These kraals were reported to be problematic during the rainy season because of the heavy accumulation of mud. They become a source of endo-parasites, predisposing cattle to footrot. However, in Namwala, the majority of cattle were not housed in the kraals, instead they were left freely grazing in the flood plains throughout the dry season and river islands in the wet season.

2.4.3 Breeding Practices

Participant choice of cattle breed was variable across different regions. For example, in Lundazi, all cattle farmers keep Angoni cattle because there are no alternative breeds in this region. However, in Namwala, farmers keep the Angoni or Brahman or both. In Chipata, a

[5] An enclosure for livestock

few farmers keep Angoni and Boran, but the majority keep Angoni. The Angoni breed is kept in all three regions.

Most cattle were found in the study to be grazing together in communal land all year round, such as the Kafue flood plains called [6]*Luntanga*. Communal bull sharing occurs at most times between neighbouring cattle farmers, as captured during a discussion among a Lundazi group of emerging cattle farmers:

"Two months ago a bull (Kuzi) from Chiwoko here was taken to Vuwu. However, we had one. It is now castrated!

What about the one at Robs place? Another farmer asked from within the group

No! That one is not counted because it is still small. Us here we have a small one but it is not yet mature. The only mature bull was the Chiwoko bull, and they did not want it to be shared and they took it to Vuwu."

(P03/01)

A large farmer in Lundazi, explained that the performance of his cattle herd had drastically reduced in terms of mature size and numbers. He recalls that in the 1990s he had more than 200 cattle and that enabled him to lease out his cattle by *herding out* to those who did not own cattle. This offered him an advantage when his cattle started dying because those areas where he sent his cattle were free from the ECF outbreak.

"You know Mr Musimuko, I had plenty of animals. More than 200 plus and as result I took some animals to my son in law, some to your auntie and other relatives. In every place, animals were producing and they were very big. Not like this, you see. Look! Look! Look at

[6] Small Islands found in Kafue flood plains

this one and it has a calf. Very small! I do not know what is happening unless you people who are educated can tell us. I would like to improve these animals to be big in size as before. Most of cattle died here except those I took to other people and they still look bigger and I am looking where I can buy a big bull.

(P03/03)

Farmers in Namwala shared similar views. Bulls were shared among the farmers because these cattle grazed together on large pieces of communal land.

The results from this study on breeding management are in agreement with most breeding practices found amongst Africa pastoralists (Frisch et al., 1986; Hanotte et al., 2002). African pastoralists have large cattle herds that are characterised by communal grazing and mating. This was commonly mentioned across the regions. Farmers shared bulls. However, one unique finding in this study is that all farmers in the same community are willing to share bulls. One particular case in the Lundazi group, one bull was transferred from one village to another to avoid the bull mating with cows from other farmers. Consequently, famers tend to use younger and more closely related bulls than the average size of the population. This drastically increases the probability that two alleles in the expected offspring to identical by descent and increase the rate of homozygosity that reveals deleterious recessive lethal effects, such as reduced vigour, fertility and size (van Arendonk, 2003). Inbreeding is feared to one of the major hindrances in genetic improvement of cattle for small-scale cattle farmers in developing countries (Rege and Gibson, 2003; Pitchford, 2007; Goddard, 2011). However, these breeding practices used by the small-scale cattle farmers can be transformed into useful tools for genetic improvement because they are the root base for exchange of genetic

material within these communities (Rege et al., 2001; Ahuya et al., 2004). With strategic planning, farmers can be encouraged to exchange bulls periodically to avoid inbreeding.

2.4.4 Disease and Parasite Management

A few major cattle diseases reported by farmers are East Coast Fever, Blackleg, Hemorrhagic septicemia and Footrot. The common disease reported in all study regions was East Coast Fever (ECF) or corridor disease, transmitted by the red hard tick, possibly *Rhipicephalus appendiculatus* as emerging cattle famer explained:

"About 90% of cattle die because of corridor disease and is the major cause of death in their cattle, characterised with various signs that included sudden death, mucus discharge from eyes and nasal, loss of appetite and dropping of ears."

(P01/01)

This report from farmers is in agreement with several studies conducted on the impact of this disease on cattle (Maloo et al., 2001; Mukhebi et al., 1992; Mwenya, 1993; Gucholi et al 2012). ECF disease is the major cause of cattle loss in Zambia and throughout Africa. Recently, ECF has been classified as a government notifiable disease and it may have a great influence on cattle genetic improvement programs.

The cost of treatment for ECF was estimated between US$8 (ZK30) for antibiotic/animal and US$20 (ZK120) for Butalex per animal across all three districts (Muuka et al., 2013). Application of acaricides to the skin surface of an animal by either spraying or dipping to kill ticks is the main method of controlling the disease. Cattle treatment with acaricides was reported as varying, often occurring once a week in Namwala or once in a month in Chipata

to several months without treatment in Lundazi. Apart from the inconsistent application of acaricide, several farmers indicated problems with interpretation of the directions for use, including mixing ratios, interval of spraying and differentiating between trade name and chemical names. Using the interview data, the cost of acaricides was estimated to be $0.6/animal sprayed. Tick control (Figure 2.4) has become a serious concern as development of acaricide-resistant ticks is possible given especially animals are communally grazed.

During the study, farmers revealed that through the ministry of agriculture and livestock departments, ECF is also controlled by vaccinating with [7]*Chitongo vaccine* (Kariuki, 1999) by six months of age at a cost of US$2 per calf. For other diseases as stated by large farmer (P01/03), such as blackleg, treatment is also administered through Zambian government. However, some farmers were reluctant to allow all their cattle to be vaccinated especially those with large numbers of animals because of the associated cost.

Figure 2.4: Emerging farmer spraying a bull to control ticks
Photo by J. Msimuko

[7] Vaccine recent developed to control East Coast Fever

2.4.5 Value of Indigenous Cattle in Zambia

The indigenous cattle were reported by all farmers to serve multiple and complex functions that differed across the three regions and within each region. In Lundazi, more farmers used cattle as a source of traction. However, in Namwala, a few farmers used cattle for traction, but also kept them to multiply and sell Cattle provided various traction attributes that included ploughing agricultural land for crop production (Table 2.1). A medium scale farmer in Lundazi explained:

"*We produce maize (Vigoma), cotton (Tonjo), groundnuts, sunflower and general vegetables. Maize was 100 x 50 bags, 30 x 80 kg bags cotton, groundnuts 25 x 50 kg and sunflower, Maize price is at* [8]*K65 000, Cotton at K3200 per kg, and groundnuts K80 000 per 50 kg bag. Sunflower, there was a loss especially that used local variety."*

(P03/04)

Not all farmers in the study areas owned cattle, therefore, during peak agricultural activities, oxen are hired out to plough neighbouring fields. Farmers, in turn, may pay cash or in kind as explained:

"We just count lines and it is K70, 000 ($14) per arce (70 lines by 100 meters). Anyway, it was only in 2003 when we tried hard to take our oxen to Muyukwa area and we managed to raise K6,000,000 ($1,200) and buy time, you it was money (money had more value to purchase more goods and services). *We had to make a camp. Without a tour these oxen will just be resting."*

(P03/03)

[8] K = Kwacha Zambian currency and the exchange rate at $1 per K5000

In Lundazi, most communities have for a long time relied on crop production as the major source of income and traction (Haggblade and Tembo 2003; Mulemba, 2009). Using the interview data from farmers (P03/01) and (P03/03), the value of traction was estimated to be approximately $4430 gross income for a pair of oxen in year. This estimated value, when expenses are deducted, is similar other estimates (CSO 2005). All farmers interviewed clearly indicated that cattle in this region serve as a source of investment, prestige and are considered important during the Shimunenga ceremonies. Cattle periodically are culled and sold to existing abattoirs and money generated is used to acquire fixed and moveable assets. Farmers may re-invest their money by purchasing pedigree Brahman bulls from commercial farmers to improve local cattle (see Figure 2.2a).

The other important reason for keeping cattle as a source of milk for most communities across the regions. The children that contributed to the discussion indicated that they preferred milk as the immediate benefit they get from cattle and the excess they sell on behalf of their parents to buy books and other school requirements. It was difficult for farmers to slaughter cattle for domestic consumption except on special occasions such as weddings, funerals and large gatherings for specific events. They preferred slaughtering goats or pigs as a source of meat explained by an emerging farmer:

"We slaughter goats for home consumption and not cattle."

(P01/02)

The indigenous cattle play a vital role in improving soil fertility in local communities through supplying plant nutrients to their crops. In all study areas, manure from cattle

contributed to production of crops even though some farmers pointed out the caveat of weeds associated with manure application, but quickly interjected during the discussion saying that weeds were not a problem as long as the cattle manure was treated prior to application by heating to kill the weed seeds. In Namwala, dry manure was used as a source of fuel and heating due to lack of firewood in the flood plains.

2.4.6 Preference of Cattle Traits

In the Namwala district, some cattle farmers preferred the Angoni breed because of its superiority in adaption and high reproduction rates as mentioned herein by a medium farmer

"From our experience, these small Angoni breeds that are locally found are good at times especially when it comes to diseases. What I have seen is that they do not easier die. You have these big animals like the Brahman in my kraal will actually die fast. They surprise me also that even in dry season, when grass is not enough, but these small breed of animals will still look good."

(P01/03)

The observations were similar to those of famers in Lundazi. Angoni cattle have developed adaptation mechanisms by changes in behaviour as well as physiological characteristics. A medium scale farmer explained some adaptation mechanisms in the Angoni breed:

"Our old animals have (are) *a problem. They tend to move a lot. Imagine when you just open the kraal, you will find that they will just run straight where there is water. In addition, they do not want to graze on small areas, but they like grazing very far, where there is grass.*

They trouble a lot moving a lot (there are a problem because of moving a lot in search of food and water)*."*

(P03/01)

Previous studies have reported that Zebu cattle are well adaptable to environments characterised by high incidence of drought and diseases (Walker, 1964; Thorpe et al., 1980; Wiener, 1994). For example, Zebu cattle are able to walk long distances to look for pasture and water, require less metabolic water and have a hump to store energy in the form of fat (Naik 1978). Reports from several farmers supported this literature (P03/01; P03/03). However, some of these adaptation features, such as walking long distances, characteristics that cattle herders may not prefer and selected against.

The reproductive performance of local breeds outperform exotic breeds in the local environments. The literature indicates that in several countries in Africa and elsewhere, local breeds have higher fertility rates than exotic breeds (Walker, 1964; Thorpe et al. 1980; Davis 1993). In Namwala, a large farmer who keeps Angoni and Brahman cattle clarified:

"*Angoni cattle do not lose weight easily during the dry season and within 2 to 3 years of age, the female Angoni cattle is able to give birth to the first calf, but the Brahman heifers takes about 4 to 5 years to give the first birth to a calf. Brahman are not strong animals, they easily die when there is an outbreak of diseases and drought."*

(P01/04)

Even though Brahman showed lower fertility rates and adaptation levels, some farmers still prefer keeping Brahman cattle as a large producer (Figure 2.2a) explained:

"Of course as I said, cattle are big business here. If numbers increase, it means more animals to sell, but also these animals should be big. Therefore, I would like to keep Brahman cattle and I even recent bought more bulls like the one you see over there, so that I can have bigger animals for sale. It is difficult again to have such animals alone. You have these local animal produce very quickly and very hard to diseases, size is small while our Brahman is big, problem they die easily.''

(P01/03)

This view was similar with a group of medium and emerging cattle farmers in Chipata (Figure 2.2b), who had the opportunity to choose between Boran and Angoni breed. For example, medium farmer (P02/01) explained:

"It is a mixture of Angoni and Boran, Angoni is good for diseases and strong but problem it has not much weight. But is (Angoni) *good when it is well looked after, but I will still choose Boran because of its more weight."*

(P02/01)

2.4.7 Overall Preferred Traits

The Chi-square test was used as a non-parametric test to examine the collected data regarding whether the preferences for cattle traits were independent between in regions. The most preferred ranking was 4 or 5 and non-preferred rankings were 1-3. The scale of 5 was assumed being the most important. Therefore, the data tested was based on yes or no criterion. The results indicate that there was no significant difference between regions in the preference for cattle traits (Figure 2.2).

Table 2.2: Chi-square values for difference in preference for cattle traits

Region	Size	Adaptability	Growth	Traction	Fertility
Namwala	1.12	0.14	0.0080	1.86	0.02
Chipata	0.13	0.0046	0.35	0.048	1.01
Lundazi	0.91	0.18	0.53	2.50	1.57
χ^2	2.17	0.32	0.89	4.41	2.60

No significant difference in the preference for cattle traits between regions

Using the quantitative data, different counts from individual traits, the raw correlations matrix between preference traits (Table 2.3) indicates that none of the traits were highly correlated with each other.

Table 2.3: Raw correlations between cattle preference traits

	Size	Adaptability	Growth	Traction	Fertility
Size	1	0.26	0.34	0.06	-0.34
Adaptability	0.26	1	0.28	0.32	0.14
Growth	0.34	0.28	1	0.34	0.10
Traction	0.06	0.32	0.34	1	0.29
Fertility	-0.34	0.14	0.10	0.29	1

None of the traits were highly correlated, Size and fertility had a slight negative correlation size and traction were very independent.

The results showed that the positive correlation ranged from as low as 0.06 (close to zero) between size and traction to moderately positive correlated (0.34) between size and growth as well as growth and traction. Size and fertility had a slightly negative correlation (-0.34).

The parametric tests for preference traits showed no significant interaction between region and category for any trait (Table 2.4). Although cattle play multiple and complex roles the overall preferred traits were not significantly different from between regions. However, preferences for size was highly significant differently (P<0.001) between categories of farmers and fertility was close to significant (P>.063) between large, medium and emerging small production cattle farmers. The large farmers to preferred large framed cattle and the emerging farmers had least preference for size, which possibly indicates they prefer smaller framed cattle. Therefore, emerging farmers in these regions are likely to prefer cattle that are docile and able to work long hours regardless of the size. Hence, size and traction were very independent (Table 2.4). Fertility, was determined, in terms of how often a cow calves and age at which a heifer gives her first calf. Emerging farmers seem to have a slightly preferred fertility, conceivably, with a view to increase the number of cattle.

Table 2.4: Parametric tests and least squares means for cattle preference traits

	Size	Adaptability	Growth	Traction	Fertility
Region	P=0.212	P=0.702	P=0.230	P=0.437	P=0.301
Namwala	3.4±0.3	2.8±0.4	3.3±0.4	2.7±0.4	2.8±0.3
Chipata	3.3±0.2	3.1±0.3	2.5±0.3	3.0±0.3	3.1±0.2
Lundazi	2.9±0.4	3.1±0.4	3.5±0.5	3.3±0.4	2.6±0.4
Category	P<0.001	P=0.169	P=0.099	P=0.870	P=0.063
Rich	4.1±0.3	3.0±0.4	2.9±0.4	3.0±0.4	2.4±0.3
Medium	2.8±0.2	3.4±0.3	2.9±0.3	2.9±0.3	3.0±0.2
Emerging	2.6±0.4	2.6±0.4	3.5±0.4	3.1±0.4	3.1±0.4

The interaction between Region and Category of farmer was not significant for any trait. Region differences were not significant. Category differences were highly significant for size and close to significant for fertility. The rich cattle holders put more emphasis on size and poor least

While the majority of large farmers were in Namwala (60%), their preference for size was similar other large farmers in other regions. This category had the highest predicted least squares mean value (4.1±0.3). Most large farmers interviewed in this region indicated that they had more preference for either Brahman cattle in Namwala or Boran in Chipata that provides a higher carcass weight despite being not highly resistant to diseases. A large farmer **(P01/04)** explained:

I would like to keep Brahman cattle and I even recent bought more bulls like the one you see over there, so that I can have bigger animals for sale. It is difficult again to have such animals alone. You have these local animal produce very quickly and very hard to diseases, size is small while our Brahman is big, problem they die easily.''

(P01/04)

Based on this large farmer's views (P01/04) their preference for the Brahman cattle is that it provides a higher carcass weight than smaller sized and disease resistant cattle. In the recent past, two meat-trading companies have opened selling outlets in Namwala, including Zambeef (Figure 2.6) which buys dressed carcasses and provides opportunities for cattle farmers to market their cattle. Conceivably, this influences most farmers in this region to prefer large framed, faster growing cattle. The cattle population is also higher than any other region in Zambia (Mwenya, 1993; CSO 2010). Interestingly, a large number (60%) of large scale cattle farmers (60%) did not show interest on fertility, suggesting that increasing the cattle population was not their priority maybe because grazing land is slowly becoming a scarce resource in this district (FAO 2006).

Figure 2.5: Sign of Zambeef Plc (Private Limited Company)
Photo by E. Musimuko

The majority of emerging farmers had the lowest preference for size. Nevertheless, since trait ranks were not highly correlated, this suggests that preference for one cattle trait, like size, had less positive influence on choosing cattle to perform various functions, such as providing work. In Chipata, according to the most important traits counts, 63% of emerging farmers, were interested in cattle that can produce a calf every year (Table 2.1). During this study, a group of emerging farmers indicated that the Zambeef Private Limited Company also opened a branch in the Chipata region (Figure 2.2b). This may have prompted farmers to develop an interest in increasing cattle numbers. Therefore, with a perceived increase in demand for cattle to be slaughtered in local abattoirs, farmers may have developed a new direction of valuing cattle more as a trading business and numbers are now a limiting factor as explained:

"It is a mixture of Angoni and Boran, Angoni is good for diseases, produce at least a calf every year and strong, but problem it has not much weight. But is (Angoni) *good when it is well looked after, but I will still choose Boran because of its more weight."*

(P02/01)

World Vision Zambia, a non-government organisation, has joined efforts to increase cattle numbers by providing dipping tanks and other handling infrastructures within small-scale cattle communities to control cattle diseases and ecto-parasites (Figure 2.7) A group of farmers discussed this during distribution of survey materials (Figure 2.2b).

Figure 2.6: Cattle dipping facility in Chipata donated by World vision Zambia
Photo by E. Musimuko.

Despite tests for significance indicated that there was no significant difference for preferred cattle traits across the regions, but based interviews data captured during this study, emerging farmers including P03/02 and P03/03 used cattle mainly for the purpose of traction. They stated that they prefer cattle that are docile, able to provide work in agricultural land and able to survive in the local environments with minimal heath care. Adaptability and traction were important. For many years, 80% of the Zambian small-scale farmers have been one of the major producers of cash crops and maize (Mason et al., 2007; Mulemba, 2009). Most rural

communities rely upon the production of agricultural crops for their livelihood and because of increased demand for food; farmers need a source of traction as a readily available power.

Nearly all cattle farmers in Lundazi area acquired cattle by selling agricultural produce and hence purchased their own cattle. Their primary cattle were oxen, used as a source of traction. The results are in agreement with other studies that reported that many small-scale farmers in Southern Africa use cattle as a source of traction (Aune et al., 2001; Haggblade and Tembo, 2003; Zulu, 2008). However, this study shows that large scale farmers do not prefer cattle for traction, but instead they preferred large framed cattle in order to sell them as carcasses. Cattle size was imperative to these farmers.

One major task in designing selection programs that can lead to animals that provide required utility is that the animal should be to able to survive in the tropical environments. To achieve this, breeding cattle for adaptation is key. Adaptation is important to consider when designing cattle improvement programs among the small-scale farmer (Rege et al., 2001). Studies indicate that animals may tend to develop small body size that makes cattle use less amount of feed required for body maintenance and hence less grazing pressure on the land (Franklin, 1986; Baker and Rege, 1994). Emerging farmers that showed stronger preference for keeping cattle to multiply indicated least preference to size. The interpretation of size and fertility shows an inverse relationship and suggests that large farmers prefer larger framed cattle over high fertility cattle (Table 2.4). This was most predominant with large farmers who fully understood the negative value of Brahman cattle over the local Angoni breed.

"*Angoni cattle do not lose weight easily during the dry season and within 2 to 3 years of age, the female Angoni cattle is able to give birth to the first calf, but the Brahman heifers takes*

about 4 to 5 years to give the first birth to a calf. Brahman are not strong animals, they easily die when there is an outbreak of diseases and drought."

(P01/04)

The literature indicates that there is a negative correlation between size and fertility (calving ease, age at first calving), associated with more difficult births, fewer number of calves per cow life span and higher maintenance costs of larger cattle (Baker and Rege 1994). Farmers were able to discuss from their experience with the Angoni and Brahman breeds.

2.5 Conclusion

Cattle farmers in this study prefer indigenous breeds. This is because indigenous breeds have proven to be well adapted, fertile and have the ability to survive and reproduce with a low investment cost in high-risk areas. Farmers indicated that cattle breeds which can walk long distances to find water and pasture and that require less veterinary care and provide a specific role, are preferred among rural communities. Strong adaptation attributes of the local breeds enables cattle to add value to the land as well providing the best alternative of land use in regions that are undesirable for crop production, like in the flood plains. Even though, lack of livestock production management skills, prevalence of diseases and poor infrastructure in the studied regions, most cattle farmers showed preference in increasing numbers in Chipata and Lundazi unlike in Namwala. However, farmers showed willingness to improve cattle through genetic selection under extremely harsh and highly variable conditions.

Chapter 3

3.0 Measuring Genetic Diversity: Population Differentiation and Structure

3.1 Introduction

Selection has created a wide diversity of breeds in domesticated animals. Charles Darwin was the first to recognise that phenotypic diversity in crops and domesticated animals occurs because breeding mimics evolution in populations subject to natural selection (Andersson, 2001). In fact, this phenotypic change during domestication was one of Darwin's strongest arguments for the evolution of new species by natural selection. Many phylogenetic studies have been conducted within closely related populations in livestock species (Meyer et al., 1990; Cano et al., 2001; Elsen 2003), and informative microsatellite DNA markers have been used for assessing genetic diversity and relatedness in cattle (Cunningham et al., 2001; Davison et al., 2009). Unique variation that occurs within closely related species is important in designing genetic improvement programs for traits such as disease resistance (Baker and Rege 1994; Davies et al., 2009), meat quality (Malau-Aduli et al., 2000; Johnston and Graser 2010); reproduction (Nicholas, 1996; Shida and Mukai, 2004; Bush et al., 2007), feed efficiency (Pitchford, 2004) and adaptation (Burrow, 2012), and for genetic conservation (Hall and Bradley 1995; Medugorac et al., 2009; Toro et al., 2009; Hoffmann, 2011).

The first ever global plan of action for conserving animal genetic resources was adopted by several international organisations in conjunction with the Food and Agriculture Organisation in 2007. According to the Commission on Genetic Resources for Food

Agriculture Organisation of the United Nations (Rege and Gibson, 2003; Dekkers, 2007), molecular genetics has become more and more significant in the characterisation of genetic diversity of most livestock species. The FAO-International Society for Animal Genetics (ISAG) working group proposed a global program for the characterisation of animal genetic resources that included more than 20 strategies (Gibson and Hanotte, 2007; Rischkowsky and Pilling, 2007). Amongst the strategic priorities for the global plan of action for animal genetic resources was to ensure that there is proper characterisation and monitoring of animal genetic diversity both in developed and developing regions are necessary in order to ensure proper assessment of the value of different breeds and as a guide to decision making when designing breeding programs for livestock genetic improvement and conservation of genetic resources (FAO, 2011). However, most of these strategies have not been realised apart from creating awareness of the need to monitor animal genetic diversity and to establish a standard approach for molecular genetic characterisation (FAO, 2011).

It is paramount that the value of animal genetic resources is well evaluated before any major decision is made in the implementation of genetic breed improvement. This is because undertaking such programs without control has proven to be detrimental in most cases (Rege and Gibson, 2003). Unique characteristics in certain breeds have been lost or depreciated significantly over time (Simianer et al., 2003). This potential erosion of animal genetic resources has become one of the major concerns for both developed and developing nations as a number of animal breeds are at risk of extinction (FAO 2006b).

Scientists in various countries have conducted independent studies to characterise locally available breeds such as Ireland (Flynn, 2009), China (Mao et al., 2008), Spain (Martín-Burriel et al., 2007), Kenya (Kios et al., 2012), Ethiopia (Dadi et al., 2008) and West Africa

(Ibeagha-Awemu and Erhardt 2004). Consequently, a wide range of molecular datasets for most livestock species are now available, such as the Domestic Animal Diversity Information System (DAD-IS). Several bioinformatics tools have been developed to help analyse such large sets of molecular data including Structure (Pritchard et al., 2000) and GenAIEx (Peakall and Smouse 2006).

3.1.2 Genetic Diversity

Genetic diversity refers to the combination of different alleles found within a population (e.g. Zambian indigenous cattle), as well as the phenotypic pattern of variation found in the populations. In natural selection, each individual has an equal chance to mate with another individual within same species, thus, increasing genetic diversity, which results in a high rate of fitness and allows the species to evolve in changing environmental conditions (Falconer, 1989). However, mating in small populations with crosses between closely related individuals (e.g. cattle stud herds) reduces genetic diversity and increases homozygosity of the individuals within the population.

There are numerous techniques for assessing genetic diversity within a population. For example, discrete phenotypes including coat colour and horn shape can be used to assess genetic diversity (Rege et al., 1999; Toro et al., 2011; Fr). However, molecular techniques involving genotyping DNA variants are more effective. Using molecular data, genetic diversity can be evaluated in several ways including determining the frequency distribution of the genotypes and alleles, the proportion of polymorphic loci, the observed and expected heterozygosity, and the allelic pattern (Toro et al., 2009; Peakall and Smouse, 2012). Genetic differentiation can be assessed based on the partition of genetic diversity between-

subpopulation and within-subpopulation components, on genetic distances (Loftus et al, 1999; Pritchard et al., 2000; Peakall and Smouse, 2006) and on fixation indices (Wrights, 1965).

From the genotype data, estimated allelic frequency distributions, mean number of alleles, effective number of alleles and private number of alleles per locus provide reliable estimates of genetic diversity within populations (Loftus et al., 1999; Peakall and Smouse, 2006) and genetic differentiation (Lynch, 2011; Pritchard et al., 2000). However, genetic comparison estimates may suffer inaccuracies due to small sample sizes, methods of sampling, methods of data analyses and the data management. Consequently, allelic richness estimates are frequently used for small sample sizes and can provide genetic diversity estimates by eliminating inaccuracies normally caused by varying sample sizes. In addition, estimates of the expected heterozygosity and observed heterozygosity within populations can provide a measure of global genetic diversity within populations.

3.1.3 Population Differentiation

From allelic frequency distributions, numerous genetic distance estimators can be determined including the Wright inbreeding indices (1965), F-statistics (Fis, Fst, Fit) and G-statistics (Nei, 1973). F-statistics are tools extensively used to characterise population genetic structures by permitting the splitting of genetic diversity within and between populations. G-statistics offers a comprehensive range of standardised estimators of genetic differentiation for small sized populations. Fst and Gst values can be compared in a pairwise matrix form to allow comparisons of multiple populations (Peakall and Smouse, 2012). Population sub-structure is assessed using Wrights fixation indices (Wright, 1965) for co-dominant data

calculated per locus basis. Fixation index values close to zero are expected in larger and random mating populations. However, values that are more positive indicate high inbreeding levels in the population, while negative values can show an excess of heterozygosity due to negative assortative mating (heterotic selection).

Fis is the inbreeding coefficient within individuals relative to the population and measures heterozygosity deficiency within population due to non-random mating within sub-populations. Fst is the inbreeding coefficient within the sub-population, relative to the total and measures the genetic differentiation among populations and Fit measures the global heterozygosity deficiency (Peakall and Smouse, 2012). Populations with a reduced effective population size suffer genetic erosion (Hall, 2004), the loss of rare alleles and random changes in allele frequencies (Falconer, 1989). Such populations can experience a 'bottleneck' because of the high level of inbreeding within a small population. Populations with high levels of inbreeding are especially important to identify for the conservation management of animal genetic resources and designing effective breeding goals, as these populations are at a higher risk of extinction (Rege and Gibson, 2003).

In population genetic studies, individuals in the study are often allocated into groups by different clustering methods (Pritchard et al., 2000). These methods allow population groups to be assessed for levels of ancestry, recent population admixture, gene migration, hybridisation or genetic uniqueness and purity within the populations. This is achieved by high throughput multi-locus genotypic data analysis tools that allow for accurate assignment of these individuals into clusters according to genetic composition and historical co-existence (Pritchard et al., 2000; Davison et al., 2009).

3.2 Materials and Methodology

3.2.1 Blood Sample Collection

The three indigenous breeds used to measure genetic diversity in Zambian cattle herein included the Angoni, Tonga and Barotse. Blood samples were collected from various sites in Zambia, but were concentrated in the Eastern Province (Lundazi, Chadiza, Katete, Petauke), Southern province (Sianazongwe and Kalomo), Western province (Kalabo, Kaoma, Lukulu and Sesheke) and Lusaka province (Figure 3.1). A total of 147 blood samples were randomly collected representing the three indigenous Zambian cattle populations. The numbers sampled were 53 Angoni, 37 Tonga and 57 Barotse. The collection of blood samples followed FAO guidelines (CGRFA-13/11/Inf.20 2011). Blood samples obtained from unrelated individuals were stored on Whatman® FTA® Elute micro cards for DNA isolation by standard protocols of ZyGEM for livestockGEM™ Storage Cards (Blood).

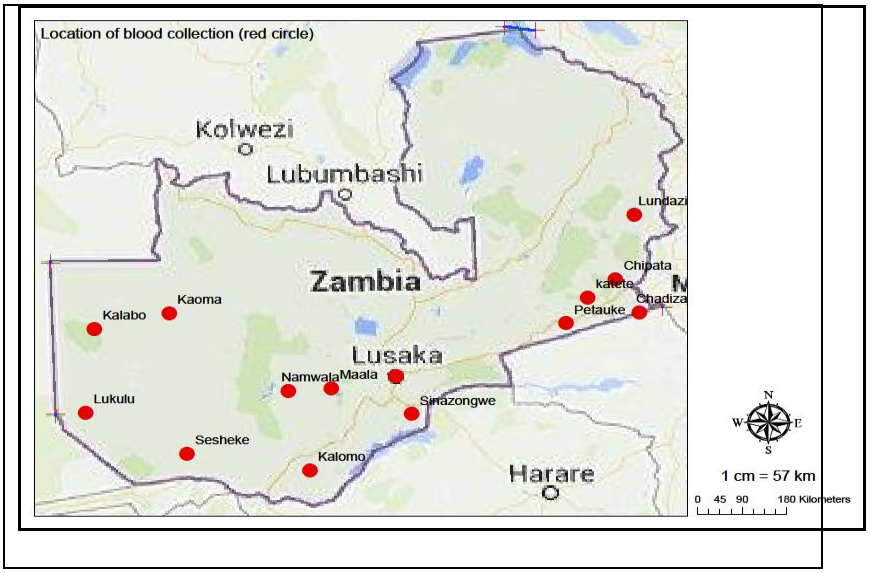


Figure 3. 1: Sampling sites (red dots) in Zambia. Samples were collected from three provinces that included the Eastern (Angoni breed n=51) Southern (Tonga n=37), Western (Barotse breed n=57), and Lusaka (pure Angoni n=2) Provinces

3.2.2 DNA Extraction and Genotyping

Three laboratories were involved in the process of DNA extraction and genotyping. DNA extraction from blood samples taken in 5 ml vacutainer tubes was first conducted in Zambia at National Scientific and Industry of Research (NSIR) following the protocols of Qiagen and Mio-Bio. Several studies have used the protocols of Qiagen in DNA extraction (Malau-Aduli et al., 2000; Marletta et al., 2006; Flynn 2009). The second DNA extraction from the blood samples stored on Whatman® FTA® Elute micro cards was by the standard protocols of ZyGEM for livestockGEM™ Storage Card (Blood) at The University of Adelaide, Roseworthy Campus molecular laboratory. However, the quality and quantity of the DNA extracted was very low for these samples and all the DNA samples were re-purified at the University of Queensland, Animal Genetics Laboratory who provided the genotyping service.

3.2.3 DNA Microsatellite Markers

The 32 microsatellite markers used in this study were: AGLA 232, BL 1043, BM 1818, BM 1824, BM203, BM 2113, BM 305, BM 5004, BMS 2047, BMS 2742, BMS 510, BMS 650, CSSM 016, CSSM 022, CSSM 036, CSSM 042, ETH 3, ETH 10, ETH 225, INRA 005, INRA 23, MGTG 4B, RM 067, RME 40, SPS 115, TGLA 057, TGLA 122, TGLA 126, TGLA 227, TGLA 263, TGLA 293 and TGLA 53. Some markers are those recommended by FAO-ISAG (Appendix 3.3) Mo DAD project (www.fao.org/dad_is). References, primer sequences, chromosome numbers and PCR product size range in base pairs are given in Appendix 3.2.

3.3 Data analyses

3.3.1 Genetic diversity analysis

Various bioinformatic tools were used for the allele frequency-based population genetic analysis from the microsatellite co-dominant genotypic data. Allele frequency based statistical procedures estimated the number of alleles (Na), effective number of alleles (Ne), information index (I), observed heterozygosity (Ho), expected heterozygosity (He) and fixation index (F) for each locus pair within population and for each pair of loci across populations. The data were analysed using GenAlEx version 6.5 (Peakall and Smouse 2012) for the F-statistics (Fis, Fst and Fit), the number of effective migrants (Nm) for each locus and mean across loci. .

Allelic patterns (APT) were also described using GenAlEx 6.5 (Peakall and Smouse, 2012), by summarising the mean and standard errors across loci for each population for Na, Na with frequency, Ne, I, number of private alleles (only those found on one breed), number of locally common alleles found in the population and He. The pairwise population matrix of Nei's genetic identity and genetic distance (Nei et al., 1974) among breeds were computed using GenAlEx 6.5 (Peakall and Smouse, 2012).

3.3.2 Population differentiation

Shannon (1948) developed a diversity index from information theory widely employed in ecology and partition genetic diversity within populations, among populations and among regions based on log 10 and 999 permutations for each locus and for loci. In this analysis of molecular variance (AMOVA) was performed following the procedures of Excoffier et al., (1992), Huff et al., (1993) and Peakall et al., (1995). AMOVA made it possible to determine

the pairwise genetic distances and genetic variation among populations and within populations by using GenAIEx 6.5 (Blyton and Flanagan, 2010) either as codom-genotype data (co-dominant, PhilPT), codom-allelic data (Fst) or codom-microsatellite data (Rst).

3.3.3 Population relatedness and structure

Genetic differentiation between populations was assessed by F-statistics (Wright 1965) and Nei's pairwise genetic identity and genetic distances (Nei, 1973), using GeneAIEx version 6.5. A Bayesian clustering method was then employed to assess population structure using the program Structure version 2.3 (Pritchard et al., 2000). This method uses multi-locus genotypes to infer the fraction of population/individual genetic ancestry that belongs to a cluster, for a given number of clusters (K). The program implements a model-based clustering method for inferring population structure using genotypic data consisting of unlinked markers (Pritchard et al., 2000). The model did not assume a particular mutation process of microsatellite markers. Three runs were performed for each K value at K=2, K=3 and K=4 and the program was run assuming a model of admixture and correlated allele frequencies. No prior information about the population origin of the animals was specified.

A burn-in period of 50000 generations followed by Markov Chain Monte Carlo (MCMC) simulations of 500000 iterations was used in all the above runs. The values of LnP(D) (the log probability of data) were estimated assigning priors from 2 to 4, and the optimal number of clusters of K was chosen based on the delta K (ΔK) value. Later, the average membership coefficients for each individual and for each pre-defined (sampled) cattle population K inferred cluster were assessed.

For this analysis, each individual in the data set was presented by a single vertical line that is partitioned into K coloured segments that represent that individual's membership fraction in each of the K inferred clusters (Pritchard et al., 2000). The ancestry vectors were plotted onto a triangle to show individuals assigned completely to one population. The MCMC method of likelihood based on estimating of admixture (Freeman et al., 2004) was employed to determine the relative contribution of each breed in each of the populations, taking into account population drift.

The proximity between individuals was measured and was presented by a dendrogram using an Agglomerative Hierarchical Clustering (AHC) program XLSTA 2013 (www.xlstat.com). The program also estimated Euclidian distances and chi-square distances proposed by Ward (1963). Eigenvalues were generated to determine the significance of microsatellites.

3.4 Results

3.4.1 Genetic diversity analysis

A total of 274 alleles (Na) were detected across the 32 microsatellite loci analysed with a mean frequency and standard error of 7.875 (±0.555) for the Angoni breed, 7.063 (±0.406) for the Tonga breed and 7.406 (±0.471) for the Barotse breed (Table 3.1). The lowest number of alleles detected per locus was 4 for the loci INRA5 and TGLA263 and the highest number of alleles per locus was for locus BM2047 in the Angoni (21), the Tonga (15) and the Barotse (19). Of the 274 alleles detected, 74 alleles were breed specific with 41 in Angoni, 17 Tonga and 16 in Barotse (Figure 3.2).

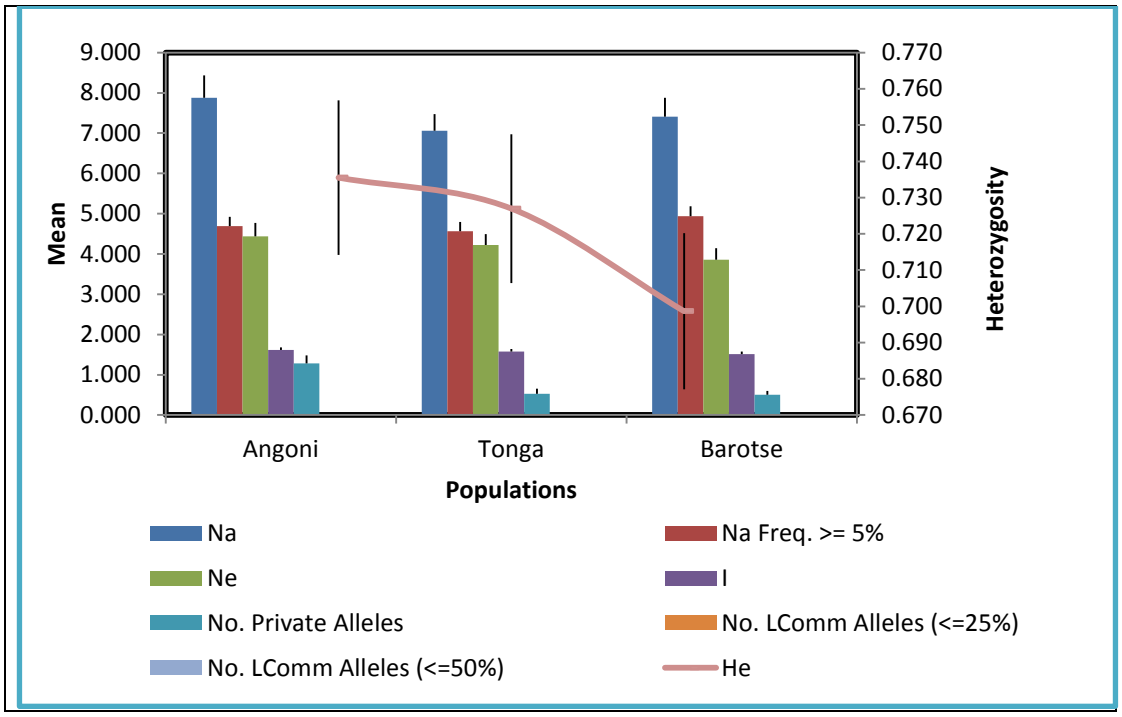


Figure 3. 2: Allelic pattern across breeds Angoni.

Angoni (n=30), Tonga (n=14) and Barotse (n=28). Na = number of different alleles; Na = number of different alleles with a frequency ≥ 5%; Ne = number of effective alleles, I = Shannon's information index; No. Private Alleles = number of alleles unique to a single population.

The estimated observed heterozygosity (Ho) and the expected heterozygosity (He) were 0.741 and 0.735 in the Angoni, 0.702 and 0.727 in the Tonga, and 0.692 and 0.699 in the Barotse (Table 3.1). In the Angoni breed, eighteen markers showed excess heterozygosity (negative F values), ranging from very little (F= -0.019 @ TGLA122 and 126) to moderate (F= -0.091@ BM 2742, F= -0.123@CSSM042) to a large excess of population differentiation (F= -0.151@TGLA293, F= -0.245@BM305). However, the overall excess of heterozygosity (F= -0.01) across all loci contributed little to the genetic differentiation in the Angoni sub-population. The interpretation of these resultant F values is based on Wright's (1978) suggested qualitative guidelines, where F = 0-0.05 indicates little population

differentiation, F= 0.05–0.15 indicates moderate differentiation, F = 0.15–0.25 indicates great differentiation, and F > 0.25 indicates very great differentiation.

The Tonga breed had an overall heterozygosity deficiency of F=0.032 across all loci. Some microsatellite markers, such as CSSM036 (F= 0.267), TGLA122 (F= 0.194), TGLA293 (F=0.208) and BM1824 (F= 0.182), contributed greatly to the genetic differentiation in the Tonga sub-population. The microsatellite marker AGLA232 showed uniqueness in the Tonga breed as it neither contributed to a deficiency nor excess heterozygosity (F= 0). However, BM203 microsatellite marker had a large excess of heterozygosity (F=-0.235) for this loci in Tonga cattle.

The Baroste breed had an overall excess heterozygosity of 0.9% and two microsatellite markers, INRA23 (F=0.355) and RM067 (0.255), greatly influenced the genetic differentiation in the Baroste breed. Markers BM2742 (F=-0.229), INRA23 (F=-0.207) and CSSM016 (F=-0.199) significantly contributed to observed heterozygosity deficit in Barotse cattle. Overall, most loci indicated an excess observed heterozygosity in all three breeds.

A total of 74 private alleles were detected within the three breeds studied. These alleles were private within the breed population data set. However, this does not prove that these alleles are private *per se* in comparison to all cattle at a global level. The results show that the Tonga breed and Barotse breed had a similar mean number of private alleles (0.5) even though the Tonga breed had a lower allelic richness (7.1) compared to the Barotse breed (7.4) (Table 3.1). The Angoni breed had the highest mean number of private alleles per locus (1.281). Also, based on the pattern of allele frequency across all three breeds, the Angoni

breed had a higher mean number of alleles per loci with an allele frequency greater or equal to 5% (Na = 7.9) than the Tonga and Barotse breeds (Table, 3.1; Figure 3.2).

Table3.I: Frequency distribution of number of alleles, heterozygosity (observed and expected) and fixation (F) for each breed

	ANGONI BREED (n= 30)					TONGA BREED (n=14)					BAROTSE BREED (n=28)				
LOCUS	Na	Pa	Ho	He	F	Na	Pa	Ho	He	F	Na	Pa	Ho	He	F
CSSM016	9	2	0.677	0.729	0.071	4	0	0.571	0.702	0.185	8	1	0.966	0.806	-0.199
CSSM022	7	2	0.774	0.723	-0.071	6	1	0.714	0.724	0.014	6	0	0.724	0.732	0.011
CSSMO36	6	0	0.71	0.736	0.036	4	1	**0.357**	0.487	**0.267**	7	1	0.655	0.618	-0.061
TGLA057	5	0	0.806	0.742	-0.086	3	0	0.5	0.584	0.144	5	0	0.724	0.64	-0.131
SPS115	5	0	0.645	0.608	-0.061	6	0	0.5	0.51	0.02	5	0	**0.276**	0.332	0.17
TGLA122	8	1	0.774	0.76	-0.019	9	0	0.571	0.709	0.194	9	0	0.862	0.785	-0.098
TGLA126	6	0	0.806	0.791	-0.019	6	0	0.786	0.806	0.025	7	0	0.655	0.826	0.207
TGLA263	4	1	**0.258**	0.235	-0.097	4	1	**0.357**	0.365	0.021	4	0	0.517	0.427	-0.21
TGLA293	8	2	0.935	0.813	-0.151	6	0	0.643	0.811	0.208	7	1	0.69	0.791	0.128
BM1818	8	1	0.839	0.817	-0.027	7	1	0.786	0.796	0.013	7	0	0.828	0.757	-0.093
BM1824	5	0	0.742	0.619	-0.198	6	1	0.571	0.699	0.182	4	0	0.621	0.625	0.007
BM2113	10	2	0.742	0.846	0.123	7	0	1	0.837	-0.195	9	1	0.759	0.863	0.121
AGLA232	9	1	0.677	0.809	0.162	7	0	0.786	0.786	0	6	0	0.621	0.7	0.114
BL1043	9	1	0.871	0.768	-0.134	9	0	0.786	0.77	-0.02	10	1	0.759	0.715	-0.062
BM203	9	2	0.839	0.817	-0.027	5	0	0.857	0.694	-0.235	7	1	0.655	0.665	0.014
BM2047	21	3	0.871	0.915	0.048	15	2	0.857	0.883	0.029	19	2	0.828	0.893	0.073
BM2742	8	2	0.839	0.768	-0.091	9	0	0.714	0.758	0.057	9	0	0.828	0.674	-0.229
BM305	9	1	0.935	0.751	-0.245	9	0	0.929	0.801	-0.159	10	1	0.655	0.724	0.094
BM5004	8	2	0.806	0.817	0.013	8	2	0.643	0.699	0.08	7	0	0.69	0.776	0.111
BMS510	8	1	0.806	0.733	-0.101	6	0	0.643	0.76	0.154	7	0	0.793	0.797	0.004
BMS650	9	3	0.613	0.751	0.184	7	0	0.643	0.719	0.106	8	1	0.517	0.53	0.024
CSSM042	7	1	0.839	0.747	-0.123	7	0	0.786	0.727	-0.081	7	0	0.759	0.672	-0.128
ETH10	6	0	0.774	0.711	-0.089	8	1	0.786	0.809	0.028	7	0	0.828	0.788	-0.05
ETH225	5	1	0.581	0.658	0.117	7	0	0.714	0.809	0.117	8	1	0.586	0.711	0.176
ETH3	7	2	0.6	0.7	0.143	6	1	0.571	0.587	0.026	5	1	0.679	0.605	-0.121
MGTG4B	9	0	0.774	0.825	0.061	9	0	0.929	0.844	-0.1	7	0	0.759	0.716	-0.06
INRA23	6	1	0.71	0.759	0.064	8	2	0.786	0.798	0.016	7	0	0.862	0.714	-0.207
INRA005	4	0	0.677	0.641	-0.057	5	0	0.643	0.686	0.063	4	0	**0.345**	0.534	0.355
RM067	6	1	**0.452**	0.563	0.198	6	1	0.571	0.635	0.1	6	1	**0.448**	0.602	0.255
RME40	11	1	0.839	0.822	-0.021	10	1	0.857	0.844	-0.015	9	1	0.793	0.823	0.036
TGLA227	7	2	0.645	0.68	0.051	7	0	0.786	0.793	0.01	8	1	0.621	0.772	0.196
TGLA53	13	5	0.867	0.883	0.019	10	2	0.929	0.829	-0.12	8	1	0.852	0.745	-0.144
MEAN	7.9	1.3	0.741	0.735	-0.01	7.1	0.5	0.705	0.727	0.036	7.4	0.5	0.692	0.699	0.009
SE	0.56	0.197	0.025	0.021	0.02	0.4	0.197	0.028	0.021	0.021	0.047	0.1	0.027	0.022	0.026

Boldfaced markers contributed significantly to heterozygosity deficit (CSSM036, TGLA 263, BM2047, INRA 5 and RM 067). Lowest number of alleles per locus detected was 4 (INRA5) and highest number of alleles per locus was 21(BM 2047). n = number of animals per breed; Na = number of alleles; Pa = private alleles; Ho = observed heterozygosity; He = expected heterozygosity; F = fixation.

3.4.2 Genetic diversity within populations

The genetic diversity with population subdivisions was assessed with Wrights (1965) F-statistics for each of the 32 loci across the populations (Table 3.2). The estimated values for fixation indices obtained from the analysis were Fis=0.01(±0.013), Fit=0.042(±0.013) and Fst=0.032(±0.003). The genetic differentiation for subdivision total (Fst) among the three breed populations ranged from 0.006 for marker RM067 to 0.077 for marker BL1043 and all loci were found to be significantly different from zero ($P<0.01$). The overall multiple locus mean (Fst) value of 0.032 obtained across breeds indicates that there is 3.2% of the genetic diversity between the three breeds and the remaining 96.8% of total genetic diversity is from genetic differentiation within each breed. The genetic differentiation among breeds (Fst) value of was moderately low (0.032), but was significantly different from zero. The overall mean Fis inbreeding value of 0.01 obtained across all loci was highly significant ($P<0.01$). This significant Fis value, which is greater than zero, suggests that there is some inbreeding overall (Wright, 1965). The results also showed a low global deficit of heterozygotes across populations (Fit) of 4.2%, which was significantly different from zero ($P<0.01$). However, as these values are low, the results indicate that there is random mating across the breeds and/or that the animals were not closely related due to geographic distance between sampling sites. The contributions to these estimates were significantly different between one locus to another locus across the cattle breeds (Table 3.2).

The Shannon tests of migration (Nm) or gene flow significance between pairwise breed populations at each locus was determined (Table 3.3). Seven loci (CSSM036, TGLA122, TGLA293, BM1818, BM1824, BM2113 and RM067) were highly significant across breeds

and showed a distinct gene flow between the three Zambia indigenous cattle breeds (Angoni, Tonga and Barotse) of between 20Nm/locus to 40.5 Nm/locus. However, results from the Shannon analysis of gene flow over the loci for all breed combinations of Nm gave different significance levels depending upon the different pairwise combinations (Table 3.3). Significant pairwise differentiation between the Angoni and Tonga breeds and between the Tonga and Barotse breeds had either significant ($P<0.05$) or non-significant (ns) loci while the Angoni and Barotse breeds only had significant loci.

Table 3.1: F- Statistics and Shannon migration estimates for three Zambian indigenous cattle breeds.

Microsatellite	Fis	Fit	Fst	Nm
CSSM016	0.010*	0.067	0.057**	4.111
CSSM022	-0.015	-0.002	0.013**	19.347
CSSM036	0.065**	0.101	0.039**	6.163
TGLA057	-0.032	0.024	0.054**	4.343
SPS115	0.021**	0.055	0.035**	6.905
TGLA122	0.020**	0.029	0.009**	26.719
TGLA126	0.073**	0.111	0.041**	5.854
TGLA263	-0.102	-0.081	0.019**	12.898
TGLA293	0.061**	0.072	0.012**	20.414
BM1818	-0.035	-0.022	0.012**	19.965
BM1824	0.005**	0.013	0.008**	30.549
BM2113	0.018**	0.032	0.015**	16.916
AGLA232	0.092**	0.107	0.017**	14.833
BL1043	-0.072	0.010	0.077**	3.016
BM203	-0.081	-0.036	0.041**	5.838
BM2047	0.050**	0.078	0.029**	8.265
BM2742	-0.082	-0.063	0.018**	13.558
BM305	-0.107	-0.059	0.043**	5.576
BM5004	0.067**	0.087	0.022**	11.306
BMS510	0.021**	0.060	0.040**	5.982
BMS650	0.114**	0.159	0.052**	4.600
CSSM042	-0.110	-0.077	0.030**	8.141
ETH10	-0.034	0.008	0.041**	5.886
ETH225	0.136**	0.181	0.051**	4.606
ETH3	0.022**	0.050	0.029**	8.441
MGTG4B	-0.032	0.011	0.041**	5.778
INRA23	-0.038	0.006	0.042**	5.695
INRA005	0.106***	0.121	0.017**	14.211
RM067	0.183***	0.188	0.006**	40.564
RME40	0.000	0.036	0.036**	6.699
TGLA227	0.086**	0.118	0.035**	6.912
TGLA53	-0.077	-0.044	0.031**	7.812
Mean	0.01	0.042**	0.032**	11.31
SE	0.013	0.013	0.003	1.537

* = $P < 0.05$; ** = $P < 0.01$; *** = $P < 0.001$, Fis is the inbreeding coefficient within individuals, Fit measures the global heterozygosity deficiency, Fst is the inbreeding coefficient within population, Nm is gene migration.

Table 3.2: Shannon analysis of breeds pairwise for all loci.

Combinations for number of migration (Nm) (gene flow) between Zambian indigenous cattle breeds (30 Angoni, 14 Tonga and 28 Barotse) using Shannon tests (1948) for 32 loci with the probability and level of significance from the chi square test.

			Nm	Chi Prob	Signif			Nm	Chi Prob	Signif			Nm	Chi Prob	Signif
LOCUS	CSSM	016				BM	2113				ETH	10			
	Angoni	Tonga	0.035	0.018	*	Angoni	Tonga	0.047	0.134	Ns	Angoni	Tonga	0.036	0.05	*
	Angoni	Barotse	0.032	0.002	**	Angoni	Barotse	0.035	0.008	**	Angoni	Barotse	0.033	0.005	**
	Tonga	Barotse	0.038	0.034	*	Tonga	Barotse	0.036	0.032	*	Tonga	Barotse	0.042	0.07	ns
LOCUS	CSSM	022				AGLA	232				ETH	225			
	Angoni	Tonga	0.034	0.02	*	Angoni	Tonga	0.04	0.035	*	Angoni	Tonga	0.04	0.049	*
	Angoni	Barotse	0.033	0.001	**	Angoni	Barotse	0.032	0.002	**	Angoni	Barotse	0.039	0.009	**
	Tonga	Barotse	0.033	0.022	*	Tonga	Barotse	0.038	0.077	Ns	Tonga	Barotse	0.034	0.02	*
LOCUS	CSSM	036				BL	1043				ETH	3			
	Angoni	Tonga	0.033	0.024	*	Angoni	Tonga	0.038	0.033	*	Angoni	Tonga	0.04	0.049	*
	Angoni	Barotse	0.035	0.007	**	Angoni	Barotse	0.033	0.002	**	Angoni	Barotse	0.03	0	***
	Tonga	Barotse	0.035	0.041	*	Tonga	Barotse	0.036	0.038	*	Tonga	Barotse	0.031	0.007	**
LOCUS	TGLA	057				BM	203				MGTG	4B			
	Angoni	Tonga	0.04	0.035	*	Angoni	Tonga	0.035	0.037	*	Angoni	Tonga	0.041	0.073	ns
	Angoni	Barotse	0.052	0.024	*	Angoni	Barotse	0.037	0.007	**	Angoni	Barotse	0.033	0.002	**
	Tonga	Barotse	0.052	0.117	ns	Tonga	Barotse	0.038	0.034	*	Tonga	Barotse	0.04	0.044	*
LOCUS	SPS	115				BM	2047				INRA	23			
	Angoni	Tonga	0.039	0.036	*	Angoni	Tonga	0.038	0.027	*	Angoni	Tonga	0.042	0.111	ns
	Angoni	Barotse	0.034	0.007	**	Angoni	Barotse	0.031	0.001	***	Angoni	Barotse	0.043	0.021	*
	Tonga	Barotse	0.047	0.144	ns	Tonga	Barotse	0.038	0.034	*	Tonga	Barotse	0.041	0.071	ns
LOCUS	TGLA	122				BM	2742				INRA	5			
	Angoni	Tonga	0.041	0.063	ns	Angoni	Tonga	0.036	0.043	*	Angoni	Tonga	0.041	0.078	ns
	Angoni	Barotse	0.038	0.011	*	Angoni	Barotse	0.033	0.004	**	Angoni	Barotse	0.035	0.007	**
	Tonga	Barotse	0.04	0.083	ns	Tonga	Barotse	0.034	0.025	*	Tonga	Barotse	0.036	0.053	ns
LOCUS	TGLA	126				BM	305				RM	067			
	Angoni	Tonga	0.047	0.186	ns	Angoni	Tonga	0.035	0.026	*	Angoni	Tonga	0.035	0.015	*
	Angoni	Barotse	0.034	0.008	**	Angoni	Barotse	0.047	0.034	*	Angoni	Barotse	0.035	0.002	**
	Tonga	Barotse	0.04	0.044	*	Tonga	Barotse	0.041	0.082	Ns	Tonga	Barotse	0.033	0.015	*
LOCUS	TGLA	263				BM	5004				RME	40			
	Angoni	Tonga	0.039	0.059	ns	Angoni	Tonga	0.051	0.156	Ns	Angoni	Tonga	0.044	0.105	ns
	Angoni	Barotse	0.035	0.003	**	Angoni	Barotse	0.047	0.044	*	Angoni	Barotse	0.037	0.009	**
	Tonga	Barotse	0.036	0.032	*	Tonga	Barotse	0.035	0.041	*	Tonga	Barotse	0.046	0.082	ns
LOCUS	TGLA	293				BMS	510				TGLA	227			
	Angoni	Tonga	0.037	0.039	*	Angoni	Tonga	0.044	0.079	Ns	Angoni	Tonga	0.048	0.072	ns
	Angoni	Barotse	0.037	0.009	**	Angoni	Barotse	0.029	0.001	**	Angoni	Barotse	0.041	0.008	**
	Tonga	Barotse	0.044	0.088	ns	Tonga	Barotse	0.04	0.047	*	Tonga	Barotse	0.054	0.145	ns
LOCUS	BM	1818				BMS	650				TGLA	53			
	Angoni	Tonga	0.042	0.062	ns	Angoni	Tonga	0.044	0.12	Ns	Angoni	Tonga	0.039	0.03	*
	Angoni	Barotse	0.032	0.001	***	Angoni	Barotse	0.034	0.006	**	Angoni	Barotse	0.034	0.002	**
	Tonga	Barotse	0.048	0.069	ns	Tonga	Barotse	0.034	0.035	*	Tonga	Barotse	0.043	0.065	ns
LOCUS	BM	1824				CSSM	042								
	Angoni	Tonga	0.039	0.045	*	Angoni	Tonga	0.041	0.112	Ns					
	Angoni	Barotse	0.035	0.008	**	Angoni	Barotse	0.043	0.044	*					
	Tonga	Barotse	0.034	0.035	*	Tonga	Barotse	0.037	0.044	*					

Nm = (0.047 / SHua)^2 (assuming Ne > 500); *p < 0.05; **p < 0.01; ***p < 0.001,.ns. = not significant

The difference between the mean and potential heterozygosity among the three breeds was measured by F statistics, assuming all individuals within population mixed and mated freely. In this study, Shannon statistics of analysis of molecular variance (AMOVA) was used to examine the patterns and degree of relatedness revealed by the F statistics. Genetic diversity was partitioned among breeds and within breeds (Table 3.4). The results revealed 2.3% genetic variation between the three breeds and 41% within breeds. Furthermore, the Angoni breed had a higher proportion of genetic diversity of 50.3%, followed by Barotse with 42.9% and Tonga with 26.7%.

Table 3.3: Shannon statistical analysis of molecular variance in Zambian indigenous cattle breeds using co-dominant microsatellite genotype data.

Source of Variation	DF[1]	G[1]	Shannon information	Diversity measure (%)	Standard divergence[3]
Between Breeds	2	244.22	1.22	2.33	0.880
All Breeds	141	1075.45	5.39	41.86	0.996
Within Angoni	61	485.77	2.43	50.27	0.996
Within Tonga	27	183.83	0.921	26.65	0.998
Within Barotse	53	405.85	2.03	42.86	0.995
Total	143	1319.67	6.61	97.73	0.997

[1] DF= Degrees of freedom, [a] breeds= Angoni (n=30), Tonga (n=14) and Barotse (n=28)
[2] G =Log-likelihood G statistic
[3] Standard divergence = divergence time (coefficients) at each node

3.4.3 Population structure

Shannon statistics revealed that there was significant genetic variation between breeds (41.86%) and within the Angoni, Tonga and Barotse breeds (Table 3.5). Results of Nei's (1992) pairwise population matrix of genetic distances to determine the degree of relationship by descent between these three breeds indicated that the Tonga breed is less

related to the Angoni (2.066) and Barotse (2.077) breeds than the Angoni and Barotse breeds are to each other (1.771, Table 3.5). Likewise, the pairwise of matrix of Nei's genetic identity also indicated that there is a closer relationship between the Angoni and Barotse breeds (0.170) than between the Tonga breed and the Angoni (0.127) or the Barotse (0.125) breeds (Table 3.5).

Table 3.4: Pairwise estimates of genetic distance and identity.

Breed	Angoni	Tonga	Barotse
Angoni	--	0.127	0.170
Tonga	2.066	-	0.125
Barotse	1.771	2.077	-

Boldface values were significantly different from others after 999 permutations and 1000 bootstraps using GenAIEx version 6.5.Below diagonal is genetic distance and above diagonal is genetic identity for three Zambia indigenous cattle breeds (*Bos indicus*) estimated using Nei's estimate (1972) from the 32 microsatellite marker genotype data for Angoni (n= 30), Tonga (n=14) and Barotse (n=28).

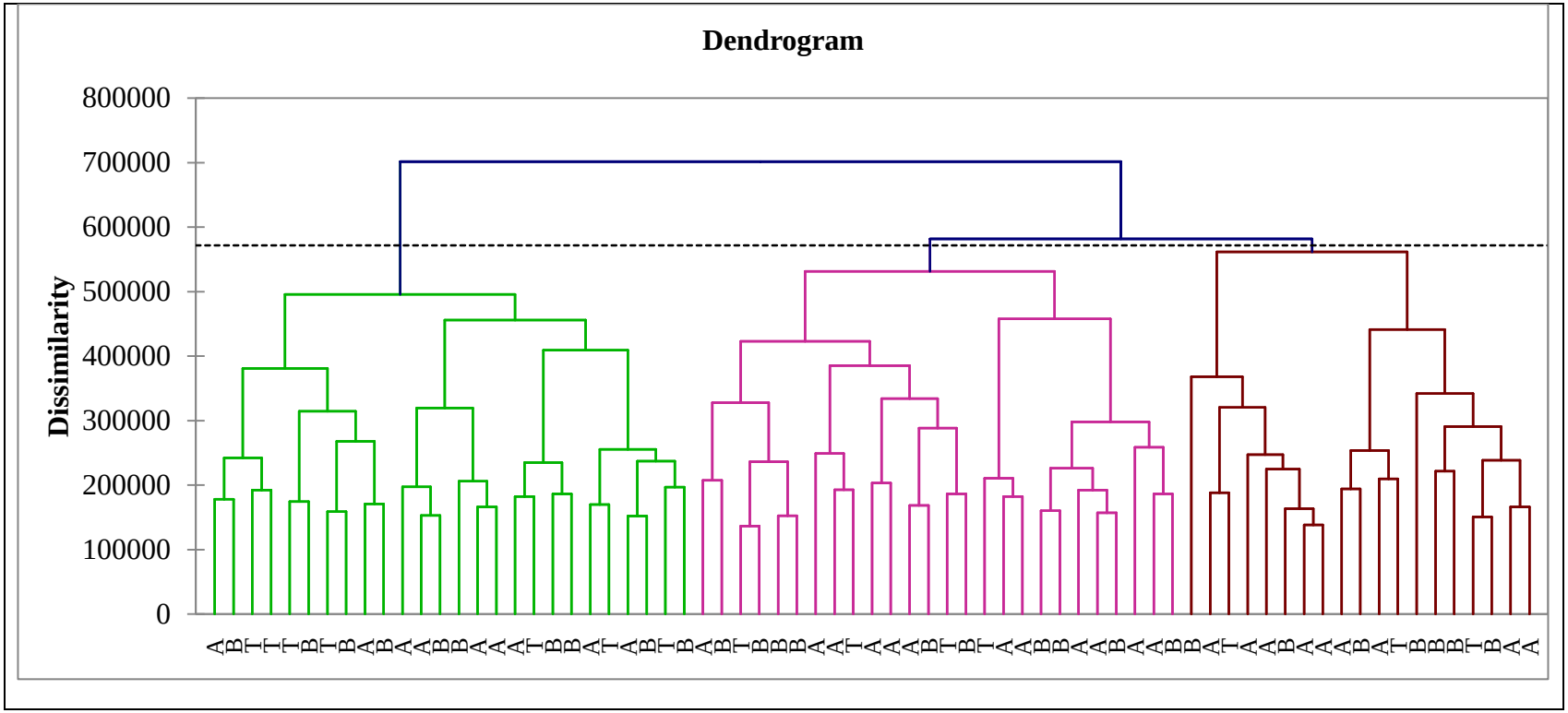


Figure 3. 3:Dendrogram.

Dendrogram constructed by agglomerative hierarchical clustering using allelic microsatellites from co-dominant genotype data obtained from 72 Zambian indigenous cattle (Angoni (n=30), Tonga (n=14) and Barotse (n=28). Dissimilarity levels were obtained using node statistics of XLSTAT version 2013. A=Angoni, B=Barotse and T=Tonga.

Agglomerative hierarchical clustering (AHC) was used for the construction of a phylogenetic tree and to estimate the proximity between individuals (Figure 3.3). There were three new distinct groups but with fragmented individual overlaps. No discrete clusters were observed perhaps because the markers used may have not shown unique signatures and because of the limited number of animals. Examination of three clusters revealed a population structure and that some individuals appear to be genetically very close to each other (Table 3.3). However, the patterns were fragmented with animals from supposedly the same breed dividing into the three distinct clusters (Figure 3.3). The dendrogram, therefore, suggests that there are no recognisable individual breeds *per se,* as the individual animals are rearranged into different groups.

The effect of microsatellite distances was also analysed using Eigenvalues above 1 to determine which markers were significant. Twenty four (24) microsatellite markers had Eigenvalues over 1 and thus, contributed significantly to the observed genetic differentiation (Figure 3.4). Together, they accounted for approximately 98% of genetic variability observed within the cattle population. This suggests that 24 of the 32 microsatellite DNA markers tested explained most of the genetic variation between the individual cattle although there is some variation occurring due individual breeds and other factors.

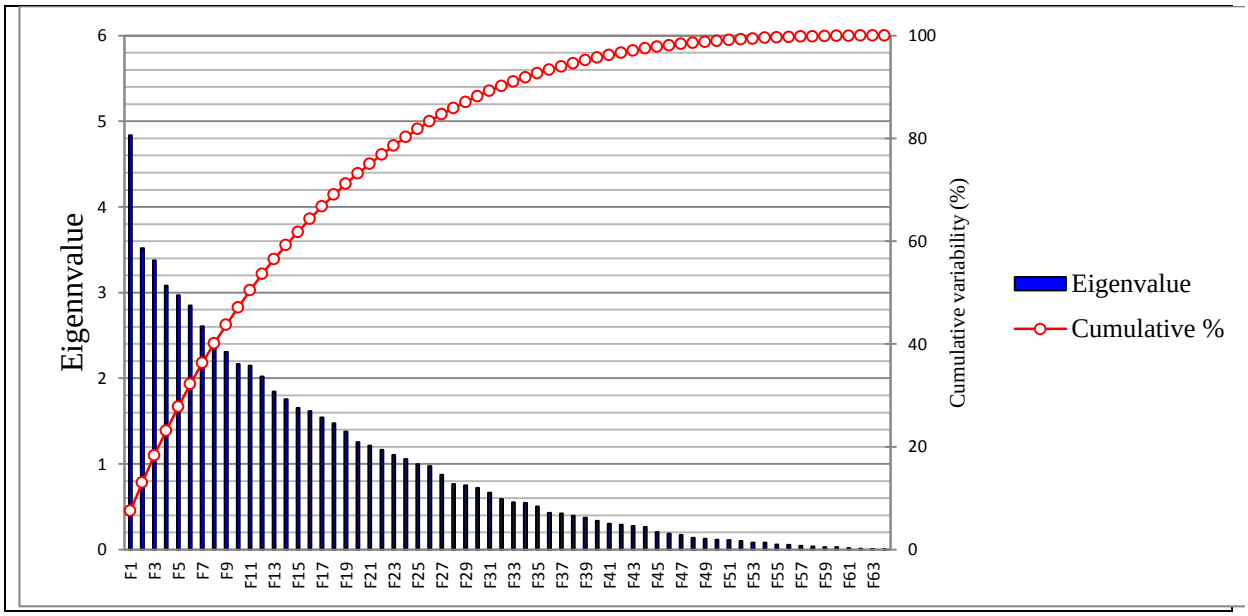


Figure 3. 4: Scree plot of Eigenvalues.

Scree plot of Eigenvalues with total genetic variance as cumulative variability in percentage for Zambian indigenous cattle obtained from the genotype data of 32 microsatellites.

Distances between pairs of individuals were estimated to categorise individuals according to dissimilarities. To quantify dissimilarities, it is expedient to define a genetic distance between individuals. Individuals with common ancestors in the recent past tend to have many genes in common and a small genetic distance between them. Genetic distance normally depends on the time since two species descended from a common ancestral species (Pritchard et al., 2000). The repeated mixing of genes in a random mating population causes the population to become homogeneous in the sense that the genetic distance between any pair of individuals. This results in genetic distances creating a tree structure representing each individual's sequence of alleles, each of which has two possible forms, inherited at random from the parents (Figure 3.3).

A Bayesian cluster analysis was performed using Structure software version 2.3 (Pritchard et al., 2000) and the most likely number of clusters from the maximised model log likelihood

data for ancestry was estimated for each animal (Figure 3.6). Individuals are assigned as a fraction of 1 (Q-value) for each cluster in the form of histogram plot (Figure 3.6). This method allows the assignment of individuals to groups based on their genetic similarity and provides an assessment of the underlying genetic diversity across the populations. The different patterns from the admixture analysis with the change in the number of clusters K from K=2 to K=4 and the posterior probabilities indicated that the most likely population value is K=2 (that is, there are 2 populations or breeds). Increasing the number of clusters (K) did not improve the average distance between loci or mean likelihood Ln log probability.

The degree of admixture using the mean value of alpha was 0.099 for K=2 and K=4, but was higher for K=3 (0.618). However, the structure also revealed average distances between individuals ranged from 0.73 to 0.76 for all K. The results indicated that Tonga breed is more closely related to Barotse breed. The breeds were divided into two distinct patterns between the Angoni and Barotse breeds after several runs of interactions. However, if K=4 (4 groups), the Tonga breed was placed in a relatively separate cluster. Using triangle Q plots showed that some Tonga individuals clustered with the Angoni cattle and others clustered with the Barotse cattle no matter the number of groups (K) (Figure 3.7).

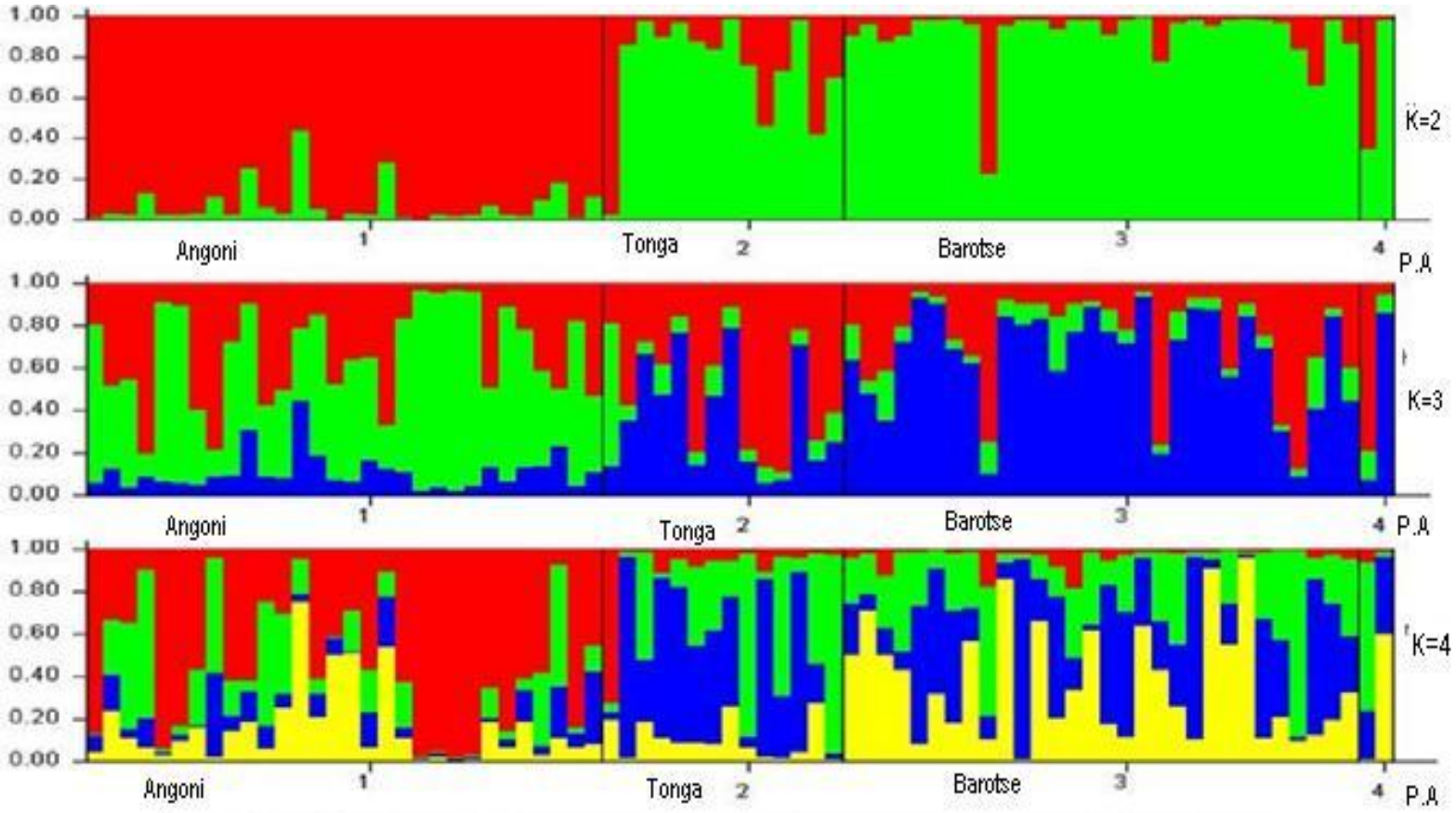
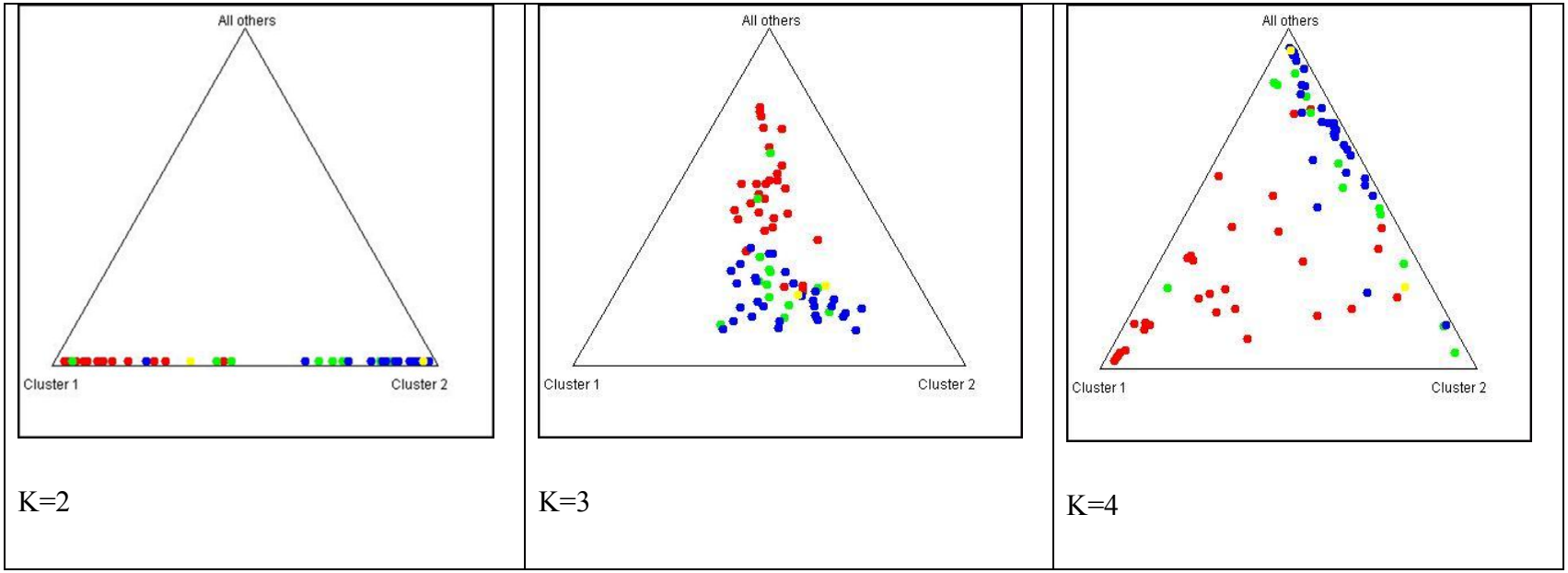


Figure 3.5: Bayesian analysis of estimates of population structure for Zambian indigenous cattle.
1= Angoni, 2=Tonga, 3= Barotse and 4-PA =pure Angoni. A single vertical line in the cluster represents each individual animal. Genotype contribution as coloured segments adds up to 1 for each of the inferred clusters. Model for top panel assumes K=2 populations, middle panel assumes K=3 populations, and bottom panel assumes K=4 populations.



K=2 K=3 K=4

Figure 3.6: The triangles plots of Q based on K=2, 3 or 4 population.
Each coloured point represents an individual corresponding to their assigned breed (red = Angoni, green = Tonga, blue = Barotse, yellow =pure Angoni).

3.5 Discussion

3.5.1 Genetic diversity

The panel of 32 microsatellite DNA markers used in this study provided adequate information to allow detailed characterisation of the three Zambian indigenous cattle breeds (Angoni, Tonga and Barotse). The genetic diversity assessment revealed that the Angoni population was the most genetically diverse breed(Table 3.2). The Angoni breed had the highest mean number of alleles, excess heterozygosity and most private alleles. The Barotse breed and Tonga had similar levels of heterozygosity (Table 3.1). However, the Barotse breed showed a higher allelic richness and a lower heterozygosity deficit than the Tonga breed. Therefore, the Barotse breed was more genetically diverse than the Tonga breed.

The Angoni population showed a consistently higher level of genetic diversity within breed compared to both the Tonga and Barotse populations (Table 3.4). This is likely to due to the Angoni's geographical location in the Eastern Province where is the majority of the population is exposed to the wider gene pool from other populations. There are no definite physical boundaries in the Eastern Province. For instance, there are no large water body boundaries in Eastern Province, unlike in the Western Province of Zambia where the Barotse cattle population is isolated by Zambezi flood plains (Figure 3.1).

The Barotse cattle populations are isolated and have been affected over time with widespread contagious bovine plural pneumonia that has caused this population to decrease greatly since 1915 (Masiga et al., 1996; Muuka et al., 2012). Isolation and the effects of disease may explain the relatively lower level of genetic diversity observed in Barotse cattle. Interestingly, the majority of Tonga cattle populations share more boundaries with beef

cattle, including the Boran and temperate cattle, and therefore, one might expect substantial dilution of the Tonga gene pool through unnoticed crossbreeding. However, the Tonga was the least genetically diverse indigenous population studied (Table 3.4) and showed the greatest overall heterozygosity deficit among the three breeds even though they are not the most isolated. On the other hand, the clustering analyses would suggest Tonga have been intermixed with both the Angoni and Barotse breeds (Figure 3.3).

The heterozygosity analysis revealed that for each of the breeds, some loci exhibited significant deviation from Hardy-Weinberg equilibrium (HWE) ($P<0.05$) although this differed for each breed. There are several possible causes for this deviation from the expected values of HWE, but it is difficult to determine the exact basis of these observed departures. However, the Angoni cattle population showed an overall excess of heterozygosity (Table 3.1) and a low high positive Fis (0.01), suggesting some occurrence of outbreeding and therefore, HWE would be expected in this population. On the other hand, the Tonga exhibited unique patterns of HWE deviation possibly because of low-frequency null alleles segregating at these loci, which can lead to a false observation of excess homozygotes. For the Barotse breed, the overall $F=0.009$ which is almost zero, indicating neither an excess heterozygosity nor a heterozygosity deficit. The observed heterozygosity was similar to the expected heterozygosity indicating that the Barotse populations have an admixture of genetic components that are passed on from one generation to another (Christiansen 1988). Using an exact test of disequilibrium in each individual showed no significant p values across the breeds. Thus, there was no evidence of linkage between loci and it can be assumed that populations were large enough and mated randomly.

The genetic diversity estimates of heterozygosity (0.699-0.735) within the Zambian indigenous cattle populations are similar to most other estimates observed within other zebu and Sanga cattle in Africa, such as in Ethiopia (MacHugh et al. 1997; Dadi et al., 2008; Zerabruk et al., 2011) and Kenya (Rege et al., 2001; Edea 2013). Other estimates of the observed heterozygosity levels for the Creole breed (0.719); continental European breeds (0.720) and Nelore breed (0.666) were also similar. On average though, the Zambian indigenous cattle showed a higher observed heterozygosity than the Indian Kandhari and Deoni breeds with mean values of 0.47 and 0.69, respectively.

The overall high-level of heterozygosity estimated in the Zambian indigenous cattle breeds provides evidence of a wide, large gene pool that exists in these local, well adapted cattle. This rich genetic diversity is assumed to have occurred because of the initial admixture of *Bos taurus* cattle and *Bos indicus* cattle during the movement of Fulani pastoralists across central Africa making zebu cattle the more predominant type in Zambia today (Payne and Williamson 1990). Zambia is a landlocked country sharing borders with eight other countries whose cattle are likely to be traded across these borders without notice, influencing the observed genetic diversity found in Zambian indigenous cattle.

The other striking reason that may influence high levels of heterozygosity obtained in this study is the Barotse population structure that showed an observed heterozygosity almost equal to expected heterozygosity (F=0.009) (Christiansen 1988). This occurs in populations that have an admixture of genetic components. The observed patterns of deviations from HWE proportions remained the same whether the population is in isolation or has recurrent immigration. The overall genetic effect leads the fixation to be equal to zero.

In relation to the high level of genetic diversity found in Zambian cattle compared to other zebu cattle, it is important to note that some of the microsatellite DNA markers have not been used previously for *Bos indicus* species. However, the results are in agreement with other studies that used similar microsatellite DNA markers (Sodhi et al., 2005; Dadi et al., 2008; Delgado et al., 2011), even though BM1818, ETH 10, INRA5,TGLA122, SPS 155markers showed different polymorphic characteristics and allele frequencies.

3.5.2 Genetic differentiation

There was overall little genetic differentiation across the loci among Zambian indigenous breeds revealed by F-statistics. Fst was highly significantly different from zero (Fst=3.2%). Although low, the Fst value is within the range reported in similar African cattle, as well as from other cattle worldwide. Numerous Fst values have been reported in African cattle, including for Ethiopian indigenous cattle populations (Fst=1.3%) (Dadi et al., 2008) and northern Ethiopian cattle breeds (Fst=1.1%) (Zerabruk et al., 2011) which are lower than the Zambian indigenous cattle estimates herein. However, higher values were obtained for Cameroon and Nigerian cattle breeds (Fst=6%) (Ibeagha-Awemu and Erhardt 2004), northern European cattle populations (Fst = 11%) (Kantanen et al., 2000), southern European beef cattle populations (Fst = 6.8%) (Jordana et al., 2003) and Indian indigenous cattle (Fst = 11%) (Sodhi et al., 2005).

Considering differences in geographical distribution of the breed populations, one might have expected a higher level of genetic differentiation amongst the breeds and high levels of inbreeding within the breeds, but this was not the case herein. The low genetic differentiation observed between these breeds would suggest a close similarity amongst the breeds and an

abundant exchange of genetic material between these breeds as revealed by the Shannon analysis of gene flow between Zambian indigenous cattle breeds (Table 3.3).

The results show these populations co-existed and the populations are characterised by overlapping generations (Figure 3.3). However, simulation models of these populations assuming different clusters (K=2 to K=4), suggests that the cattle were actually divided into two breeds (Figure 3.6). Correspondingly, the Tonga cattle were observed to share alleles with both the Angoni and Barotse cattle (Figure 3.7). Seven microsatellite DNA markers exhibited a highly significant level of genetic exchange across the breeds (CSSM036, TGLA122, TGLA293, BM1818, BM1824, BM2113 and RM067). However, the overall Fis value (0.01) was very low, though significantly higher than zero. This indicates a departure from panmixia because of inbreeding within the populations.

The classical genetic differentiation estimators of genetic distances and genetic identity (Nei, 1973) provided pairwise differentiation estimates, allowing comparative analysis to be carriedout. The Nei's pair-wise estimates indicated a strong and significant differentiation among breeds. However, these high levels of differentiation between the breeds varied and the most apparent observation was that the Angoni breed was the most genetically distant and the Tonga and Barotse populations were the least genetically distant. This genetic isolation observation was not supported by the Bayesian cluster analysis (Pritchard et al., 2000) (Figure 3.6).

Notably, although the placement of the Angoni breed in one cluster and the Barotse and Tonga in other Bayesian cluster at K=2 is an indication of the existence of divergent multi-locus genetic mixtures between the groups, the analysis also displayed isolated clustering of

individuals within their associated populations for Angoni and to a lesser isolated degree for Tonga and Barotse individuals (Figures 3.5-3.6). Similarly, although the Zambian indigenous cattle proved to be sub-divided into three independent genetic clusters using the agglomerative hierarchical clustering (Figure 3.3), there were many individuals that did not cluster within breeds. There was overlap between breeds within the clusters and one of the clusters was particularly genetically undistinguishable for the Angoni, Tonga and Barotse breeds. The clustering results show one particular individual may be somehow incorrectly assigned or may phenotypically looked like Angoni, but in fact genetically. For example, for number 31 clearly belong in cluster 1 (Angoni breed) instead of the Tonga breed as labelled. Alternatively and most likely, the results may reflect that fact the markers are not providing a sufficiently distinctive breed signature (Figure 3.3).

The absence of distinct clusters within breeds though is strong support of the results that showed high levels of gene flow between these breeds, with their historical coexistence and management (Payne and Williamson, 1990; Hanotte et el., 2002). According to Hanotte et al. (2002) and Payne and Williamson (1990), zebu cattle were dispersed from east Africa to central and southern Africa by Fulani pastoralists. In the process, zebu cattle were crossbred with Sanga cattle to become the predominant cattle in Zambia. Consequently, the results of the cluster analysis are in agreement with this historical pattern. In most areas where this study was conducted, cattle are usually grazed together and share drinking water without any defined breeding objective and this management system is likely to influence the high level of gene flow, maintaining a high level of shared genetics and hence low genetic differentiation among breeds. A study in European cattle supports these findings where

different breeds within very close proximity had low genetic differentiation (Canon et al., 2001; Jordan et al., 2003).

The fact that these groups coexisted for some time is probably the cause of inter-population gene flow and it is reasonable to expect that some overlap or allele sharing occurred because cross-breeding. The crossbreeding might be undetected at the phenotypic level, especially given the peculiarities of the brindle coat pattern. The old ways of raising cattle characterised by communal grazing and herding out practices facilitates gene flow within populations.

The population structure analysis was largely supported by the clustering analyses as a high percentage of individuals from these three populations can be assigned to their population of origin. The combination of this clustering and a high re-assignment percentage to populations of origin would indicate that the Angoni breed displayed the highest level of purity followed by the Barotse and then the Tonga. However, significant levels of inbreeding were not detected in any population examined. Even the Tonga population, which displayed the lowest levels of genetic diversity, showed no significant inbreeding. The relatively low inbreeding level obtained across the three breeds though might be attributed to the selective sampling practised herein to achieve good representation of each breed and was done by avoiding sampling of closely related animals. Therefore, locally the inbreeding might be higher.

Despite the fact that most of the analyses herein are in agreement, the results are quite preliminary and only indicative at best. The major problem is that very few animals were sampled from each breed and the sample sizes were not the same (Angoni=30, Tonga= 14 and Barotse = 28). Most importantly, there were a large number of different microsatellite

alleles (274) but quite a limited number of alleles genotyped for each of the 32 microsatellite loci (72x2=144). Thus, all the analyses suffer from having a large dimension feature space compared to the size of the sample and the results must be viewed with caution.

3.6 Conclusion

Genetic diversity studies are considered a priority area for breed development and conservation for future use. This area is of importance especially when dealing with locally well-adapted populations and lesser-known cattle breeds with low genetic diversity. This study reveals hidden genetic diversity in the Zambian indigenous breeds (Angoni, Tonga and Barotse). Although breed purity and uniqueness is not high, these three breeds offer a highly valuable genetic resource with apparently no significant inbreeding. The genetic closeness between the breeds would suggest that there is gene flow between these breeds. However, these breeds display sufficient levels of genetic differentiation that individuals with specific characteristics should be considered for conservation of their genotypes for future use.

Future research requires a much large number of samples with further breed classification and analyses. This should be based additional microsatellite markers and perhaps sequencing of the mitochondrial DNA D-loop fragment. It would be important to include other tropical breeds (such as Boran and Brahman) in Zambia that have co-existed for a period of time. It is also important that levels of taurine and indicine genetics be documented in the Zambian indigenous breeds by using either microsatellite or SNP markers that distinguish between the 2 sub-species.

Chapter 4.0

4.0 Measuring genetic parameters for growth traits

4.1 Introduction

Appropriate evaluation of genetic parameters for production traits is needed in order to effectively improve cattle productivity through genetic selection. A routine evaluation of genetic parameters is essential to help predict the genetic progress (Goddard and Hayes, 2009). For many years, animal breeders have manipulated the genetic composition of livestock species by making use of the variation that exists within breeds and within populations to improve animal growth and production (Hall, 2004; Goddard and Hayes, 2009; Eggen, 2012). In the quest to improve the productivity of livestock populations, traditional breeding practices do not employ molecular selection of DNA genotypes known to be associated with specific traits. Instead, animal breeders achieve enhanced production by selecting superior animals as progenitors in the next generation based on estimated breeding values that are calculated from the phenotypic records of related individuals (Dekkers, 2004). In addition to phenotypic records, pedigree records and heritability estimates are necessary for predicting the genetic progress based on estimated breeding values (Henderson, 1975; Green et al., 2006; Goddard and Hayes, 2009).

Production traits are complex in nature, usually quantitative, and controlled by many genes with small effects. That is, they are polygenic and show both additive genetic effects and environmental effects (Falconer, 1989; Falconer and Mackay, 1996). Substantial evidence from quantitative genetics studies has shown there is a statistical connection between a

phenotype and its genotypic basis, even though the exact genes determining the quantitative traits are generally not known (Falconer and Mackay, 1996; Lynch and Walsh, 1998).

Koots et al. (1996) and Gutierrez et al. (1997) showed that genetic parameters can vary significantly from one breed to another and from one property to another. The effect was first reported in dairy cattle herds (Spike and Freeman, 1978Bobe et al., 1998). The literature since suggests that the genetic models used in analysing data within a given structure affect the genetic parameter estimates (Clement et al., 2001; Haile et al., 2011).

There has been an unprecedented increase in demand for meat and other livestock products during the past few decades in Africa and a corresponding need to improve cattle production. Consequently, several studies have been conducted to assess genetic parameters for growth rate in different African breeds of cattle in different regions and countries of Africa (Table 4.1). Although similar information on production traits has been recorded for several years in Zambia, the information has not been used to estimate the breeding values for Zambian cattle. Therefore, estimating genetic parameters for production traits in Zambian cattle breeding programs would be useful to predict genetic progress of the local beef cattle and to quantify the amount of genetic improvement that can be achieved within a specific time frame.

Determination of genetic progress and genetic effects over a specific period of time is a vital component in designing breeding programs for cattle because phenotypic variance is either attributed to direct genetic effects, maternal effects or interactions between direct and maternal genetic effects (Willham, 1972; Meyer and Hill, 1997; Roughsedges et al., 2005).

Table 4.1: Genetic parameter estimates for beef cattle weaning weights in cattle

Breed	Estimated genetic parameters for weaning weight									
	σ^2_a	σ^2_m	σ^2_e	σ^2_p	h^2_a	h^2_m	r_{am}	σ_{am}	h^2_t	Source
Brahman	84.86	35.66	422.96	618.6	0.14	0.06	-	-	0.17	Pico et al., 2004
Gudali	180.00	80.66	548.96	710.00	0.25	0.11	-0.42	-23.16	-	Ndofor-Foleng et al., 2012
Nguni	219	149.2	627.3	869.44	0.25	0.17	-0.85	-	-	Assan and Masache, 2012
Kenya Boran	47.33	101.33	444.06	631.50	0.17	0.16	-0.66	-45.72	-	Wasike et al., 2006
Tswana	93.0	66.71	296.48	456.20	0.20	0.15	0.64	-	-	Raphaka and Dzama 2010
Ethiopia Boran	452.86	182.84	235.37	707.3	0.64	0.26	-0.84	-241.7	-	Wasike et al., 2007
Ethiopia Boran	449.6	222.4	217.1	1043	0.43	0.21	-0.57	-	-	Haile et al., 2011

σ^2_a =direct additive genetic variance, σ^2_m =maternal additive genetic variance, σ_{am} =direct-maternal genetic correlation, σ^2_e =residual σ^2_p =Total Phenotypic variance, h^2_a =direct heritability, h^2_m=maternal heritability, r_{am} =direct-maternal genetic correlation, h^2_t =Total heritability, LogL likelihood standard deviation estimates in genetic models.

Several genetic and non-genetic factors influence overall performance of offspring from the time of birth to the date of weaning. For example, in cattle, during conception, the sire and dam contribute 50% of their genetic material (direct genetic effects) to the offspring (Hall, 2004). In addition to the direct genetic effect, the dam provides the prenatal environment and postnatal milk to the calf, thus contributing maternal genetic effects to the final weaning weight. Thus, in suckling species, the dam plays a dual role as compared to the sire. In addition to genetic effects, the presence of diseases, availability of feed, sex and age of the calf influence the final weaning weight of calf as environmental effects (Koch and Clark, 1955; Manzi et al., 2002).

If the maternal effect is positively correlated with the direct effect on traits such as growth, cattle improvement through selection is feasible. In contrast, where a large negative genetic correlation exists between the direct effect and maternal effect, selection will be more difficult as the selection for one trait reduces the other trait (Willham, 1972; Swalve 1993). This negative relationship is one of the major constraints in designing selection programs because by improving one trait, another trait will be selected against. However, if the negative correlation is low, the effect may be minimal (Falconer and Mackay, 1996).

Numerous studies have been carried out to determine genetic parameters for growth traits in African cattle, for example, in South Africa (Pico et al., 2004), Botswana (Raphaka and Dzama 2010), Kenya (Wasike et al., 2006) and Zimbabwe (Assan and Masache 2012), but not in Zambia. For effective development of sound breeding objectives and implementation of cattle improvement programs through selection, genetic parameter estimates are required for the traits within the breeding objective. Consequently, the aim of this work herein was to

estimate the genetic variance components for growth in Zambian beef cattle as a preliminary study to demonstrate similarities with other trials and specifically to estimate the direct and maternal effects on weaning weight for both Angoni and Boran stud cattle reared on the same property.

4.2 Materials and Methods

4.2.1 Study site

Data for this study were acquired from the Lilayi Stud farm, owned by Alan Miller, located at Latitude S 15° 31' 7.57 and Longitude E 28° 18' 4.90 in Zambia (Figure 4.1). The farm is located at an average 1272 meters above sea level, with temperature ranges between 10^{o}C to 31^{o}C and the annual rainfall is approximately 800mm per year (Mulemba, 2009). All pedigree cattle were registered with the Herd Book Society of Zambia (HSBZ). HSBZ guidelines require that stud farm owners provide notification of births with full identification of cattle in terms of breed, species details, and tattoo marks within 30 days of birth.

The farm was opened in 1926 and in 1985; the Angoni stud herd was introduced as a second stud herd to Boran. During the data collection, 303 cattle (62 pure Angoni breed, 136 pure Boran breed and 105 crossbreds) were kept on the farm. Animals were managed on natural and improved pastures of giant star grass (*Cynodon plectostachynus*) or Rhodes grass (*Chloris gayana*) mixed with legumes, such as Stylo (Stylosanthes *guianensis*) or Siratro (*Macroptilium atropurpureum*) for grazing and hay.

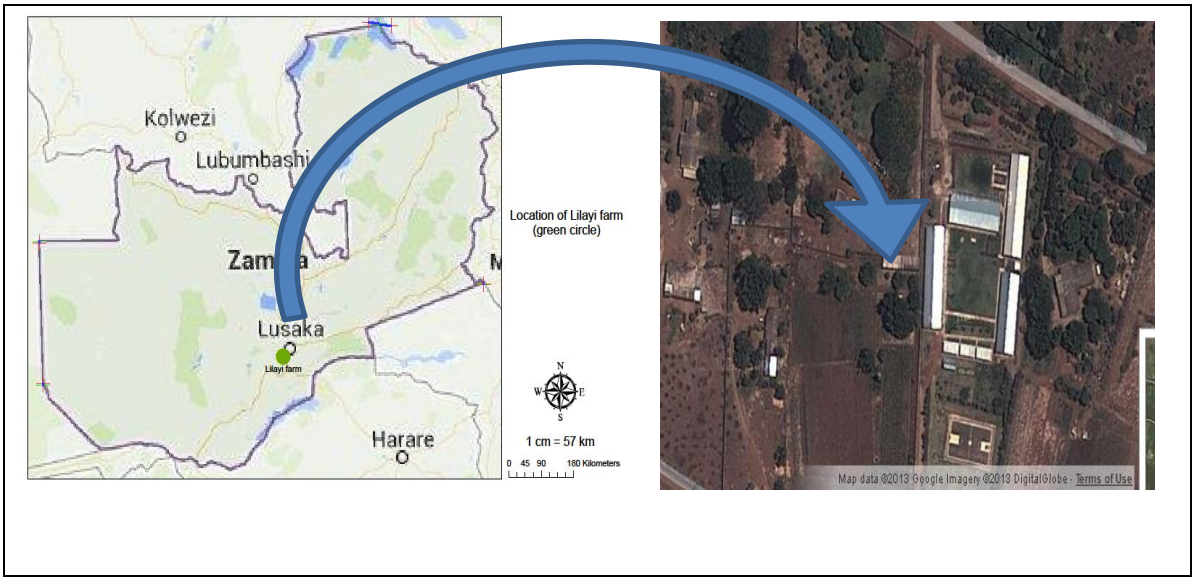


Figure 4.1: Location of Liyayi Farm
Source : <https://maps.google.com.au>.

4.2.2 Cattle management

Lilayi farm herds include a Boran stud (45%), an Angoni stud (20%), a commercial herd (30%) and a dairy herd (5%). Most of year, stud bulls and cows are raised separately in different paddocks (Figure 4.2). Natural mating is frequently used in the stud herds. Several parameters are considered when selecting a specific bull to mate with a certain cow on heat, such as relatedness and ages of the cow and bull. Mating occurs in small paddocks designed for mating activities for at least two days for proper identification of the sire.

Figure 4.2: A herd of bulls from Lilayi Farm in Zambia.
Photo by E. Musimuko 2013.

The main breeding season is restricted and runs for approximately 90 days, commencing in December and ending in March, known as summer breeding. This season is preferred because of the rising plane of nutrition, relative cool temperatures and availability of water during the rainy season. Most calves are born from September to November when the land is usually dry, and a few months later, the pastures improve when the lactation period reaches its peak (Payne, 1970).

All calves are identified using metal ear tags, tattoo marks and breed marks recorded within 48 hours after birth. Records of date of birth, sex, dam and sire are entered in the calf record book according to the Zambia Herd Book Society Standard Recording System (Appendix 4.1). In addition, individual animals are ear notched with numbers representing the year and month of birth. Selection of replacement heifers is carried out in different phases. At birth,

calves are immediately culled if they show physical and genetic deformities including lameness or lack of pigmentation on the muzzle. During weaning, based on weight and physical assessment, additional heifers are culled. At the time of joining, heifers are required to reach 66% of their mature weight.

At approximately 7-9 months, calves are weighed and weaned from their dams. Weaning weight in kilograms (kg) is recorded for each weaned calf in the calf record book. In addition to weaning weight, other information recorded includes the date weaning, health of the calf and any abnormities. Cattle performance data records range from production records (yearling weight, joining weight and mature weight) and reproduction records (conception rates, calving rates, calving interval, stillbirths and age at first calving). Thereafter, performance indices are calculated and entered in the calf record book. For the Angoni stud herd, records started in 1985 when the stud herd was first introduced.

4.2.3 Data collection and analysis

Numerous data sheets were scrutinised for dates of birth, weaning weights and dates, identities for each individual animal and coding system prior to data entry for analysis. Twelve animals without proper sire or dam records were excluded from data analysis after the edit checks and the data from the years 1995 to 2009 were retained in this study (Figure 4.2). The data prior to 1995 were not included as there were only a low number of records available prior to 1995.

Data edit and analysis for weaning weight in kilograms was assessed using ASREML version 3.0 (Gilmour et al. 2009). After the data edit, the herd structure was determined from

the Angoni and Boran pedigrees. All detected duplicate records were removed from the data analysis. Within the herd, there were 1128 calves from 39 sires, 11 paternal grandsires, paternal 12 grand dams, 389 dams, 25 maternal grandsires and 148 maternal grand dams were retained over five generations (Table 4.2).

Table 4.2: Herd structure of data for Zambian zebu cattle (Bos indicus) from Lilaya Farm

Item	Category	Size	Number
Animal Records		1128	
Sire	Angoni	39	11
	Boran		28
Dam	Angoni	872	266
	Boran		606
Sex of calves weaned	Female	2	452
	Male		420
Year of Birth		15	
*Generations		5	

*Generation interval- average age of parents at birth of their offspring for the period 1995 to 2009. Classification of these data used Wald statistics with an adapted ASREML version 3.0 by Meuwissen and Luo (1992).

Eight different models were fitted to estimate genetic parameters using univariate ASREML procedures (Meyer and Hill, 1997). The models varied in their inclusion or exclusion of maternal genetic effects and the correlation between direct and maternal genetic effects. Weaning weight was analysed for genetic parameters using a univariate REML procedure (Gilmour et al., 2009). Comparison of the different univariate models was made using log-likelihood ratio tests to determine the best model to fit the weaning weight data. The

difference in log likelihood ratio between pairs of models was doubled and tested against chi-square values with a 95% significance level (Gilmour et al., 2009). All calculations were carried out using the restricted maximum likelihood method (Thompson 1998; Meyer and Hill, 1997). For each trait in the analysis, convergence was considered to have been reached when the variance of function values (−2*logL) was less than 10^{-8}. The (co)variance components $\sigma^2_{Aa,}$ $\sigma^2_{Ma,}$ $\sigma^2_{Ab,}$ $\sigma^2_{Mb,}$ $\sigma_{A.Ma,}$ $\sigma_{A.Mb}$ σ^2_{Ea} and σ^2_{Eb} were derived at convergence variance of 10^{-8}, using standard symmetric matrix notation.

The direct-maternal genetic correlations ($r_{A.M}$) and the total heritabilities (h^2_T) were calculated after convergence. Total-additive heritability used in the total heritability calculation was defined by Willham (1972) as $h^2_T = (\sigma^2_A + 0.5\ \sigma^2_M + 1.5\ \sigma_{A.M})/\ \sigma^2_p$. The estimated covariance components were used to obtain direct heritability (h^2), maternal heritability (m^2), the covariance between direct and maternal effects as a proportion of the phenotypic variance for each breed (Angoni and Boran) (c_{AM}) and direct-maternal additive genetic correlation as $r_{A.M} = \sigma_{A.M\ /}\ (\sigma^2_A \text{ x } \sigma^2_M)^{1/2}$. However, based on Swalve (1993), the statistical analysis of likelihood-ratio-test (LRT) was applied by multiplying the difference by -2 and then comparing the results to chi-square (χ^2) test statistics with the number of parameters taken as the degrees of freedom.

Henderson (1973) described the notation as follows:

$LR_{ij} = -2\log_e (L_j/L_i) = 2\log_e L_i - 2\log_e L$ Equation 1

where L_{ij}= likelihood of maximum models that would be compared corresponding models. Weaning weight was analysed by fitting a linear mixed model was using ASREML v3.0

(Gilmour et al. 2009) with fixed effects as listed below and various random effects as outlined in Table 4.3:

$Y_{ijk} = \mu + B_i + S_j + Y_k + G_l + (AB)_{(i)} + S(B) + Y(B) + B(G) + \varepsilon_{ijk}$

where:

Y_{ijkl} = given weaning weight,

μ = overall mean,

B_i = fixed effect of breed season (i= Angoni, Boran),

S_j = fixed effect of sex levels (j= female, male),

Y_k = fixed effect of the year (k= 1995, 1996…2009),

G_s = fixed effect of season (season) (s= winter, summer),

A (B) = fixed effect of age at weaning nested within breed,

S (B) = fixed effect of sex of calf nested within breed,

Y (B) = fixed effect of year of birth nested within breed,

B (G) = fixed effect of breed nested within season (season),

and

ε_{ijkl} = random error.

Variance components were estimated using the ASREML programme of Gilmour et al. (1999). The expected estimate parameters were determined using the method that involves maximizing the likelihood function given the data (Table 4.3).

Table 4.3: Description of models fitted.

Parameters	Model							
	1	2	3	4	5	6	7	8
σ^2_{Aa}	✓	✓	-	✓	-	-	✓	✓
σ^2_{Ab}	✓	✓	-	✓	-	-	✓	✓
σ^2_{A}	-	-	✓	-	✓	✓	-	✓
σ^2_{Ma}	✓	✓	✓	-	-	-	-	
σ^2_{Mb}	✓	✓	✓	-	-	-	-	
σ^2_{M}	-	-	-	✓	✓	✓	-	
$\sigma_{A,Ma}$	✓	-	-	-	-	-	-	
$\sigma_{A,Mb}$	✓	-	-	-	-	-	-	
$r_{A.Ma}$		-	-	-	-	-	-	
$r_{A.Mb}$		-	-	-	-	-	-	
σ^2_{Ea}	✓	✓	✓	✓	✓	-	✓	✓
σ^2_{Eb}	✓	✓	✓	✓	✓	-	✓	✓
σ^2_{E}						✓	-	✓

σ^2_{Aa} =direct additive genetic variance (Angoni); σ^2_{Ma}= maternal additive genetic variance (Angoni); σ^2_{A}= direct additive genetic variance; σ^2_{Ab}= direct additive genetic variance (Boran); σ^2M_b= maternal additive genetic variance (Boran); $\sigma_{A,Ma}$= direct-maternal genetic covariance (Angoni); $\sigma_{A,Mb}$ = direct-maternal genetic covariance (Boran); σ^2_{M} = maternal additive genetic variance; σ^2_{Ea} = residual error variance (Angoni); σ^2_{Eb} =residual error variance (Boran); σ^2_{Pa} =Phenotypic variance(Angoni); σ^2_{Pb}= Phenotypic variance (Boran); σ^2_{p}=Total Phenotypic variance; σ^2_{E}= residual; LogL= Log likelihood standard deviation estimates in genetic models; $r_{A\cdot Ma}$ =direct-maternal genetic correlation (Angoni); $r_{A\cdot Mb}$=direct-maternal genetic correlation (Boran). All variance components were estimated using ASREML (Gilmour et al. 2009).

4.3 Results

4.3.1 Distribution of births

Descriptive statistical analysis indicated that breeding occurred throughout entire year (Figure 4.3).The highest number of calves were born in 1995 (85) and lowest recorded in 2009 (26). Note that in 2002 and 2009 only Boran calves were born and in 2007 only Angoni calves were born. However, Boran calves had highest proportion (69.5%) of all the total number of calves born between 1995 and 2009.

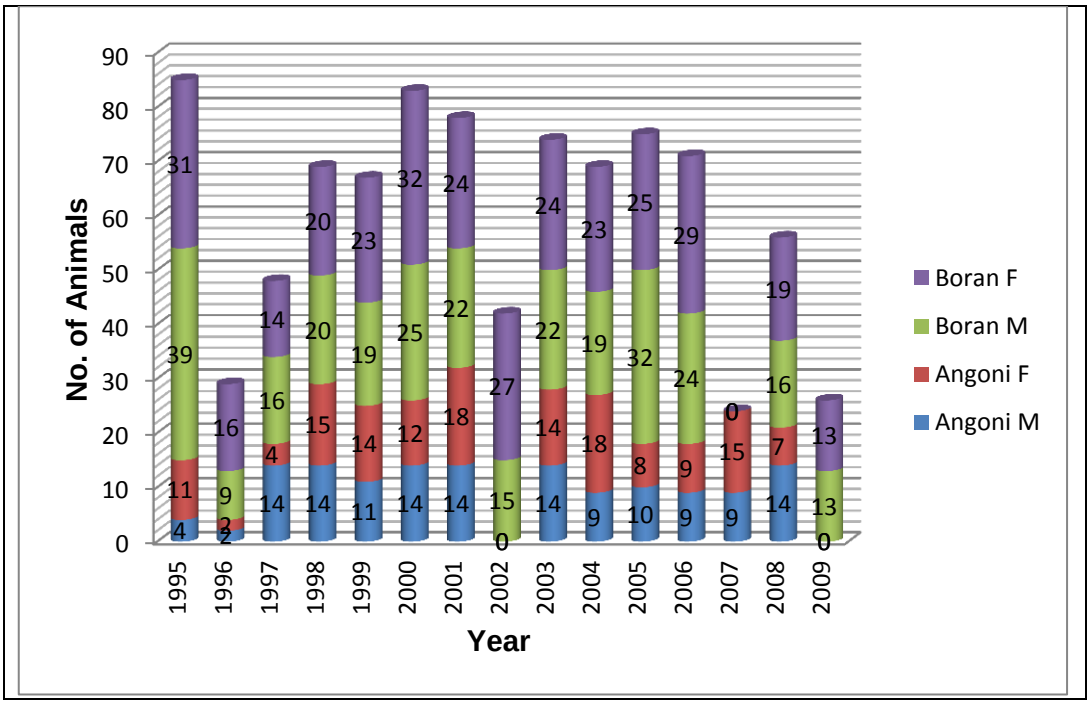


Figure 4.3: Distribution of birth records from 1995 to 2009 on the Lilayi farm in Zambia. Courtesy of Alan Miller (2012).

4.3.2 Weaning Weight

The contribution of weaning weight to the genetic improvement of growth in beef cattle is significant because the weight of a calf at weaning reflects both the ability for it to grow and the mothering ability of the dam. Tests of significance of fixed effects of year of birth,

season (winter and summer), breed (Angoni and Boran) and sex (male and female) were determined (Table 4.4). All main effects were highly significant but the interactions were not significant.

Table 4.4: Statistical analysis of variance for zebu cattle from Liyayi farm.

Source of variation	Degrees of Freedom	F-probability
Age	1	50.01**
Sex	1	59.66**
YOB	14	17.44**
Breed	1	50.89**
Age.Breed	1	0.09
Sex.Breed	1	0.14
YoB.Breed	10	1.24
Breed.Season	2	0.03

**P < 0.001; YOB= year of birth; DF= degrees of freedom. Breed =Angoni and Boran cattle

The year with the highest weaning weight was 1998 (152±3.3 kg), while the lowest was in 1996 (105±4.2 kg) (Figure 4.4). The data further indicated at weaning that the Boran calves were heavier than the Angoni (19%, 142 vs 119 kg); steers were heavier than heifers (7%, Boran 146 vs 137 kg and Angoni 124 vs 114 kg) (Appendix 4.2). The average age at weaning was 212 days and weaning weight was 137 kg. Based on the regression of weaning weight on age, the average daily gain was 0.19 kg/d for the Angoni calves and 0.26 kg/d for the Boran calves.

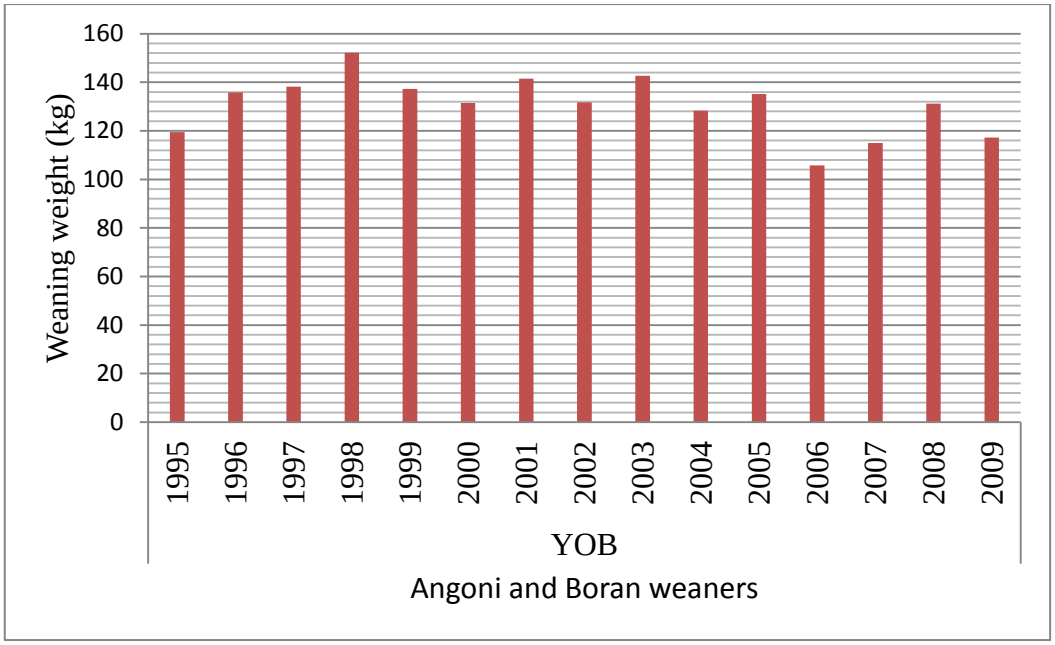


Figure 4.4: Annual variation in weaning weight for Angoni and Boran calves born 1995 to 2009. Data courtesy of Alan Miller (2012). YOB = year of birth.

4.3.4 Estimates of covariance components and genetic parameters

The covariance components and genetic parameters for weaning weight for Angoni and Boran cattle were estimated (Table 4.5). Model 6 estimated 3 components: the additive, maternal and residual components. Models 1-5 tested for significant improvements by including additional components for breed differences in each of the components in Model 6 and also for the covariance between additive and maternal effects. Thus, Model 1 had 8 components. However, adding any of these additional 5 components was not a significant improvement in the fit except for possibly model 5 which had 4 components: a common direct and maternal genetic effect but separate residual variances for the two breeds.

Model 8 differed from Model 6 by dropping the maternal component and included only an additive and residual effect (2 components) but there was a significant deviation indicating the maternal effect should be included. Model 7 was similar to Model 8, but had separate breed effects for the additive and residual components (for a total of 4), but was no better than Model 8. Although not presented, a common covariance was also tested in addition to the 3 components in Model 6 but it was not significant. Thus, it was clearly demonstrated that common variance components can be used across the breeds and that both an additive and maternal genetic effect on weaning weight should be included.

The results indicate no significant difference in the heritability between the Angoni and Boran breeds although model 5 (with common genetic effects but different residual variances) resulted in slightly different heritabilities (Table 4.5). For Model 6, the direct heritability for Angoni and Boran obtained was 20% and the maternal heritability was 19%.

Table 4.5: Estimated genetic parameters for weaning weight in zebu cattle (*Bos indicus*).

Parameters	MODEL[e]							
	1	2	3	4	5	**6**	7	8
σ^2_{Aa}	46.7±0.9	52.4±0.9	-	77.3±1.1	-	-	70.8±3.6	
σ^2_{Ab}	96.4±1.6	73.7±1.9	-	70.8±1.9	-	-	77.7±3.9	
σ^2_{A}	-	-	70.3±2.11	-	71.8±2.3	**71.1±2.2**	-	149.4
σ^2_{Ma}	50.5±1.2	76.9±2.4	72.3±2.44	-	-	-	-	
σ^2_{Mb}	71.7±1.8	51.7±2.9	52.3±2.22	-	-	-	-	
σ^2_{M}	-	-	-	61.4±3.1	62.1±3.2	**64.5±3.3**	-	
$\sigma_{A,Ma}$	28.1±0.8	-	-	-	-	-	-	
$\sigma_{A,Mb}$	-25.9±-0.6	-	-	-	-	-	-	
$r_{A\cdot Ma}$	0.58	-	-	-	-	-	-	
$r_{A,Mb}$	-0.31	-	-	--	-	-	-	
σ^2_{Ea}	194.1±5.4	189.6±4.8	180.7±6.4	179.4±4.3	182.3±6.5	-	152.73±4.8	
σ^2_{Eb}	218.7±6.4	256.7.2±8.9	258.4±9.5	254.1±8.9	253.3±3	-	222.4±7.1	
σ^2_{E}	-	--	-	-	-	**231.1±10**	-	
$^a\sigma^2_{Pa}$	319.8	318.9	323.3	318.1	316.2	-	223.5	
$^a\sigma^2_{Pb}$	360.6	382.1	377.0	386.3	387.2	-	300.1	
$^a\sigma^2_{P}$	-	-	-	-	-	**348.7**	-	373.3
$^bh^2_{Aa}$	14.6	16.4	21.7	24.3	22.7	-	31.7	
$^bh^2_{Ab}$	26.7	19.3	18.6	18.9	18.5	-	25.9	
$^bh^2_{A}$	-	-	-	-	-	**20.4**	-	40.0
$^ch^2_{Ma}$	15.8	24.1	22.4	19.3	19.6	-	-	
$^ch^2_{Mb}$	19.9	13.5	13.9	15.9	16.0	-	-	
$^ch^2_{M}$	-	-	-	-	-	**18.5**	-	
$^dh^2_{Ta}$	35.7	-	-	-	-	-	-	
$^dh^2_{Tb}$	25.9	-	-	-	-	-	-	
LogL	-2914.6	-2915.0	-2915.0	-2915.2	-2915.2	**-2917.8**	-2923.3	-2924.4
LRij		(0.78)	(0.04)	(0.28)	(0.04)	**(5.2)**	(11.1)**	2.2
LRij B					18.4**	**13.2****	2.2	

p<0.01; [a]subscript($\sigma^2_{p)} = \Sigma(\sigma^2_A + \sigma^2_M + \sigma_{A.M} + r_{A\cdot M} + \sigma^2_E)$; [b] subscript ($h^2_{A)} = \sigma^2_A/\sigma^2_p$);[c] subscript ($h^2_M$)= σ^2_M/σ^2_p; [d] subscript(h^2_T)=(σ^2As + 0.5σ^2Ms 1.5$\sigma_{A.Ms}$)/ σ^2_p [e] MODEL –description of all models are in the text. Fully Parameters are explained (Table 4.2) $LR_{ij}=2\log_e L_i - 2\log_e L$, **LRijB indicate difference between 8 and other models in question.

4.4 Discussion

4.4.1 Genetic parameters for weaning weight in zebu cattle

The results are not in agreement with some studies (Pico et al., 2004). The direct and maternal heritability estimates herein (20 and 19% respectively) were different from another study of Brahman cattle (Pico et al., 2004) which found a 14% direct heritability and 6% maternal heritability, but they were similar to the estimates of 20% and 15% for Tswana indigenous cattle in Botswana (Raphaka and Dzama, 2010). These studies indicated that maternal heritability significantly differed from direct heritability using different models. Moreover, Praharani (2009) demonstrated that there was significant difference in the co-variances between additive and maternal effects in Bali cattle. The direct and maternal heritability estimated were 30% and 8%, respectively. One major factor that possibly could cause a large difference in direct and maternal heritability estimates would have been that the Bali cattle were largely been supplemented throughout the season such that environmental factors would contribute largely to the final weaning weight. This was different from Angoni and Boran cattle herein that were pastures fed only.

Diop and Van Vleck (1998) found the same heritability estimate as herein (20%) for zebu Gobra (*Bos indicus)* cattle in Senegal, and the heritability estimated for Brahman cattle in Venezuela was only slightly lower (16%) (Plasse et al., 2002). The direct (24%) and maternal (13%) heritabilities of Boran obtained in the study by Koots et al. (1996) were also similar to the Zambian cattle in this study. The results herein are also comparable to the indigenous Tswana cattle in Botswana, with direct heritability estimates of 20% and maternal heritability estimates of 25%. However, the heritability estimates of the Boran cattle herein (direct =19%-27% and maternal =14-20%) were lower than the Boran

heritability estimates in Kenya reported by Wasike et al., (2006) (direct =31% and maternal =16-23%).

Several factors may have been responsible for the differences in the heritability estimates between the Kenya Boran and Zambian Boran, including the differences in the size of the data sets (Wright et al., 1985) and in the models applied to estimate the genetic effects. The direct and maternal heritability (45% and 5%, respectively) estimated in Asturiana de los Valles beef cattle (Gutierrez, 1997) using an animal model that included additive and maternal effects were different from estimates in this study, even though the `best' animal model were chosen according to the significant difference in the likelihood values similar to herein. The underlying reason may be attributed to the different types of breeds. The Asturiana is a double muscling taurine breed while the Zambian breeds are zebu and not doubled muscled. Interestingly, Meyer and Hill (1997) reported direct heritability (19-22%) and maternal heritability (14-18%) in Hereford cattle similar to this study. This is significant because by employing the appropriate genetic improvement program, Zambian cattle should achieve the same genetic gains observed in Hereford.

The significant maternal component is supported by most other studies analysing weaning weight that have used various models to measure the genetic parameters for growth traits in cattle (Nester et al., 1996; Meyer 1997; Wasike, 2006). Interestingly, the heritability levels were moderate but comparable to other breeds suggesting the lower observed post-weaning, joining and mature weights are attributed to environmental variance rather the lack of genetic variance. This further supports the finding of Thorpe et al. (1980) and Walker (1964) who reported that Angoni cattle are more efficient in terms of calf weaned per cow than Boran cattle (Chapter 1).

4.4.2 Non genetic parameters

Effect of year of birth

Weaning weights were consistently higher from 1998 to 2006 and lower from 2007 to 2009 (Figure 4.4). Numerous factors could have contributed to the variation in weaning weights observed over this 15 year period. For example, in sub-Sahara Africa regions, including Zambia, there has been a wide variation of annual rainfall and distribution patterns within seasons that are usually characterised by long droughts and heavy rainfalls (Marlowe and Gains 1958). The long persistent droughts and heavy storms that results in floods affect both the quantity and quality of pastures produced (Okantah, 1992; Sottie et al., 2009). This has a direct relationship with cattle output, affecting the weights of calves weaned in a particular year. Pauw and Thurlow (2011) showed that the quantity of maize yield was strongly positively correlated to the patterns of rainfall in a study on climate change, reflecting the effects of varying periods of drought that influence the availability of pastures and feed. Similar year effects on weaning weight ($P<0.01$) were obtained in a study of Bali cattle (Praharani, 2009).

The results of this study suggest that the season of birth has only a slight influence on weaning weight (Appendix 3.2). Comparing the two seasons (winter and summer) using simple averaging statistics indicates a difference of 2 kg between the 2 seasons. The calves weaned in the winter season had a mean overall weaning weight of 131.85±1.89 kg versus those weaned in summer with a mean overall weaning weight of 129.86±1.89 kg. The higher weights obtained in winter seasons are similar to those reported in other studies (Koch and Clark, 1955; Manzi et al., 2002; Pico et al., 2004; Sottie et al., 2009). The calves born in winter may have a better chance of utilising good pastures prior to weaning. Calves born in winter are also usually weaned when the rumen is probably fully

functional, six months after the date of birth (Heinrichs 2009). It is likely that the difference in weaning weight between the winter season and summer season may be influenced by environmental factors rather than genetic factors (Marlowe and Gains 1958).

Effect of sex

The results in this study indicate a significant difference ($P<0.001$) in mean weight between weaner steers (135.7±2.15kg) and weaner heifer (126.1± 2.15kg). The difference in weaning weight between males and females has long been explained by the action of testosterone circulating in the blood system of males responsible for secondary sexual characteristics (e.g. skeletal conformation and muscle size) acting as a growth hormone. However, the sex by breed interaction on weaning traits was not significant herein. Therefore, the indigenous Angoni breed should still respond favourably, similar to the improved Boran cattle subjected to same management systems.

Effect on breed

At weaning, the Boran calves were 19% heavier than Angoni (142 vs 119kg; Appendix 3.2). These results are in agreement with other studies that have found Boran calves have greater weaning weights than Angoni calves (Thorpe et al., 1981; Mwenya, 1993). Studies in Kenya showed significant differences between the weaning weights even in the small Boran cattle versus the improved Boran cattle (Mason and Maule, 1960; Haile-Mariam and Kassa-Mersha, 1995). However, Walker (1972) showed that when weaning weights are translated as a total output of a cow-calf unit, there was no statistically significant difference between the Angoni and Boran breeds ($P>0.05$). This suggests that even though the Angoni breed has lower weaning weights than the Boran, the Angoni

breed is likely to be as efficient and productive as the Boran. Nesting breed with each of other fixed effects (sex, year of birth and season) within the models showed no statistical difference under similar management systems.

4.5 Conclusion

Weaning weight was analysed as a model for other traits to quantify genetic variation in Zambian breeds under Zambian conditions. This study has confirmed that weaning weights are affected by both additive and maternal genetics and separate parameters for breeds are not necessary despite them differing in weaning weight by 19%. Common fixed effects of age, sew, season and year of birth have been also quantified. The results are similar to studies in other countries and breeds and the moderate heritability estimates demonstrate is there is ample opportunity for making genetic improvement in weaning weight.

Chapter 5

5.0 Summary

The global plan of action for the World Animal Genetic Resources of the Food and Agriculture Organisation (FAO 2007) aims to ensure the characterisation, utilisation and conservation of animal genetic diversity worldwide. Genetic diversity is significant to the food supply throughout the world as it is essential for the genetic improvement of domesticated species (Busch et al., 2007; Oldenbroek, 2007). Unique livestock genetic characteristics found in developing countries, including sub-Saharan Africa, are a valuable resource that needs to be managed well and preserved for future use. Specific examples are N'Dama cattle that are trypanotolerant and have the ability to survive in harsh environments and still provide milk and meat to the local people (De Joel et al., 1992). In Zambia, the Angoni cattle are able to produce a calf nearly every year under harsh conditions and still provide power to cultivate agricultural lands for long periods of time (Walker 1964; Thorpe et al., 1989).

This study provides preliminary insight into the level of genetic diversity within Zambian indigenous cattle populations (Chapter 3). The results indicate that when genotyped of 32 microsatellite panel the three breeds studied (Angoni, Barotse and Tonga) share some common genotypes so there may be some overlap between the breeds (Figure 3.3). They were placed into two rather than three main clusters (Figures 3.6 and 3.7). The overlap could be due to the crossbreeding with the Sanga that occurred during cattle dispersion from east Africa to central Africa (Hanotte et al., 2002; Hanotte and Jianlin, 2006). The Tonga breed appears to be more diverse than the Angoni and Barotse breeds. Thus, breed conservation may not be relevant for the Tonga. Interestingly, the Barotse cattle have

been isolated in the Zambezi flood plan, with a fixation index of almost zero indicating the population may be exhibiting a Wahlund effect (Christiansen, 1988). This is a significant finding for this study because the allele frequencies for the Barotse will remain constant in the near future so genetic improvement and conservation programs need to consider that some genes may be fixed.

Historical perspective indicate that cattle have adapted to different environments through natural selection (Murray, 2004; Franklin et al., 2006; Blackburn, 2012). Despite selection, the results indicate that Zambian indigenous cattle appear to have a large amount of genetic diversity that can be exploited in breeding programs without the need to introduce other genetic material from elsewhere. The indigenous Zambian cattle possess desirable characteristics such as a reduced susceptibility to diseases and the ability to survive and reproduce in hash environmental conditions with little veterinary attention (Thorpe et al., 1980). It should be possible to retain these desirable characteristics and still improve various production traits through genetic breeding programs. For example, the Nandi zebu cattle are tolerant to most external parasites (such as ticks, biting flies) and are resistant to tick-borne diseases, yet have been bred for increased milk production (Hanotte et al., 2000; Payne and Williamson, 1990). Another example is in Gambia, a successful breeding program that involved local cattle farmers has been implemented, resulting in genetic gain for body weight and milk yield in the locally adapted N'Dama cattle (Ahunu et al., 1997; Dempfle and Jaitner 2000).

The choice of production trait breeding objectives in such genetic improvement programs is difficult. This is because cattle are used for multiple purposes by the rural people in Sub-Saharan Africa (Thorthon 2002; Gibson et al., 2006, Mulemba, 2009). Knowledge of the most important attributes of cattle is required to achieve effective genetic

improvement progress in any breeding program (Smith 1988). A social science study was conducted herein using both qualitative and quantitative techniques to determine producer preferences with regards to production traits in cattle (Chapter 2). This is critical because breed improvement programs must take farmer preferences into account if the programs are to be successful. Using both parametric and non-parametric tests (Chapter 2), it was found that preferences were consistent across the different regions in Zambia, but differed between large and small-scale breeders (Table 2.4). Large scale cattle farmers (60%, Table 2.1) are mostly predominant in the pastoral communities and practice transhumance similar to habitants of the Namwala areas who raise Angoni and Brahman cattle (Mwenya 1993). More emerging small scale farmers were found in Chipata and had less than 50 cattle but the results were similar in the other districts. The larger scale cattle farmers ranked animal size more highly than fertility, whereas the emerging small-scale cattle farmers were opposite. Having established that animal size and fertility were preferred differently depending upon the scale of the production this information can help develop selection indices for such traits in the Zambian cattle breeding programs to benefit the rural populations in Zambia.

In addition to establishing farmer preferences, measurement of genetic gain is key to any genetic breeding program to improve the livelihood of cattle farmers. Smith (1988) stated that estimating production parameters for growth traits provides a way of monitoring and evaluating the progress of selection and demonstrates to the farmers that the effort is worthwhile. The results of the study herein indicate that both the direct and maternal heritability of weaning weight are moderate but sufficient for good genetic progress. Given that weaning weight has similar genetic variances to other studies, it is assumed this would be the case for other traits and breeding programs could be designed without extensive local parameter estimation for all traits in the breeding objectives.

Efforts that focus on developing sustainable genetic improvement programs for local and well-adapted breeds taking into account the preferred attributes, available genetic diversity, and estimated genetic parameters will be beneficial to cattle farmers and help implement sound conservation of genetic diversity. Numerous organisations are likely to be involved in cattle improvement programs as reported in the Zambian Parliamentary Committee on Agriculture (Committee on Agriculture, 2013). However, appropriate roles need to be clearly defined in order to circumvent misinterpretation in the process of implementation of the breeding programs. It will be important to learn lessons from the experience of successful breeding schemes in Africa (Aluya et al., 2005; Bradley et al., 2006).

Opening up nucleus breeding schemes by involving local farmers who are willing to join the schemes is very important. However, the farmers highlighted numerous caveats during the study, such as inadequate veterinary services, poor infrastructure and little knowledge of cattle management practices. As changes in the average performance of cattle are the product of combination of genetic change with environmental factors, these problems need to be addressed at the inception of designing the cattle breeding programs for each specific region. Other limitations that were found are common among developing countries and included the lack of proper guidelines on land property rights, poor access or no access to clean water throughout the year, and uncontrolled breeding (Kosgey et al., 2006; FAO 2011). The lack of disease prevention and control also significantly contributes to cattle loss throughout the regions as noted by others (Gall 1997). Therefore, it is important to involve several farmers in co-operatives (Smith 1988) or as groups of individual farm units with a considerable number of animals from which replacements can be obtained. Implementing cattle breeding programs that involve local

farmers as an integral part of the production system from inception are more likely to be successful (Aluya 2005; van Arendonk, 2003).

Using cattle that survive, reproduce, and provide multiple functions can improve the standard of living for cattle farmers in Zambia. However, in the future, this will depend on developing flexible and operational breeding programs that suit local farmers. This is because the indigenous cattle breeds will continue to be raised under traditional management systems without feed supplementation and minimal use of animal health treatments. So access to global markets will only be possible if farmers are provided with opportunities to improve their local, well-adapted cattle. The programs will need to be flexible in the sense that large scale farmers and small scale farmers are likely to have different breeding objectives (eg size versus fertility). The differences in preference may also affect breed choice. The study herein determined that large scale cattle farmers in Zambia have a strong preference for size while small scale farmers slightly prefer fertility, and thus, large scale farmers are likely to prefer the larger Barotse and the small scale farmers are likely to prefer the more fertile Angoni.

In most developing countries, record keeping is poorly undertaken and information transmission mostly depends on hearsay. Therefore, using data from commercial farms that keep traditional cattle breeds and good records will be useful in estimating genetic parameters for traits. Moreover, the results herein are similar to studies in other countries and the moderate heritability estimates indicate there is room for genetic improvement in traits such as weaning weight. Thus, it is feasible to develop selection indices that incorporate growth and reproductive performance while also at least maintaining adaptability and requirements for traction in the improvement of Zambian cattle. Given the different emphasis identified, a strategy could be to improve the locally adapted,

fertile Angoni for emerging small scale farmers and the locally adapted, large Barotse for large scale cattle farmers using such selection indices and genetic parameter estimates from Zambian commercial farm data.

The survey herein was conducted for six months and the respondents were purposely selected due to the limited time and resources available for data collection. Hence, a moderate sample size was used herein. This may not have greatly affected the content analysis, but the sample size may have affected the outcome of the parametric tests. Therefore, a similar study should be conducted which can includes more individuals to clearly quantify the trait preferences of farmers.

Although the genetic diversity results were comparable to other studies, more work is also required on classification the Zambian indigenous cattle based on microsatellite genotyping by including much larger and balanced populations with many more representatives of each breed at each location. The markers used herein would allow the breed diversity to be compared with other breeds and other regions in Zambia or sharing borders with Zambia as they included markers in common with the ISAG panel. Using a larger panel of 32 microsatellites herein provided better genome coverage than is commonly achieved, but if feasible, the gold standard would be to use a cattle SNP chip.

Measuring genetic parameters for production traits is most important. Herein the direct and maternal heritability were estimated for only one trait, weaning weight, and used data from a limited number of individuals. To develop a large national cattle breeding program, genetic parameters need to be estimated for other traits (e.g pre-weaning weight, calving interval, heifer joining weight) using a larger data set that includes many different properties in the country.

Therefore, it is recommended that there is:

1. Ongoing work on economic values and trait preferences to enable development of clear breeding objectives;

2. Parameter estimation conducted for a wider range of traits that affect productivity;

3. Genotyping of a larger number of animals from each breed to gain a greater understanding of breed origin and diversity;

4. Sequencing of influential sires to develop genomic tests for ongoing breed improvement; and

5. Development of strategies for low-cost recording of pedigree and measurement of key traits.

References

Ahunu, B, Arthur, P, Kissiedu, H (1997) Genetic and phenotypic parameters for birth and weaning weights of purebred and crossbred Ndama and West African Shorthorn cattle. *Livestock Production Science* **51**, 165-171.

Ahuya, CO, Okeyo, AM, Mwangi, N, Peacock, C (2005) Developmental challenges and opportunities in the goat industry: The Kenyan experience. *Small Ruminant Research* **60**, 197-206.

Alroe, HF, Kristensen, ES (2002) Towards a systemic research methodology in agriculture: rethinking the role of values in science. *Agriculture and Human Values* **19**, 3-23.

Amer, PR, Mpofu, N & Bondoc, O 1998, Definition of breeding objectives for sustainable production systems, Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, Armidale, NSW, Australia, 11-16 January, 1998. Volume 28: Animal genetic resources and sustainable development. 6WCGALP/FAO Symposium

Anderson, J (1949) Artificial insemination in cattle breeding in Kenya. *East African Agricultural Journal* **14**, 148-150.

Andersson, L (2001) Genetic dissection of phenotypic diversity in farm animals. *Nature Reviews Genetics* **2**, 130-138.

Animal Husbandry Research Division (1976) Annual report of the Animal Husbandry Research Division, Department of Agriculture, Central Research Station, Mazabuka, for the period 1st October, 1975 to 30th September, 1976. (Zambia Department of Agriculture: Lusaka).

Araya, A, Habtu, S, Hadgu, KM, Kebede, A, Dejene, T (2010) Test of AquaCrop model in simulating biomass and yield of water deficient and irrigated barley (*Hordeum vulgare*). *Agricultural Water Management* **97**, 1838-1846.

Assan, N (2012) Genetic improvement and utilization of indigenous cattle breeds for beef production in Zimbabwe: past, present and future prospects. *Scientific Journal of Agriculture* **1**, 1-13.

Aune, JB, Bussa, MT, Asfaw, FG, Ayele, AA (2001) The ox ploughing system in Ethiopia: can it be sustained? *Outlook on Agriculture* **30**, 275-280.

Baker, RL, Rege, JEO (1994) Genetic resistance to diseases and other stresses in improvement of ruminant livestock in the tropics. *Proceedings, 5th World Congress, University of Guelph, Guelph, Ontario, Canada, 7-12 August, 1994. Volume 20. Poultry breeding; avian biotechnology; behaviour genetics; reproductive biotechnology; immunogenetics and disease resistance genetics; breeding in the tropics and extreme environments.* 405-412.

Barendse, W, Vaiman, D, Kemp, SJ, Sugimoto, Y, Armitage, SM, Williams, JL, Sun, HS, Eggen, A, Agaba, M, Aleyasin, SA, Band, M, Bishop, MD, Buitkamp, J, Byrne, K, Collins, F, Cooper, L, Coppettiers, W, Denys, B, Drinkwater, RD, Easterday, K, Elduque, C, Ennis, S, Erhardt, G, Ferretti, L, Flavin, N, Gao, Q, Georges, M, Gurung, R, Harlizius, B, Hawkins, G, Hetzel, J, Hirano, T, Hulme, D, Jorgensen, C, Kessler, M, Kirkpatrick, BW, Konfortov, B, Kostia, S, Kuhn, C, Lenstra, JA, Leveziel, H, Lewin, HA, Leyhe, B, Lil, L, Burriel, IM, McGraw, RA, Miller, JR, Moody, DE, Moore, SS, Nakane, S, Nijman, IJ, Olsaker, I, Pomp, D, Rando, A, Ron, M, Shalom, A, Teale, AJ, Thieven, U, Urquhart, BGD, Vage, DI, VandeWeghe, A, Varvio, S, Velmala, R, Vikki, J, Weikard, R, Woodside, C, Womack, JE, Zanotti, M, Zaragoza, P (1997) A medium-density genetic linkage map of the bovine genome. *Mammalian Genome* **8**, 21-28.

Barrett, T, Rossiter, P (1999) Rinderpest: the disease and its impact on humans and animals. *Advances in Virus Research* **53**, 89-110.

Barriball, KL, While, A (1994) Collecting data using a semi structured interview a discussion paper. *Journal of Advanced Nursing* **19**, 328-335.

Bebe, BO, Udo, HMJ, Thorpe, W (2008) Characteristics of feeding and breeding practices for intensification of smallholder dairy systems in the Kenya highlands. *Livestock Research for Rural Development* **20**, 20023-20023.

Bijma, P (2006) Estimating maternal genetic effects in livestock. *Journal of Animal Science* **84**, 800-806.

Bishop, SC (2012) Possibilities to breed for resistance to nematode parasite infections in small ruminants in tropical production systems. *Animal* **6**, 741-747.

Blackburn, HD (2012) Genetic Selection and Conservation of Genetic Diversity. *Reproduction in Domestic Animals* **47**, 249-254.

Bobe, G, Beitz, D, Freeman, A, Lindberg, G (1999) Effect of milk protein genotypes on milk protein composition and its genetic parameter estimates. *Journal of Dairy Science* **82**, 2797-2804.

Boston, EJ (1961) The Indigenous Livestock of Eastern and Southern Africa. By I. L. Mason and J. P. Maule (Book Review). 61: 118.

Bradley, D, Hanotte, O, Otsen, M, Lenstra, J (1999) Satellite DNA polymorphisms and AFLP correlate with Bos indicus-taurus hybridization. *Animal genetics* **30**, 265-273.

Bradley, DG, Loftus, RT, MacHugh, DE, Cunningham, P (1997) The molecular evolution of domestic cattle. In 'International Symposium on Mediterranean Animal Germplasm and Future Human Challenges: A Joint Eaap - Fao - Ciheam International Symposium.' (Eds D Matassino, J Boyazoglu, A Cappuccio.) pp. 55-59.

Brady, NC, Weil, RR (2010) Elements of the nature and properties of soils'. (Pearson Prentice Hall UK

Bruford, MW, Bradley, DG, Luikart, G (2003) DNA markers reveal the complexity of livestock domestication. *Nature Reviews Genetics* **4**, 900-910.

Bryman, A (2007) Barriers to Integrating Quantitative and Qualitative Research. *Journal of Mixed Methods Research* **1**, 8-22.

Buckman, HO, Brady, NC (1960) The nature and properties of soils. *Soil Science* **90**, 212.

Burrow, HM (2012) Importance of adaptation and genotype X environment interactions in tropical beef breeding systems. *Animal* **6**, 729-740.

Busch, DC, Williamson, DJ, Schafer, DJ, Leitman, NR, Haden, JK, Ellersieck, MR, Smith, MF, Patterson, DJ (2007) Comparison of progestin-based estrus synchronization protocols before fixed-time artificial insemination on pregnancy rate in beef heifers. *Journal of Animal Science* **85**, 1933-1939.

Butterworth, MH, McNitt, JI (1983) Slaughter and carcass characteristics of malawi-zebu steers and some observations on hindquarter conformation. *Tropical Agriculture* **60**, 221-223.

Byrne, TJ, Amer, PR, Fennessy, PF, Hansen, P, Wickham, BW (2012) A preference-based approach to deriving breeding objectives: applied to sheep breeding. *Animal* **6**, 778-788.

Caballero, A, Toro, MA (2002) Analysis of genetic diversity for the management of conserved subdivided populations. *Conservation Genetics* **3**, 289-299.

Calus, MPL (2010) Genomic breeding value prediction: methods and procedures. *Animal* **4**, 157-164.

Campbell, D, Bernatchez, L (2004) Generic scan using AFLP markers as a means to assess the role of directional selection in the divergence of sympatric whitefish ecotypes. *Molecular Biology and Evolution* **21**, 945-956.

Canon, J, Alexandrino, P, Bessa, I, Carleos, C, Carretero, Y, Dunner, S, Ferran, N, Garcia, D, Jordana, J, Laloe, D, Pereira, A, Sanchez, A, Moazami-Goudarzi, K (2001) Genetic diversity measures of local European beef cattle breeds for conservation purposes. *Genetics Selection Evolution* **33**, 311-332.

Cardellino, RA, Boyazoglu, J (2009) Research opportunities in the field of animal genetic resources. *Livestock Science* **120**, 166-173.

Central Statistical Office (2010),census of population and housing. volume 11. national descriptive tables published by Central Statistical Office< <www.zamstats.gov.zm/.../Census/2010/2010%20Census%20of%20Popul...accessed on 20th June, 2013>

Chilonda, P, Van Huylenbroeck, G, D'Haese, L, Samui, KL, Musaba, EC, Imakando, M, Ahmadu, B (1999) Cattle production and veterinary care systems in Zambia. *Outlook on Agriculture* **28**, 109-116.

Christiansen, FB (1988) The Wahlund effect with overlapping generations. *The American Naturalist* **131**, 149-156.

Clément, V, Bibé, B, Verrier, É, Elsen, J-M, Manfredi, E, Bouix, J, Hanocq, É (2001) Simulation analysis to test the influence of model adequacy and data structure on the estimation of genetic parameters for traits with direct and maternal effects. *Genetics Selection Evolution* **33**, 369-396.

Committee on Agriculture Zambia (2013) Report of the Committee on Agriculture for the second session of the eleventh National Assembly appointed on Thursday 27th September, 2012. Available at: http://www.parliament.gov.zm/index.php?option=com_docman&task=doc_download&gid=1100 (verified 20 February 2013).

Conway P Clarke, George R.; Shah, Manu Kedia; Sheppard, Marie; Munro, Juliet; Pearson Jr., Roland V.. 2010. Who's productive in Zambia's private sector? - Evidence from the Zambia Business Survey. Vol. 2 of Zambia - Zambia Business Survey. Washington, DC: World Bank. http://documents.worldbank.org/curated/en/2010/06/16362743/zambia-zambia-business-survey-vol-2-5-whos-productive-zambias-private-sector-evidence-zambia-business-survey

Dadi, H, Tibbo, M, Takahashi, Y, Nomura, K, Hanada, H, Amano, T (2008) Microsatellite analysis reveals high genetic diversity but low genetic structure in Ethiopian indigenous cattle populations. *Animal Genet* **39**, 425-31.

Davies, G, Genini, S, Bishop, SC, Giuffra, E (2009) An assessment of opportunities to dissect host genetic variation in resistance to infectious diseases in livestock. *Animal* **3**, 415-436.

Davis, G (1993) Genetic parameters for tropical beef cattle in Northern Australia: a review. *Crop and Pasture Science* **44**, 179-198.

Davis, GP, DeNise, SK (1998) The impact of genetic markers on selection. *Journal of Animal Science* **76**, 2331-2339.

Davison, D, Pritchard, JK, Coop, G (2009) An approximate likelihood for genetic data under a model with recombination and population splitting. *Theoretical Population Biology* **75**, 331-345.

de Albuquerque, G (2001) Estimates of direct and maternal genetic effects for weights from birth to 600 days of age in Nelore cattle. *Journal of Animal Breeding and Genetics* **118**, 83-92.

Dekkers, J (1992) Asymptotic response to selection on best linear unbiased predictors of breeding values. *Anim. Prod* **54**, 351-360.

Dekkers, JCM (2003) Commercial application of marker- and gene-assisted selection in livestock: Strategies and lessons. *Journal of Dairy Science* **86**, 5-5.

Dekkers, JCM (2004) Commercial application of marker- and gene-assisted selection in livestock: strategies and lessons. *Journal of animal science* **82 E-Suppl**, E313.

Dekkers, JCM (2007) Prediction of response to marker-assisted and genomic selection using selection index theory. *Journal of Animal Breeding and Genetics* **124**, 331-341.

Dekkers, JCM (2012) Application of Genomics Tools to Animal Breeding. *Current Genomics* **13**, 207-212.

Dekkers, JCM, Hospital, F (2002) Multifactorial genetics the use of molecular genetics in the improvement of agricultural populations. *Nature Reviews Genetics* **3**, 22-32.

Dekkers, JCM 2007, 'Prediction of response to marker-assisted and genomic selection using selection index theory', Journal of Animal Breeding and Genetics, vol. 124, no. 6, Dec, pp. 331-341.

Dekkers, JCM 2012, 'Application of Genomics Tools to Animal Breeding', Current Genomics, vol. 13, no. 3, May, pp. 207-212.Delgado, JV, Martinez, AM, Acosta, A, Alvarez, LA, Armstrong, E, Camacho, E, Canon, J, Cortes, O, Dunner, S, Landi, V, Marques, JR, Martin-Burriel, I, Martinez, OR, Martinez, RD, Melucci, L, Munoz, JE, Penedo, MCT, Postiglioni, A, Quiroz, J, Rodellar, C, Sponenberg, P, Uffo, O, Ulloa-Arvizu, R, Vega-Pla, JL, Villalobos, A, Zambrano, D, Zaragoza, P, Gama, LT, Ginja, C (2012) Genetic characterization of Latin-American Creole cattle using microsatellite markers. *Animal Genetics* **43**, 2-10.

Demeke, S, Neser, F, Schoeman, S (2004) Estimates of genetic parameters for Boran, Friesian and crosses of Friesian and Jersey with the Boran cattle in the tropical highlands of Ethiopia: reproduction traits. *Journal of Animal Breeding and Genetics* **121**, 57-65.

Dempfle, L (1992) Report on genetic improvement of trypanotolerant livestock in West and Central Africa. In 'FAO Animal Production and Health Paper; Proceedings of the FAO expert consultation on the genetic aspects of trypanotolerance.' Vol. 94 pp. 77-121.

Dennis, ES, Ellis, J, Green, A, Llewellyn, D, Morell, M, Tabe, L, Peacock, WJ (2008) Genetic contributions to agricultural sustainability. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences* **363**, 591-609.

Desta, TT, Ayalew, W, Hegde, BP (2011) Breed and trait preferences of Sheko cattle keepers in southwestern Ethiopia. *Tropical Animal Health and Production* **43**, 851-856.

Diop, M, Van Vleck, L (1998) Estimates of genetic parameters for growth traits of Gobra cattle. *Animal Science* **66**, 349-356.

Drucker, AG, Gomez, V, Anderson, S (2001) The economic valuation of farm animal genetic resources: a survey of available methods. *Ecological Economics* **36**, 1-18.

Ducrocq, V, Quaas, RL (1988) Prediction of genetic response to truncation selection across generations. *Journal of Dairy Science* **71**, 2543-2553.

Duguma, G, Mirkena, T, Haile, A, Okeyo, AM, Tibbo, M, Rischkowsky, B, Soelkner, J, Wurzinger, M (2011) Identification of smallholder farmers and pastoralists' preferences for sheep breeding traits: choice model approach. *Animal* **5**, 1984-1992.

Edea, Z, Dadi, H, Kim, S-W, Dessie, T, Lee, T, Kim, H, Kim, J-J, Kim, K-S (2013) Genetic diversity, population structure and relationships in indigenous cattle populations of Ethiopia and Korean Hanwoo breeds using SNP markers. *Frontiers in Genetics* **4**,15-20

Eggen, A (2012) The development and application of genomic selection as a new breeding paradigm. *Animal Frontiers* **2,** 10-15.

Eler, J, Van Vleck, LD, Ferraz, J, Lôbo, R (1995) Estimation of variances due to direct and maternal effects for growth traits of Nelore cattle. *Journal of Animal Science* **73**, 3253-3258.

Elsen, JM (2003) Utilization of genomic information in livestock improvement. *Outlook on Agriculture* **32**, 241-245.

Epstein H. (1971) The Origin of the Domesticated Animals of Africa, Vol. I. African Publishing Corporation, New York.

Epstein H. & Mason I.L. (1984) Cattle. In: Evolution of Domesticated Animals (Ed. by I.L. Mason), pp. 6–27. Longman, New York.

European Environment, A, European Environment, A (2006) 'Progress towards halting the loss of biodiversity by 2010.' FAO 2011

Excoffier, L, Laval, G, Schneider, S (2005) Arlequin (version 3.0): an integrated software package for population genetics data analysis. *Evolutionary Bioinformatics Online* **1**, 47.

Falconer, D. S., and T. F. C. Mackay (1996) In 'Introduction to Quantitative Genetics'. 4th ed. Addison Wesley Longman, Essex, UK.

Falconer, DS (1989) In 'Introduction to Quantitative Genetics.' (Longman: London)

Falush, D, Stephens, M, Pritchard, JK (2007) Inference of population structure using multilocus genotype data: dominant markers and null alleles. *Molecular Ecology Notes* **7**, 574-578.

Fernandez, J, Toro, MA (2006) A new method to estimate relatedness from molecular markers. *Molecular Ecology* **15**, 1657-1667.

Fielder, RJ (1973) Role of cattle in Ila economy - conflict of views on uses of cattle by ila of namwala. *African Social Research* 327-361.

Fisher, J, Tozer, P, Abrecht, D (2012) Livestock in no-till cropping systems - a story of trade-offs. *Animal Production Science* **52**, 197-214.

Flynn, P (2009) 'Characterisation of rare Irish cattle breeds by comparative molecular studies using nuclear and mitochondrial DNA markers.' PhD thesis, University College Dublin.

Franklin, IR (1986) Breeding ruminants for the tropics. *3rd World Congress on Genetics applied to Livestock Production, Lincoln, Nebraska, USA, July 16-22, 1986. XI. Genetics of reproduction, lactation, growth, adaptation, disease, and parasite resistance.* 451-461.

Freeman, AR, Bradley, DG, Nagda, S, Gibson, JP, Hanotte, O (2006) Combination of multiple microsatellite data sets to investigate genetic diversity and admixture of domestic cattle. *Animal Genetics* **37**, 1-9.

Frisch, JE & Vercoe, JE 1986, Genetic improvements to productivity of cattle in tropical Africa, Nuclear and related techniques for improving productivity of indigenous animals in harsh environments. Proceedings of an advisory group meeting held in Ankara from 3 to 8 June 1985.

Fynn, RWS, O'Connor, TG (2000) Effect of stocking rate and rainfall on rangeland dynamics and cattle performance in a semi-arid savanna, South Africa. *Journal of Applied Ecology* **37**, 491-507.

Gibson, J, Ayalew, W, Hanotte, O (2007) Measures of Diversity as Inputs for Decisions in Conservation of Livesctock Genetic Resources. *Managing Biodiversity in Agricultural Ecosystems. Bioversity International, Columbia University Press, New York* 117-140.

Gibson, J, Gamage, S, Hanotte, O, Iñiguez, L, Maillard, J, Rischkowsky, B, Semambo, D, Toll, J (2006) Options and strategies for the conservation of farm animal genetic resources: Report of an international workshop (7–10 November 2005, Montpellier, France). *CGIAR System-wide Genetic Resources Programme (SGRP)/Bioversity International, Rome, Italy* 5.

Gill, WJ (1999) The Doubly Green Revolution: food for all in the twenty-first century. *Geographical Journal* **165**, 233-234.

Gilmour, AR, Gogel, B, Cullis, B, Thompson, R (2009) ASReml user guide release 3.0. *VSN International Ltd, Hemel Hempstead, UK*

Goddard, M (2009) Genomic selection: prediction of accuracy and maximisation of long term response. *Genetica* **136**, 245-257.

Goddard, ME (2012) Uses of genomics in livestock agriculture. *Animal Production Science* **52**, 73-77.

Goddard, ME, Hayes, BJ (2009) Mapping genes for complex traits in domestic animals and their use in breeding programmes. *Nature Reviews Genetics* **10**, 381-391.

Golden, BL, Garrick, DJ, Benyshek, LL (2009) Milestones in beef cattle genetic evaluation. *Journal of Animal Science* **87**, E3-E10.

Gomez-Romano, F, Villanueva, B, Rodriguez de Cara, MA, Fernandez, J (2013) Maintaining genetic diversity using molecular coancestry: the effect of marker density and effective population size. *Genetics, Selection, Evolution* **45**, (2 October 2013)-(2 October 2013).

Grapes, L, Dekkers, JCM, Rothschild, MF, Fernando, RL (2004) Comparing linkage disequilibrium-based methods for fine mapping quantitative trait loci. *Genetics* 166, 1561-1570.

Greene, WH, Hensher, DA, Rose, J (2006) Accounting for heterogeneity in the variance of unobserved effects in mixed logit models. *Transportation Research Part B-Methodological* **40**, 75-92.

Groeneveld, LF, Lenstra, JA, Eding, H, Toro, MA, Scherf, B, Pilling, D, Negrini, R, Finlay, EK, Jianlin, H, Groeneveld, E, Weigend, S, Consortium, G (2010) Genetic diversity in farm animals - a review. *Animal Genetics* **41**, 6-31.

Gunawan, A, Sari, R, Parwoto, Y, Uddin, M (2011) Non genetic factors effect on reproductive performance and preweaning mortality from artificially and naturally bred in Bali Cattle. *Journal of the Indonesian Tropical Animal Agriculture* **36**, 83-90.

Gutiérrez, J, Canon, J, Goyache, F (1997) Estimation of direct and maternal genetic parameters for pre-weaning traits in the Asturiana de los Valles beef cattle breed through animal and sire models. *Journal of Animal Breeding and Genetics* **114**, 261-266.

Gwakisa, PS, Kemp, SJ, Teale, AJ (1994) Characterization of zebu cattle breeds in Tanzania using random amplified polymorphic dna markers. *Animal Genetics* **25**, 89-94.

Haan, Cd (2001) 'Livestock Development: A Strategy Paper for the World Bank.' (World Bank Publications:

Habier, D, Fernando, RL, Dekkers, JCM (2009) Genomic Selection Using Low-Density Marker Panels. *Genetics* **182**, 343-353.

Habier, D, Tetens, J, Seefried, FR, Lichtner, P, Thaller, G (2010) The impact of genetic relationship information on genomic breeding values in German Holstein cattle. *Genetics Selection Evolution* **42**,

Haggblade, S, Tembo, G (2003) Conservation farming in Zambia. Available at: http://www.google.com.au/url?sa=t&rct=j&q=&esrc=s&frm=1&source=web&cd=1&cad=rja&ved=0CC0QFjAA&url=http%3A%2F%2Fwww.fao.org%2Fprods%2Fgap%2Fdatabase%2Fgap%2Ffiles%2F327_CONSERVATION_FARMING_IN_ZAMBIA.PDF&ei=18kGU7PPBsiulQWfnIDIAQ&usg=AFQjCNEJo1ZfgGISqV3Qabo3Z7lxYNTXWw&bvm=bv.61725948,d.dGI(13 March 2013)

Haile, A, Joshi, B, Ayalew, W, Tegegne, A, Singh, A (2009) Genetic evaluation of Ethiopian Boran cattle and their crosses with Holstein Friesian in central Ethiopia: milk production traits. *Animal* **3**, 486-493.

Haile-Mariam, M, Kassa-Mersha, H (1995) Estimates of direct and maternal (co) variance components of growth traits in Boran cattle. *Journal of Animal Breeding and Genetics* **112**, 43-52.

Hall, SJ, Bradley, DG (1995) Conserving livestock breed biodiversity. *Trends in Ecology & Evolution* **10**, 267-270.

Hall, SJG, Ruane, J (1993) Livestock breeds and their conservation - a global overview. *Conservation Biology* **7**, 815-825.

Hall., SJG (2004) In 'Livestock Biodiversity: Genetic Resources for the Farming of the Future.' Vol. 1 (Blackwell Science, United Kingdom)

Hammond, K (1998) Animal genetic resources for the twenty-first century. *Acta Agriculturae Scandinavica Section a-Animal Science* 11-18.

Hanotte, O, Bradley, DG, Ochieng, JW, Verjee, Y, Hill, EW, Rege, JEO (2002) African pastoralism: Genetic imprints of origins and migrations. *Science* **296**, 336-339.

Hanotte, O, Jianlin, H (2006) Genetic characterization of livestock populations and its use in conservation decision-making. *The role of biotechnology in exploring and protecting agricultural genetic resources. FAO, Rome, Italy* 89-96.

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

Hartemink, AE, Veldkamp, T, Bai, ZG (2008) Land cover change and soil fertility decline in tropical regions. *Turkish Journal of Agriculture and Forestry* **32**, 195-213.

Hassen, F, Bekele, E, Ayalew, W, Dessie, T (2007) Genetic variability of five indigenous Ethiopian cattle breeds using RAPD markers. *African Journal of Biotechnology* **6**,

Hayes, B, Goddard, ME (2001) The distribution of the effects of genes affecting quantitative traits in livestock. *Genetics Selection Evolution* **33**, 209-229.

Hayes, BJ, Visscher, PM, McPartlan, HC, Goddard, ME (2003) Novel multilocus measure of linkage disequilibrium to estimate past effective population size. *Genome Research* **13**, 635-643.

Hedrick, PW, Kalinowski, ST (2000) Inbreeding depression in conservation biology. *Annual Review of Ecology and Systematics* **31**, 139-162.

Heinrichs, A, Lesmeister, K, Garnsworthy, P (2005) In 'Rumen development in the dairy calf, Calf and heifer rearing: principles of rearing the modern dairy heifer from calf to calving. 60th University of Nottingham Easter School in Agricultural Science, Nottingham, UK. 23rd-24th March, 2004.'. (Nottingham University Press, United Kingdom)

Henderson, CR (1973) 'Sire evaluation and genetic trends, Proceedings of the animal breeding and genetics symposium in honor of Dr. Jay L. Lush.' Biometrics 423-447.

Henderson, CR (1975) Best linear unbiased estimation and prediction under a selection model. *Biometrics* 423-447.

Hensher, DA (1994) Stated preference analysis of travel choices - the state of practice. *Transportation* **21**, 107-133.

Hensher, DA, Greene, WH (2003) The Mixed Logit model: The state of practice. *Transportation* **30**, 133-176.

Herskovits, MJ (1926) The cattle complex in east Africa*. *American Anthropologist* **28**, 230-272.

Hiendleder, S, Bauersachs, S, Boulesteix, A, Blum, H, Arnold, GJ, Frohlich, T, Wolf, E (2005) Functional genomics: tools for improving farm animal health and welfare. *Revue Scientifique Et Technique-Office International Des Epizooties* **24**, 355-377.

Hocquette, JF, Lehnert, S, Barendse, W, Cassar-Malek, I, Picard, B (2007) Recent advances in cattle functional genomics and their application to beef quality. *Animal* **1**, 159-173.

Hodges, J (2003) Livestock, ethics, and quality of life. *Journal of Animal Science* **81**, 2887-2894.

Hoffmann, I (2011) Livestock biodiversity and sustainability. *Livestock Science* **139**, 69-79.

Honda, T, Katsuta, T, Mukai, F (2009) Simulation Study on Parentage Analysis with SNPs in the Japanese Black Cattle Population. *Asian-Australasian Journal of Animal Sciences* **22**, 1351-1358.

Ibeagha-Awemu, EM, Erhardt, G (2005) Genetic structure and differentiation of 12 African Bos indicus and Bos taurus cattle breeds, inferred from protein and microsatellite polymorphisms. *Journal of Animal Breeding and Genetics* **122**, 12-20.

Ibeagha-Awemu, EM, Erhardt, G (2006) An evaluation of genetic diversity indices of the Red Bororo and White Fulani cattle breeds with different molecular markers and their implications for current and future improvement options. *Tropical Animal Health and Production* **38**, 431-441.

Ibeagha-Awemu, EM, Jann, OC, Weimann, C, Erhardt, G (2004) Genetic diversity, introgression and relationships among West/Central African cattle breeds. *Genetics Selection Evolution* **36**, 673-690.

Johnston, DJ, Graser, HU (2010) Estimated gene frequencies of GeneSTAR markers and their size of effects on meat tenderness, marbling, and feed efficiency in temperate and tropical beef cattle breeds across a range of production systems. *Journal of Animal Science* **88**, 1917-1935.

Kahi, A, Thorpe, W, Nitter, G, Baker, R (2000) Crossbreeding for dairy production in the lowland tropics of Kenya: I. Estimation of individual crossbreeding effects on milk production and reproductive traits and on cow live weight. *Livestock Production Science* **63**, 39-54.

Kariuki, D (1999) 'East Coast fever (ECF) immunisation in Kenya, Live Vaccines for Theileria Parva: Deployment in Eastern, Central and Southern Africa: Proceedings of an FAO/OAU-IBAR/ILRI Workshop Held at ILRI, Nairobi, Kenya, 10-12 March 1997.' (ILRI (aka ILCA and ILRAD):

Karlsen, A, Ruane, J, Klemetsdal, G, Heringstad, B (2000) Twinning rate in Norwegian cattle: Frequency (co)variance components, and genetic trends. *Journal of Animal Science* **78**, 15-20.

Karlsson, EK, Baranowska, I, Wade, CM, Salmon Hillbertz, NHC, Zody, MC, Anderson, N, Biagi, TM, Patterson, N, Pielberg, GR, Kulbokas, EJ, Comstock, KE, Keller, ET, Mesirov, JP, von Euler, H, Kampe, O, Hedhammar, A, Lander, ES, Andersson, R, Andersson, L, Lindblad-Toh, K (2007) Efficient mapping of mendelian traits in dogs through genome-wide association. *Nature Genetics* **39**, 1321-1328.

Kassie, GT, Abdulai, A, Wollny, C (2009) Valuing Traits of Indigenous Cows in Central Ethiopia. *Journal of Agricultural Economics* **60**, 386-401.

Kebede, B (1985) Review of the Ethiopian Borana breed. *Animal genetic resources in Africa. High potential and endangered livestock. Second OAU Expert Committee Meeting on Animal Genetic Resources in Africa, 24-28 November, 1983, Bulawayo, Zimbabwe.* 48-53.

Kim, JJ, Farnir, F, Savell, J, Taylor, JF (2003) Detection of quantitative trait loci for growth and beef carcass fatness traits in a cross between Bos taurus (Angus) and Bos indicus (Brahman) cattle. *Journal of Animal Science* **81**, 1933-1942.

Kios, D, van Marle-Koester, E, Visser, C (2012) Application of DNA markers in parentage verification of Boran cattle in Kenya. *Tropical Animal Health and Production* **44**, 471-476.

Koch, RM, Clark, R (1955) Influence of sex, season of birth and age of dam on economic traits in range beef cattle. *Journal of Animal Science* **14**, 386-397.

Koots, KR, Gibson, JP (1996) Realized sampling variances of estimates of genetic parameters and the difference between genetic and phenotypic correlations. *Genetics* **143**, 1409-1416.

Kosgey, IS, Rowlands, GJ, van Arendonk, JAM, Baker, RL (2008) Small ruminant production in smallholder and pastoral/extensive farming systems in Kenya. *Small Ruminant Research* **77**, 11-24.

Lampkin, GH, Lampkin, K (1960) Studies on the production of beef from zebu cattle in East Africa. II. Milk production in suckled cows and its effect on calf growth. *Journal of Agricultural Science* **55**, 233-239.

Lande, R, Thompson, R (1990) Efficiency of Marker-Assisted Selection in the Improvement of Quantitative Traits. *Genetics* **124**, 743-756.

Lasley, JF (1987) In 'Genetics of Livestock Improvement' (4th Ed.). (Englewood Cliffs: New Jersey)

Leland H. Hartwell, lH, Michel L. Goldbery, Ann E. Reynolds, Lee M Silver Ruth C. Veres (2008) In 'Genetics: From Genes to Genomics' (3rd Ed.). (McGraw Hill: New York)

Liu, L, Harris, B, Keehan, M, Zhang, Y (2009) Genome scan for the degree of white spotting in dairy cattle. *Animal Genetics* **40**, 975-975.

Loftus, RT, Machugh, DE, Bradley, DG, Sharp, PM, Cunningham, P (1994) Evidence for 2 independent domestications of cattle. *Proceedings of the National Academy of Sciences of the United States of America* **91**, 2757-2761.

Lungu, JCN, 2003, 'Animal Genetic Resources Policy Issues in Zambia', *Paper presented at a Workshop Meeting to Strengthen Capacity for Developing Policies* Affecting Genetic Resources, 5–7 September, 2003, Rome, Italy

Lwoga, ET, Ngulube, P, Stilwell, C (2010) Managing indigenous knowledge for sustainable agricultural development in developing countries: Knowledge management approaches in the social context. *International Information and Library Review* **42**, 174-85.

Lynch, M, Abegg, A (2010) The Rate of Establishment of Complex Adaptations. *Molecular Biology and Evolution* **27**, 1404-1414.

Lynch, M., and B. Walsh. 1998. Genetics and Analyses of Quantitative Traits. Sinauer, Sunderland, MA.

Machado, MA, Azevedo, ALS, Teodoro, RL, Pires, MA, Peixoto, MGCD, de Freitas, C, Prata, MCA, Furlong, J, da Silva, MVGB, Guimaraes, SEF, Regitano, LCA, Coutinho, LL, Gasparin, G, Verneque, RS (2010) Genome wide scan for quantitative trait loci affecting tick resistance in cattle (Bos taurus x Bos indicus). *Bmc Genomics* **11**, 233-241

MacHugh, DE, Loftus, RT, Cunningham, P, Bradley, DG (1998) Genetic structure of seven European cattle breeds assessed using 20 microsatellite markers. *Animal Genetics* **29**, 333-340.

Mader, TL, Frank, KL, Harrington Jr, JA, Hahn, GL, Nienaber, JA (2009) Potential climate change effects on warm-season livestock production in the Great Plains. *Climatic Change* **97**, 529-541.

Maillard, J-C, Kiem Phan, V, Tung, N, Thu Nhu, V, Berthouly, C, Libeau, G, Kwiatek, O (2008) Examples of Probable Host-Pathogen Co-adaptation/Co-evolution in Isolated Farmed Animal Populations in the Mountainous Regions of North Vietnam. In 'Animal Biodiversity and Emerging Diseases: Prediction and Prevention.' (Eds OAE Sparagano, JC Maillard, JV Figueroa.) Vol. 1149 pp. 259-262.

Malau-Aduli, AEOS, B. D; Bottema, C. D. K; Pitchford, W. S (2000) Heterosis, sex and breed differences in the fatty acid composition of muscle phospholipids in beef cattle. *Journal of Animal Physiology and Animal Nutrition* **83**, 113-120.

Maloo, SH, Ngumi, P, Mbogo, S, Williamson, S, Thorpe, W, Rowlands, GJ, Perry, BD (2001) Identification of a target population for immunisation against East Coast fever in coastal Kenya. *Preventive Veterinary Medicine* **52**, 31-41.

Manzi M, Junga J O, Ebong C and Mosi R O 2012**:** Factors affecting pre and post-weaning growth of six cattle breed groups at Songa Research station in Rwanda. *Livestock Research for Rural Development. Volume 24, Article #68.* Retrieved February 21, 2014, from http://www.lrrd.org/lrrd24/4/manz24068.htm (27th June 2013)

Mao, Y, Chang, H, Yang, Z, Zhang, L, Xu, M, Chang, G, Sun, W, Song, G, Ji, D (2008) The analysis of genetic diversity and differentiation of six Chinese cattle populations using microsatellite markers. *Journal of Genetics and Genomics* **35**, 25-32.

Mapiye, C, Chimonyo, M, Muchenje, V, Dzama, K, Marufu, MC, Raats, JG (2007) Potential for value-addition of Nguni cattle products in the communal areas of South Africa: a review. *African Journal of Agricultural Research* **2**, 488-495.

Marletta, D, Tupac-Yupanqui, I, Bordonaro, S, Garcia, D, Guastella, AM, Criscione, A, Canon, J, Dunner, S (2006) Analysis of genetic diversity and the determination of relationships among western Mediterranean horse breeds using microsatellite markers. *Journal of Animal Breeding and Genetics* **123**, 315-325.

Marlowe, TJ, Gaines, JA (1958) The influence of age, sex, and season of birth of calf, and age of dam on preweaning growth rate and type score of beef calves. *Journal of Animal Science* **17**, 706-713.

Marshall, K, Quiros-Campos, C, van der Werf, JHJ, Kinghorn, B (2011) Marker-based selection within smallholder production systems in developing countries. *Livestock Science* **136**, 45-54.

Martín-Burriel, I, Rodellar, C, Lenstra, JA, Sanz, A, Cons, C, Osta, R, Reta, M, De Argüello, S, Sanz, A, Zaragoza, P (2007) Genetic diversity and relationships of endangered Spanish cattle breeds. *Journal of Animal Science 16, 716-723.*

Masiga, W, Domenech, J, Windsor, R (1996) Manifestation and epidemiology of contagious bovine pleuropneumonia in Africa. *Revue scientifique et technique (International Office of Epizootics)* **15**, 1283.

Mason, IL, Maule, JP (1960) The indigenous livestock of Eastern and Southern Africa. Available at: http://www.cabdirect.org.proxy.library.adelaide.edu.au/abstracts/19600403595.html(26th February 2013)

Mason, NM, Jayne, TS, Chapoto, A, Donovan, C (2011) Putting the 2007/2008 global food crisis in longer-term perspective: Trends in staple food affordability in urban Zambia and Kenya. *Food Policy* **36**, 350-367.

Mbulu, R-S, Tjipura-Zaire, G, Lelli, R, Frey, J, Pilo, P, Vilei, EM, Mettler, F, Nicholas, RA, Huebschle, OJ (2004) Contagious bovine pleuropneumonia (CBPP) caused by

vaccine strain T1/44 of Mycoplasma mycoides subsp mycoides SC. *Veterinary Microbiology* **98**, 229-234.

Medugorac, I, Medugorac, A, Russ, I, Veit-Kensch, CE, Taberlet, P, Luntz, B, Mix, HM, Forster, M (2009) Genetic diversity of European cattle breeds highlights the conservation value of traditional unselected breeds with high effective population size. *Molecular Ecology* **18**, 3394-3410.

MacHugh, D, Bradley, D (1994) Genetic characterization and West African cattle. *World Animal Review* **78**, 59-66.

Meuwissen, THE (1989) A deterministic model for the optimization of dairy-cattle breeding based on blup breeding value estimates. *Animal Production* **49**, 193-202.

Meuwissen, THE, Goddard, ME (2000) Fine mapping of quantitative trait loci using linkage disequilibria with closely linked marker loci. *Genetics* **155**, 421-430.

Meuwissen, THE, Goddard, ME (2001) Prediction of identity by descent probabilities from marker-haplotypes. *Genetics Selection Evolution* **33**, 605-634.

Meuwissen, THE, Hayes, BJ, Goddard, ME (2001) Prediction of total genetic value using genome-wide dense marker maps. *Genetics* **157**, 1819-1829.

Meyer, K (1992) Variance components due to direct and maternal effects for growth traits of Australian beef cattle. *Livestock Production Science* **31**, 179-204.

Meyer, K (2007) WOMBAT—A tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *Journal of Zhejiang University Science B* **8**, 815-821.

Meyer, K, Hill, WG (1997) Estimation of genetic and phenotypic covariance functions for longitudinal or 'repeated'records by restricted maximum likelihood. *Livestock Production Science* **47**, 185-200.

Moll, HA, Staal, SJ, Ibrahim, M (2007) Smallholder dairy production and markets: A comparison of production systems in Zambia, Kenya and Sri Lanka. *Agricultural systems* **94**, 593-603.

Moore, SS, Hansen, C (2003) Genomics: delivering added value to the beef industry? *Outlook on Agriculture* **32**, 247-252.

Morgan, DL (2007) Paradigms Lost and Pragmatism Regained Methodological Implications of Combining Qualitative and Quantitative Methods. *Journal of Mixed Methods Research* **1**, 48-76.

Moyo, S (1993) Relative productivity of indigenous, exotic and crossbred cattle at Matopos Research Station. *Journal of the Zimbabwe Society for Animal Production* **5**, 23-28.

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

Mtetwa, R (1978) Myth or reality: the 'cattle complex'in South East Africa, with special reference to Rhodesia. Available at: http://digital.lib.msu.edu/projects/africanjournals/html/itemdetail.cfm?recordID=1548 (3rd July 2013 ???).

Mubaya, CP, Njuki, J, Mutsvangwa, EP, Mugabe, FT, Nanjad, D (2012) Climate variability and change or multiple stressors? Farmer perceptions regarding threats to livelihoods in Zimbabwe and Zambia. *Journal of Environmental Management* **102**, 9-17.

Mulder, HA, Calus, MPL, Veerkamp, RF (2010) Prediction of haplotypes for ungenotyped animals and its effect on marker-assisted breeding value estimation. *Genetics, Selection, Evolution* **42**, 210-211

Muuka, GM, Songolo, N, Kabilika, S, Fandamu, P, Buonavoglia, D, Scacchia, M (2013) Private sector involvement in the control of contagious bovine pleuropneumonia (CBPP) in the Kazungula district of Zambia benefitted the community and the control strategy. *Tropical Animal Health and Production* **45**, 699-703.

Mwacharo, J, Okeyo, A, Kamande, G, Rege, J (2006) The small East African shorthorn zebu cows in Kenya. I: Linear body measurements. *Tropical Animal Health and Production* **38**, 65-74.

Mwenya, WNM (1993) The impact of the introduction of exotic cattle in east and southern Africa. FAO 2006

Naik, S (1978) Origin and domestication of Zebu cattle (< i> Bos indicus</i>). *Journal of Human Evolution* **7**, 23-30.

Ndofor-Foleng, H, Ebangi, A, Agu, C, Okenyi, N (2012) Estimation of genetic parameters for preweaning and postweaning growth traits in the Gudali beef cattle using multiple trait derivative free restricted maximum likelihood. *African Journal of Biotechnology* **11**, 14410-14416.

Nei, M (1972) Genetic distance between populations. *American Naturalist* **106**, 283-291&.

Nei, M, Roychoud.Ak (1973) Sampling variances of heterozygosity and genetic distance. *Genetics* **76**, 379-390.

Newman, S, Morris, CA, Baker, RL, Nicoll, GB (1992a) Genetic-improvement of beef-cattle in new-zealand - breeding objectives. *Livestock Production Science* **32**, 111-130.

Nicholas, FC (2005) Animal breeding and disease. *Philosophical Transactions of the Royal Society of London. Series B, Biological sciences* **360**, 1529-1536.

Nicholas, FW (1996) Genetic improvement through reproductive technology. *Animal Reproduction Science* **42**, 205-214.

Nielsen, HM, Christensen, LG, Odegard, J (2006) A method to define breeding goals for sustainable dairy cattle production. *Journal of Dairy Science* **89**, 3615-3625.

Notter, DR (1999) The importance of genetic populations diversity in livestock populations of the future. *Journal of Animal Science* **77**, 61-69.

Oldenbroek, K (2007) In 'Utilisation and conservation of farm animal genetic resources.' (Wageningen Academic Publishers: Wageningen)

Olesen, I, Groen, AF, Gjerde, B (2000) Definition of animal breeding goals for sustainable production systems. *Journal of Animal Science* **78**, 570-582.

Olsen, HG, Hayes, BJ, Kent, MP, Nome, T, Svendsen, M, Lien, S (2010) A genome wide association study for QTL affecting direct and maternal effects of stillbirth and dystocia in cattle. *Animal Genetics* **41**, 273-280.

Ouma, E, Abdulai, A, Drucker, A (2007) Measuring heterogeneous preferences for cattle traits among cattle-keeping households in East Africa. *American Journal of Agricultural Economics* **89**, 1005-1019.

Owens, FN, Dubeski, P, Hanson, C (1993) Factors that alter the growth and development of ruminants. *Journal of Animal Science* **71**, 3138-3150.

Pauw, K, Thurlow, J (2011) Agricultural growth, poverty, and nutrition in Tanzania. *Food Policy* **36**, 795-804.

Payne, WJA (1970) In 'Cattle production in the tropics: Vol. 1. General introduction and breeds and breeding, (Longman Scientific & Technical, Harlow, Essex, England).

Payne, WJA, Williamson, G (1990) In 'An introduction to animal husbandry in the tropics.' (Longman Scientific & Technical: Harlow, Essex, England)

Peakall, R, Smouse, PE (2006) GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. *Molecular Ecology Notes* **6**, 288-295.

Peakall, R, Smouse, PE (2012) GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. *Bioinformatics* **28**, 2537-2539.

Phocas, F, Bloch, C, Chapelle, P, Bécherel, F, Renand, G, Ménissier, F (1998) Developing a breeding objective for a French purebred beef cattle selection programme1. *Livestock Production Science* **57**, 49-65.

Phocas, F, Laloë, D (2003) Evaluation models and genetic parameters for calving difficulty in beef cattle. *Journal of Animal Science* **81**, 933-938.

Pico, B, Neser, F, Van Wyk, J (2004) Genetic parameters for growth traits in South African Brahman cattle. *South African Journal of Animal Science* **34**, 44-46.

Pitchford, WS (2004) Genetic improvement of feed efficiency of beef cattle: what lessons can be learnt from other species? *Animal Production Science* **44**, 371-382.

Pitchford, WS (2007) Improving accuracy of selection ofyoung bulls by Pastoralists. *Livestock Science* **110**, 141-147.

Plasse, D, Verde, O, Fossi, H, Romero, R, Hoogesteijn, R, Bastidas, P, Bastardo, J (2002) (Co) variance components, genetic parameters and annual trends for calf weights in a pedigree Brahman herd under selection for three decades. *Journal of Animal Breeding and Genetics* **119**, 141-153.

Ponzoni, RW, Newman, S (1989) Developing breeding objectives for Australian beef cattle production. *Animal Science* **49**, 35-47.

Praharani, L (2009) Estimation of direct and maternal effects for weaning and yearling weights in Bali cattle1). *Indonesian Journal of Agriculture* **2**, 74-81.

Pritchard, JK, Stephens, M, Donnelly, P (2000) Inference of population structure using multilocus genotype data. *Genetics* **155**, 945-959.

Pryce, JE, Bolormaa, S, Chamberlain, AJ, Bowman, PJ, Savin, K, Goddard, ME, Hayes, BJ (2010) A validated genome-wide association study in 2 dairy cattle breeds for milk production and fertility traits using variable length haplotypes. *Journal of Dairy Science* **93**, 3331-3345.

R. A. Afolayan, WSP, M. P. B. Deland and W. A. McKiernan (2007) Breed variation and genetic parameters for growth and body development in diverse beef cattle genotypes. *Animal* **1**, 1320.

Raphaka, K, Dzama, K (2010) Genetic analyses for growth traits of two indigenous beef cattle breeds in Botswana. *Livestock Science* **129**, 194-199.

Rege, J, Ayalew, W, Getahun, E, Hanotte, O, Dessie, T (2006) DAGRIS (Domestic Animal Genetic Resources Information System). International Livestock Research Institute, Addis Ababa, Ethiopia.

Rege, J, Lipner, ME (1992) In 'African Animal Genetic Resources: Their Characterisation, Conservation, and Utilisation: Proceedings of the Research Planning ILCA, Addis Ababa, Ethiopia.

Rege, JEO (1999) The state of African cattle genetic resources I. Classification framework and identification of threatened and extinct breeds. *Animal Genetic Resources Information* 1-25.

Rege, JEO, Gibson, JP (2003) Animal genetic resources and economic development: issues in relation to economic valuation. *Ecological Economics* **45**, 319-330.

Rege, JEO, Tawah, CL (1999) The state of African cattle genetic resources II. Geographical distribution, characteristics and uses of present-day breeds and strains. *Animal Genetic Resources Information* 1-25.

Reist-Marti, S, Simianer, H, Gibson, J, Hanotte, O, Rege, J (2003) Weitzman's approach and conservation of breed diversity: an application to African cattle breeds. *Conservation Biology* **17**, 1299-1311.

Rewe, TO, Herold, P, Kahi, AK, Zarate, AV (2009) Breeding indigenous cattle genetic resources for beef production in Sub-Saharan Africa. *Outlook on Agriculture* **38**, 317-326.

Rewe, TO, Indetie, D, Ojango, JMK, Kahi, AK (2006) Breeding objectives for the Boran breed in Kenya: Model development and application to pasture-based production systems. *Animal Science Journal* **77**, 163-177.

Robinson, D (1996) Estimation and interpretation of direct and maternal genetic parameters for weights of Australian Angus cattle. *Livestock Production Science* **45**, 1-11.

Roosen, J, Fadlaoui, A, Bertaglia, M (2005) Economic evaluation for conservation of farm animal genetic resources. *Journal of Animal Breeding and Genetics* **122**, 217-228.

Roughsedge, T, Amer, P, Thompson, R, Simm, G (2005) Development of a maternal breeding goal and tools to select for this goal in UK beef production. *Animal Science-Glasgow Then Penicuik-* **81**, 221.

Ruto, E, Garrod, G, Scarpa, R (2008) Valuing animal genetic resources: a choice modeling application to indigenous cattle in Kenya. *Agricultural Economics* **38**, 89-98.

Scarpa, R, Ruto, ESK, Kristjanson, P, Radeny, M, Drucker, AG, Rege, JEO (2003) Valuing indigenous cattle breeds in Kenya: an empirical comparison of stated and revealed preference value estimates. *Ecological Economics* **45**, 409-426.

Schaeffer, LR (2006) Strategy for applying genome-wide selection in dairy cattle. *Journal of Animal Breeding and Genetics* **123**, 218-223.

Schoeman, S, Jordaan, G (1999) Multitrait estimation of direct and maternal (co) variances for growth and efficiency traits in a multibreed beef cattle herd. *South African Journal of Animal Science* **29**,

Scholtz, MM, McManus, C, Okeyo, AM, Theunissen, A (2011) Opportunities for beef production in developing countries of the southern hemisphere. *Livestock Science* **142**, 195-202.

Scoones, I (1992) The economic value of livestock in the communal areas of southern Zimbabwe. *Agricultural systems* **39**, 339-359.

Simianer, H, Marti, S, Gibson, J, Hanotte, O, Rege, J (2003) An approach to the optimal allocation of conservation funds to minimize loss of genetic diversity between livestock breeds. *Ecological Economics* **45**, 377-392.

Singogo, LP (1989) Case study management of research teams in national agricultural research systems: the Zambian experience. *Proceedings of the SACCAR/ISNAR regional workshop on human resource management in National Agricultural Research Systems.* 179-186.

Sodhi, M, Mukesh, M, Ahlawat, SPS, Sobti, RC, Gahlot, GC, Mehta, SC, Prakash, B, Mishra, BP (2008) Genetic diversity and structure of two prominent zebu cattle breeds adapted to the arid region of India inferred from microsatellite polymorphism. *Biochemical Genetics* **46**, 124-136.

Sodhi, M, Mukesh, M, Mishra, BP, Mitkari, KR, Prakash, B, Ahlawat, SPS (2005) Evaluation of genetic differentiation in Bos indicus cattle breeds from Marathwada region of India using microsatellite polymorphism. *Animal Biotechnology* **16**, 127-137.

Solberg, TR, Sonesson, AK, Woolliams, JA, Meuwissen, THE (2008) Genomic selection using different marker types and densities. *Journal of Animal Science* **86**, 2447-2454.

Soller, M (1995) Marker-assisted selection in animal biotechnology. *Agricultural Biotechnology* 387-406.

Sottie, E, Darfour-Oduro, K, Okantah, S (2009) Comparative studies on growth traits of Sanga and Friesian-Sanga crossbred calves raised on natural pasture on the Accra Plains of Ghana. *Tropical Animal Health and Production* **41**, 321-328.

Spike, P, Freeman, A (1978) Prediction of genetic differences among herds with estimates of breeding value. *Journal of Dairy Science* **61**, 1476-1482.

Steele, MC (1981) The economic function of African-owned cattle in colonial Zimbabwe. *Zambezia* **9**, 29-48.

Steinfeld, H, Wassenaar, T, Jutzi, S (2006) Livestock production systems in developing countries: status, drivers, trends. *Revue Scientifique Et Technique-Office International Des Epizooties* **25**, 505-516.

Suárez, MJ, Cantet, RJC (2011) Bayesian estimation in maternally ancestral animal models for weaning weight of beef cattle. *Journal of Animal Science* **89**, 3859-3871.

Swalve, H (1993) Estimation of direct and maternal (co) variance components for growth traits in Australian Simmental beef cattle. *Journal of Animal Breeding and Genetics* **110**, 241-252.

Tano, K, Kamuanga, M, Faminow, MD, Swallow, B (2003) Using conjoint analysis to estimate farmer's preferences for cattle traits in West Africa. *Ecological Economics* **45**, 393-407.

Tawah, C, Mbah, D, Rege, J, Oumate, H (1993) Genetic evaluation of birth and weaning weight of Gudali and two-breed synthetic Wakwa beef cattle populations under selection in Cameroon: genetic and phenotypic parameters. *Animal Production* **57**, 73-73.

Team, S, Team, S (2003) 2. Livelihood Dynamics: Rural Mozambique, South Africa and Zimbabwe. *IDS Bulletin* **34**, 15-30.

Thompson, R (2008) Estimation of quantitative genetic parameters. *Proceedings of the Royal Society B-Biological Sciences* **275**, 679-686.

Thomsen, H, Lee, HK, Rothschild, MF, Malek, M, Dekkers, JCM (2004) Characterization of quantitative trait loci for growth and meat quality in a cross between commercial breeds of swine. *Journal of Animal Science* **82**, 2213-2228.

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

Thornton, PK, Herrero, M (2010) The inter-linkages between rapid growth in livestock production, climate change, and the impacts on water resources, land use, and deforestation. *Policy Research Working Paper - World Bank* 82 pp.-82 pp.

Thornton, PK, Kruska, RL, Henninger, N, Kristjanson, PM, Reid, RS, Atieno, F, Odero, AN, Ndegwa, T (2002) Mapping poverty and livestock in the developing world. *Mapping poverty and livestock in the developing world* **12,** 118-119

Thorpe, W, Cruickshank, DKR, Thompson, R (1979) The growth and carcass characteristics of crosses of Hereford and Friesian with Angoni, Barotse and Boran cattle in Zambia. *The Journal of Agricultural Science* **93**, 423-430.

Thorpe, W, Cruickshank, DKR, Thompson, R (1980a) Genetic and environmental-influences on beef-cattle production in Zambia .1. factors affecting weaner production from angoni, Barotse and Boran dams. *Animal Production* **30**, 217-234.

Thorpe, W, Cruickshank, DKR, Thompson, R (1980b) Genetic and environmental-influences on beef-cattle production in Zambia .2. live weights for age of purebred and reciprocally crossbred progeny. *Animal Production* **30**, 235-243.

Thorpe, W, Cruickshank, DKR, Thompson, R (1980c) Genetic and environmental-influences on beef-cattle production in Zambia .3. carcass characteristics of purebred and reciprocally crossbred castrated males. *Animal Production* **30**, 245-252.

Thorpe, W, Cruickshank, DKR, Thompson, R (1981) Genetic and environmental-influences on beef-cattle production in Zambia .4. weaner production from purebred and reciprocally crossbred dams. *Animal Production* **33**, 165-177.

Tisdell, C (2003) Socioeconomic causes of loss of animal genetic diversity: analysis and assessment. *Ecological Economics* **45**, 365-376.

Toosi, A, Fernando, RL, Dekkers, JCM (2010) Genomic selection in admixed and crossbred populations. *Journal of Animal Science* **88**, 32-46.

Toro, MA, Fernandez, J, Caballero, A (2006) 'Scientific basis for policies in conservation of farm animal genetic resources.' *Livestock Science* 118, 1160-185.

Toro, MA, Fernandez, J, Caballero, A (2009) Molecular characterization of breeds and its use in conservation. *Livestock Science* **120**, 174-195.

Toro, MA, Meuwissen, THE, Fernandez, J, Shaat, I, Maki-Tanila, A (2011) Assessing the genetic diversity in small farm animal populations. *Animal* **5**, 1669-1683.

Van Dongen, S, Backeljau, T (1997) Bootstrap tests for specific hypotheses at single locus inbreeding coefficients. *Genetica* **99**, 47-58.

Van Onselen, C (1972) Reactions to Rinderpest in Southern Africa, 1896-97. *Journal of African History* **13**, 473-488.

van Overbeek, LS, Wellington, EMH, Egan, S, Smalla, K, Heuer, H, Collard, JM, Guillaume, G, Karagouni, AD, Nikolakopoulou, TL, van Elsas, JD (2002) Prevalence of streptomycin-resistance genes in bacterial populations in European habitats. *Fems Microbiology Ecology* **42**, 277-288.

Van Raden, PM, Van Tassell, CP, Wiggans, GR, Sonstegard, TS, Schnabel, RD, Taylor, JF, Schenkel, FS (2009) Invited review: Reliability of genomic predictions for North American Holstein bulls. *Journal of Dairy Science* **92**, 16-24.

Walker, CA (1957) Studies of the cattle of Northern Rhodesia. 1. The growth of steers under normal veld grazing, and supplemented with salt and protein. *Journal of Agricultural Science* **49**, 394-400.

Walker, CA (1964) The growth and development of the beef qualities of Angoni cattle (East African zebu). *The Journal of Agricultural Science* **63**, 135-154.

Ward Jr, JH (1963) Hierarchical grouping to optimize an objective function. *Journal of the American statistical association* **58**, 236-244.

Wasike, C, Ilatsia, E, Ojango, JM, Kahi, A (2006) Genetic parameters for weaning weight of Kenyan Boran cattle accounting for direct-maternal genetic covariances. *South African Journal of Animal Science* **36**, 275-281.

Wasike, C, Indetie, D, Ojango, J, Kahi, A (2009) Direct and maternal (co) variance components and genetic parameters for growth and reproductive traits in the Boran cattle in Kenya. *Tropical Animal Health and Production* **41**, 741-748.

Weir, BS, Cockerham, CC (1984) Estimating F-statistics for the analysis of population-structure. *Evolution* **38**, 1358-1370.

Willham, R (1972) The role of maternal effects in animal breeding: III. Biometrical aspects of maternal effects in animals. *Journal of Animal Science* **35**, 1288-1293.

Williamson, RT (2003) Biodiversity of domestic livestock in the Republic of Yemen. *Tropical Animal Health and Production* **35**, 27-46.

Wood, AP (1989) Cattle and development in western Zambia. *Paper - Pastoral Development Network* 28pp.-28pp.

Wright, A (1985) Diallel designs, analyses, and reference populations. *Heredity* **54**, 307.

Wright, S (1965) The interpretation of population-structure by f-statistics with special regard to systems of mating. *Evolution* **19**, 395-420.

Wright, S (1978) In Evolution and the genetics of populations, Volume 4, University of Chicago Press, Chicago.

Young, ND (1999) A cautiously optimistic vision for marker-assisted breeding. *Molecular Breeding* **5**, 505-510.

Zambia, DoA (1977) In Annual report of the Research Branch 1973-74. *Annual report of the Research Branch 1973-74.*

Zander, KK, Drucker, AG, Holm-Mueller, K (2009) Costing the conservation of animal genetic resources: The case of Borana cattle in Ethiopia and Kenya. *Journal of Arid Environments* **73**, 550-556.

Zerabruk, M, Li, MH, Kantanen, J, Olsaker, I, Ibeagha-Awemu, E, Erhardt, G, Vangen, O (2012b) Genetic diversity and admixture of indigenous cattle from North Ethiopia: implications of historical introgressions in the gateway region to Africa. *Animal Genetics* **43**, 257-266.

Zulu, DN (2008) In 'Genetic characterization of Zambian native cattle breeds.' Master of Science Thesis, Virginia Polytechnic Institute and State University, Blacksburg, Virginia

Appendix 1. 1: Zambian population size, distribution and average growth rate for each province from 1990 – 2010.

	1990			2000				2010			
Province	Male	Female	Total	Male	Female	Total	Average annual Growth 1990-2000	Male	Female	Total	Average annual Growth 2000-2010
Central	385,230	386,588	771,818	510,501	501,756	1,012,257	2.7	626,823	640,980	1,267,803	2.3
Copperbelt	739,519	718,940	1,458,459	799,402	781,819	1,581,221	0.8	973,770	984,853	1,958,623	2.2
Eastern	492,909	511,784	1,004,693	648,676	657,497	1,306,173	2.6	836,165	871,566	1,707,731	2.7
Luapula	278,222	286,271	564,493	387,825	387,528	775,353	3.2	467,613	491,363	958,976	2.1
Lusaka	498,704	492,522	991,226	705,778	685,551	1,391,329	3.4	1,080,152	1,118,844	2,198,996	4.7
Northern	456,865	469,000	925,865	629,976	628,720	1,258,696	3.1	861,628	897,972	1,759,600	3.4
North-western	212,826	225,390	438,216	290,856	292,494	583,350	2.9	345,025	361,437	706,462	1.9
Southern	474,488	491,103	965,591	601,440	610,684	1,212,124	2.3	786,394	820,399	1,606,793	2.9
Western	302,813	335,943	638,756	371,844	393,244	765,088	1.8	416,885	464,639	881,524	1.4
Total	**3,841,576**	**3,917,541**	**7,759,117**	**4,946,298**	**4,939,293**	**9,885,591**	**2.4**	**6,394,455**	**6,652,053**	**13,046,508**	**2.8**

Appendix 2.1: Adapted and modified SADC Questionnaire

Date of interview / /2012

Enumerator			**Code no.**
Supervisor			Code no.
1	Province		Code no.
2	District		Code no.
3	Ward		Code no.
4	Village (VIDCO)		Code no.
5	Farm type	Communal Small-scale commercial Large-scale	
6	GPS reading	*(to be filled in later)*	
7	Household	No	
8	Wealth category	Rich medium Poor Not classified	*(tick one)*

The overall objective of the survey**,** which is determine preference traits in both traditional and cattle management systems in order to develop breeding objectives. This will help in development of multiple selection indexes that will improve selection accuracy of young bulls. Furthermore, the survey will enable the rapid implementation of cattle breed genetic improvement and conservation-breeding programs within the local population size and distribution of farm animal breed resources. In addition, the survey will enable establish aspects of causes of loss of genetic diversity of local- well adapted cattle breed as well as to determine management/ production and socio-cultural practices employed by farmers in raising these animals. The surveys will enable simple, regular updating of breed information and facilitate updating of the role and traits farmers perceive most important. With this information, Zambia will be able to:

• develop comprehensive plans for improving and managing Cattle genetic resources

• facilitate development of appropriate animal recording systems and sustainable breeding programs,

• facilitate development and implementation of relevant conservation activities.

AuSAID through the Australia Awards funded the Study, in collaboration with The University of Adelaide, Roseworthy Campus, Adelaide, South Australia.

Date of interview / /2012

HOUSEHOLD General Information		
1.1. Interviewee _____ 2. Household head		
1.☐Position in household	☐Male	
2.☐Spouse of head	☐ Female	
3.☐Brother		
4.☐Sister	Age (yrs) ☐≤ 30	
5.☐Son	☐31-40	
6.☐Daughter	☐41-50	
	☐51-60	
Other (specify)	☐ 61-70	
	☐> 70	
7. _____	☐Not known	
3. 3.Tribe	4. Number of people residing in household	
Name _____	Males	
	Females	
Code	Children < 15 yrs	
5. 5.Land holding / farm size	6. Land ownership	
(enter X in box in first column	*(Tick one or more)*	
If (not known)		
	☐Own	
	☐ Lease	
Area Units *(tick)*	☐Other (specify) ____	
Crops ☐ Acres ☐		
Grazing ☐ Hectares☐		
Forest ☐	9. Livestock kept	Most important
Total size☐	*(Enter numbers*	species
	in first column)	*(rank up to 3)*
Other than communal	Number	1,2,3
	1. Cattle ☐	☐
	2. Sheep ☐	☐
7. Livestock activity	3. Goats ☐	☐
	4. Chickens ☐	☐
Is livestock the major activity on your farm?	5. Pigs ☐	☐
Yes No	6. Donkeys ☐	☐
	7.Other ☐	☐
8. Sources of income		
(Tick first column as		
Appropriate, rank		
level of source of income in second column – 1-4.)		
1. ☐ Crops		

2. ☐ Livestock and products *

3. ☐ Home industries

4. ☐ Salary / wages

5. _____ Other (specify)

10. Livestock production category

	Dairy	Meat	Dual purpose	
1. Cattle	☐	☐	☐	
2. Sheep	☐	☐	☐	
3. Goats	☐	☐	☐	

** Include the value of non-cash outputs or products e.g manure, traction etc.*

11. System of production

1. Industrial/intensive.	☐	1 2. Mobility 1. Sedentary	☐
2. Semi-intensive	☐	*(Tick one or more)* 2.Transhumant	☐
3. Extensive/pastoral	☐	3. Nomadic	☐
4. Free range	☐	___	☐
5. _____			

13. Purpose of keeping cattle

Ask an open question and tick any purpose considered in first half of box - one or more boxes to be ticked. Then rank top three by writing in second half of a box 1 for primary purpose, 2 for second, 3 for third.

Head	☐	Head/spouse	☐	
1. Meat	☐	Sons	☐	☐
2. Milk	☐	Daughters	☐	
3. Work/draft	☐	Others *	☐	☐
4. Stud breeding	☐			
5. Manure	☐			
6. Blood	☐			
7. Hide	☐			
8. sales	☐			
9. Investment	☐			
10. Dowry	☐			
11. Ceremonies	☐			
12. Cultural	☐			
13. _____	☐			

14. Members of household who own cattle *(Tick one or more)*

Spouse	☐
Head/spouse	☐
Sons	☐
Daughters	☐
Others *	☐

15. Members of household responsible for cattle activities

(Tick as appropriate; more than one column in a row may be ticked)

	Adults		Boys	Girls	Hired
	Males	Females	(<15y)	(<15y)	labour
1. Purchasing cattle	☐	☐	☐	☐	☐
2. Selling	☐	☐	☐	☐	☐
3. Herding	☐	☐	☐	☐	☐
4. Breeding	☐	☐	☐	☐	☐
5. Feeding	☐	☐	☐	☐	☐

6. Milking	☐	☐	☐	☐	☐	
7. Making dairy products	☐	☐	☐	☐	☐	
8. Selling dairy products	☐	☐	☐	☐	☐	
9. Animal health	☐	☐	☐	☐	☐	
10. Other (specify)	☐	☐	☐	☐	☐	

16. Season Grazing/feeding			17. Housing			
	Dry	Wet	Dry season		Wet season	
1. Herded	☐	☐	1. Kraal	☐	☐	
2. Paddock	☐	☐	2. Stall/shed	☐	☐	
3. Tethered	☐	☐	3. Yard	☐	☐	
4. Stall	☐	☐	4. None	☐	☐	
5. Yard	☐	☐	5. _____	☐	☐	
6. Freely	☐	☐	Other (specify)			
7. _____	Are calves housed together with adults? Yes ☐ No ☐					

Are calves grazed/fed together with adults?

Yes ☐ No ☐

CATTLE Production system

If animals not housed go to question 17.

18. Materials used for housing *(Tick one or more)*		19. Form of housing *(Tick if present)*		
1. Untreated poles	☐	1. Roof	☐	
2. Treated wood	☐	2. Solid wall	☐	
3. Iron sheets	☐	3. Floor	☐	
4. Bricks	☐	a. concrete	☐	
5. Mud	☐	b. wooden	☐	
6. Wire	☐	c. Earth	☐	
Other (specify)	☐			
7. _____	☐			

21. How cattle are watered

				Dry	Wet
20. Supplementation regime *(Tick as appropriate)*			1. Animals go to water	☐	☐
	Dry	Wet	2. Water is provided	☐	☐
1. Roughage	☐	☐	3. Both	☐	☐
2. Minerals	☐	☐			
3. Concentrates	☐	☐	Comments		
4. None	☐	☐			
Other (specify)	☐	☐			
5.	☐	☐			

22. Source of Water

23. Distance to farthest watering point

1. Borehole	☐	☐	1. At household	☐	☐
2. Dam/pond	☐	☐	2. <1km	☐	☐
3. River	☐	☐	3. 1-5 km	☐	☐
4. Water well	☐	☐	4. 6-10 km	☐	☐

5. Spring	☐	☐	5. >10 km	☐	☐
6. unicipal/piped	☐	☐			
Other (specify)	☐	☐			

24. Frequency of watering			25. Water quality (season) *(Tick one or more)*		
	Dry	Wet		Dry	Wet
1. Freely available	☐	☐	1. Good/clear	☐	☐
2. Once a day	☐	☐	2. Muddy	☐	☐
3. Twice a day	☐	☐	3. Salty	☐	☐
4.Every other day	☐	☐	4. Smelly	☐	☐

25. CATTLE Health

1. Access to veterinary services

(Tick as appropriate)

1. Government vet. ☐
2. Private vet. ☐
3. Veterinary drug supplier ☐
4. Extension service ☐
5. None ☐
Other (specify) ☐
6. _____ ☐

27. Prevalent diseases that occur on farm (*i.e. diseases that are seen by farmer in his animals)*

If none tick this box ☐

Local name or symptoms of disease

(Rank, most common first) Are animals treated when sick?

	Code *	Yes	No	Treatment given (if known)*
☐	☐	☐		
☐	☐	☐		
☐	☐	☐		
☐	☐	☐		
☐	☐	☐		

**(code to be entered later from list of diseases)*

3. Vaccinations/preventive treatments given

If none tick this box ☐

Local name or symptoms of disease	`Code	Routinely	when need arises *(Tick as appropriate)*
1. _____	☐	☐	☐
2. _____	☐	☐	☐
3. _____	☐	☐	☐
4. _____	☐	☐	☐
5. _____	☐	☐	☐
6. _____	☐	☐	☐

**(code to be entered later from list of diseases)*

4. Ectoparasite control						
			Done when need arises	Done routinely	*If done routinely specify*	
Method						
	(Tick)	dry	wet	dry	wet	dry wet
1. None	☐					
2. Dip	☐	☐	☐	☐	☐	☐ weeks ☐
3. Spray	☐	☐	☐	☐	☐	☐ weeks ☐
4. Pour-on	☐	☐	☐	☐	☐	☐ weeks ☐
5. Hand	☐	☐	☐	☐	☐	☐ weeks ☐
6. Injectable	☐	☐	☐	☐	☐	☐ weeks ☐
7. Traditional	☐	☐	☐	☐	☐	☐ weeks ☐
If traditional method specify _____ Code ☐ *(to be entered from list of traditional methods)*						
Name external parasites		rank				
		☐				
		☐				
		☐				
Name of internal parasite		rank				
		☐				
		☐				
		☐				
		☐				
CATTLE		Castration/entries/exits/culling				
1. Castration						
Do you castrate? Yes ☐		No ☐				
2. Numbers of entries within last 12 months(*for Q2 and Q3 if information is not known mark x and if known mark 0 on general information)*						
					Adults	Total
If yes, say why you castrate. (*Tick one or more boxes)*		Calves	Weaners	Males	Females	W + A
1. Control breeding	☐	1. Born		☐		
2. Improve meat quality	☐	2. Bought		☐	☐	☐ ☐ ☐
3. Better price	☐	3. Donated/gift		☐	☐	☐ ☐ ☐
4. Better draft power	☐	4. Exchanged/lent		☐	☐	☐ ☐ ☐
5. Better temperament	☐					
* *to include bride price and dowry*						
Other (specify)						
At what age do you castrate?						Adults
		Calves	Weaner	M	F	T
< 3 months	☐					

3-6 months ☐ 1. Died	☐	☐	☐	☐	☐
6-12 months ☐ 2. Sold	☐	☐	☐	☐	☐
> 12 months ☐ 3. Slaughtered	☐	☐	☐	☐	☐
4. Donated/gift	☐	☐	☐	☐	☐
5. Exchanged/lent	☐	☐	☐	☐	☐
6. Stolen	☐	☐	☐	☐	☐
Sale outlet					

(if sold in last 12 months)

Were animals sold? Yes ☐ No ☐

* *to include bride price and dowry*

If yes tick one or more boxes.

1. Sold at auction ☐
2. Sold to butcher ☐
3. Sold privately ☐
4. Sold to abattoir ☐

Other (specify)

5. _____ ☐

5. Reasons for selling, culling / disposal.

Ask as open question and tick any answers given in first half of box, one or more boxes to be ticked. Then rank top three by writing in second half of box 1 for primary reason for culling, 2 for second and 3 for third.

Trait	Males	Females
1. Size	☐☐	☐☐
2. Conformation / shape	☐☐	☐☐
3. Colour	☐☐	☐☐
4. Temperament	☐☐	☐☐
5. Health	☐☐	☐☐
6. Body condition	☐☐	☐☐
7. Performance	☐☐	☐☐
8. Old age	☐☐	☐☐
9. Poor fertility	☐☐	☐☐

28. CATTLE BREEDING

2.0 Mating (tick one or more boxes)

1. Primary reason for keeping bull(s) *(Tick one)*

1. Breeding ☐
2. Socio-cultural ☐
3. Work / draft ☐
4. Other (specify) ☐

1. Uncontrolled ☐
2. Restricted ☐
3. Group mating ☐
4. A.I ☐

3. Reasons for choice of bull(s) for breeding (if breeding not done proceed to next page

Ask an open question and tick any reason for choice *considered in first half of box, one or more boxes to be ticked. Then rank top three by writing in second half of box1 for*

primary reason for choice, 2 for second and 3 for third.						
	Rank	Excellent	Good	Fair	Poor	Sex
1. Size	☐☐	☐				
2. Conformation/shape	☐☐	☐	☐	☐	☐	☐
3. Colour	☐☐	☐	☐	☐	☐	☐
4. Horns	☐☐	☐	☐	☐	☐	☐
5. Temperament	☐☐	☐	☐	☐	☐	☐
6. Performance	☐☐	☐	☐	☐	☐	☐
7. Availability (nochoice)	☐☐	☐	☐	☐	☐	☐
8.Calf every year	☐☐	☐	☐	☐	☐	☐

4. Source and breed(s) of bull(s) used in the herd

Breed name(s) *(Specify if known – crosses can be included.)*

Breed type 1		Breed type 2	
Tick one or more boxes			
Code*	Common name	Code*	Common name
1. Own bull (bred) ☐	_____	☐☐	_
2. Own bull (bought) ☐	_____	☐☐	_
3. Bull donated	☐_	☐☐	
4. Bull borrowed	☐_	☐☐	
5. A.I. ☐	_____	☐☐	_____
6. Communal area bull ☐	_____	☐☐	_____

29.CATTLE BREED/AGE/SEX STRUCTURE

Number

BREED 1	BREED 2
(from list of breeds)	*(from list of breeds)*
1. Common breed name	1. Common breed name
Local breed name	Local breed name
2. Trend within herd *(tick one)*	2. Trend within herd *(tick one)*
Increasing ☐ Decreasing ☐	Increasing ☐ Decreasing ☐
Stable ☐ Unknown ☐	Stable ☐ Unknown ☐
3. Numbers by age and sex	3. Numbers by age and sex
(Enter X in box if not known)	(Enter X in box if not known)
Calves Weaners Adults	Calves Weaners Adults
Intact male ☐ ☐ ☐	Intact male ☐ ☐ ☐
Castrate ☐ ☐ ☐	Castrate ☐ ☐ ☐
Female ☐ ☐	Female ☐ ☐ ☐
How old is the oldest animal? years ☐	How old is the oldest animal? years ☐
4. Origin/source of breed	4. Origin/source of breed
1. Inherited ☐	1. Inherited ☐
2. Communal area farm ☐	2. Communal area farm ☐
3. Commercial farm ☐	3. Commercial farm ☐

4. Market * ☐			4. Market * ☐	
** specify location*			** specify location*	
5. Quality of traits perceived by owner *(Ask each question and for each trait tick one box, poor, fair, good, Excellent)*				
BREED				
	Poor	Fair	Good	Excellent
1. Size				
2. body shape				
3. Colour				
4. Horns				
5. Disease tolerance				
6. Drought tolerance				
7. Heat tolerance				
8. Temperament				
9. Work rate				
10. Milk yield				
11. Meat				
12. Growth rate				
13. Fertility				
14. Calf/year				
16. Progeny type				

Appendix 2.3: In-depth interview Questionnaire

I.0 General Information and Introductions

Date of interview:

Region:

Name of Farmer/household/group:

Chief/ Location:

2.0 History of cattle farming and their use

2.1 Do you own cattle or have intention to own cattle?

2.2 How you first acquired your cattle and when?

2.3 How do you keep your cattle? Do they graze on their own or you share grazing land? Explain

2.4. what main roles do cattle play in your life?

3.0 Sharing ideals and detail understand constraints associated with cattle management

3.1 What are the main problems you face in relation with cattle keeping?

3.2 How do you manage the animal health care?

3.3 What are the common diseases you experience around your area?

3.4 How do you spray your cattle ?

3.5 how often do you deworm your cattle?

3.6 How clean is your water for cattle and how long does it take cattle to reach the drinking place?

3.7 How frequently do you access veterinary services?

4.0 Grazing and housing

4.1 How do you own the land where your cattle graze?

4.2 How do you graze your cattle??

4.3. Do you allow calves to grazing with old cattle throughout the year?

4.4. What material did you use to build your cattle kraal (Housing) and do you have problems with your Kraal?

4.5 Do you give your cattle extra food during dry season?

4.6 Do you castrate male calves? who does the castration?

4.7 Do you sale some of your cattle? If so, how do you decide which animal to be sold?

5.0 Cattle breeding and preference for cattle traits

5.1 What cattle breeds do you keep?

5.2 How many animals do you have including small ones?

5.3 Why do you like the breed(s) from your own experience?

5.4 What most important characteristics do you look for or you like from your cattle? For example, Size, animals that grow fast or animals that do not lose weight in dry season or animals that are easy to handle or those that give birth frequently. Please Explain.

6.0 Follow up questions

6.1 if you sale you animals, how much do you earn from one animal?

6.2 If you use cattle for ploughing fields, how many of bags of crops did you earn from a pair of oxen?

6.3 Do you hire out your oxen?

6.4 How much does cost to buy drugs to treat your cattle?

6.5 What are your plans? Are you interested to improve your cattle through proper genetic selection?

7.0 Acknowledgments

7.1 Is there anything you wish to say?

Appendix 2.2: Participant Information Sheet

Participant Information Sheet

Project Title: Designing breeding objectives for genetic selection in Zambian Cattle; Preference studies with cattle breeders in Zambia.

I, Ellison Musimuko, am currently undertaking research program in Zambia as part of my Master of Philosophy program in the School of Animal and Veterinary Sciences at The University of Adelaide, Australia. My study is looking at two main aspects:

1. Understanding your cattle preferred traits i.e. attributes of cattle, for example growth rate, fertility status, ability to survive in a given environment. I am hoping to able to speak with several of farmers within your community.

2. Blood or hair samples will be collected from cattle to determine animal genetic diversity in your local breed.

The study results may help to improve cattle management and also assist both the government and non-government organisations to effectively implement a breeding program in your area, but I cannot guarantee that you or your community will benefit from the directly study.

The study is completely **confidential and voluntary**, so nothing that you say will be reported in a way that will identify you or your remarks about any person or organization, unless you agree to be identified. If you do not wish to be identified, no personal or identifying information about you will be included in my thesis, and I will use an invented name to attach to your interview notes.

The way that I will carry out the study will be to organise a time and place to meet that suits you. The meeting should take 30-60 minutes and will be more like a conversation than a formal interview. I would like to tape our conversation if you agree. If you do not wish to be identified, your real name would not be connected with the tape. The tape

would be erased as soon as I have finished using it to make notes of our conversation. If you would prefer not to be tape-recorded, I am happy just to take notes. If you wish to check a copy of my notes before I use them in my study, then please indicate this on the attached Consent Form.

If you decide to participate in the study you are free to change your mind and withdraw at any time before the study has been completed. Also, you are not obliged to answer questions or to discuss any issues that you do not wish to discuss. You are free to withdraw your interview material up until the time that I have finished all the interviews. You do not have to give me any reason if you do decide to withdraw from the study.

Please don't hesitate to contact me if you want more information about the study. If you have concerns that you do not wish to discuss with me directly, contact ***Professor Gordon Howarth*** who is the Post Graduate Co-ordinator of the Masters program for which I am conducting this study or ***Associate Professor Wayne Pitchford*** who is my Principal Supervisor

CONTACT DETAILS: **Ellison Musimuko** Student, Master of Philosophy, School of Animal and Veterinary Sciences, University of Adelaide Ph. +61424446281 E-mail ellison.musimuko@adelaide.edu.au	Assoc Professor Wayne Pitchford School of Animal and Veterinary Sciences University of Adelaide Roseworthy SA 5371 Ph +61-8-83137642 Mob +61-418809688 Email wayne.pitchford@adelaide.edu.au Professor- Gordon Howarth Postgraduate Co-ordinator' University of Adelaide Ph. 831337885 E-mail gordon.howarth@adelaide.edu.au

Human Research Ethics Committee (HREC)

CONSENT FORM

I .....have read the attached Information Sheet and agree to take part in the following research project:

Title:	**Designing breeding objectives with genomic selection in Zambian Cattle; Preference studies with cattle breeders in Zambia**
Ethics Approval Number:	

1. I have had the project, so far as it affects me, fully explained to my satisfaction by the research worker Ellison Musimuko. My consent is given freely.

2. I have been given the opportunity to have a member of my family or a friend present while the project was explained to me.

3. Although I understand the purpose of the research project it has also been explained that my involvement may not be of any direct benefit to me or family members.

4. I have been informed that, while information gained during the study may be published, I will not be identified and my personal results will not be divulged.

5. I understand that I am free to withdraw from this project at any time and that this will not affect my right to run cattle in this region, now or in the future.

6. I agree to the interview being audio/video recorded.Yes ☐ No ☐

7. I am aware that I should keep a copy of this Consent Form, when completed, and the attached Information Sheet.

Participant to complete:

Name:----------Signature:----------Date:----------

Rsearcher/Witness to complete:

I have described the nature of the research to----------P*rint name of participant)*

and in my opinion she/he understood the explanation.

Signature:---------- Position: ----------Date----------

Appendix 3.2: Microsatellites for Bovine Breed Identification

ISAG RECOMMENDED MICROSATELLITES FOR BOVINE BREED IDENTIFICATION						
No.	NAME	Chr	Primer Sequence (5' -> 3') Forward Reverse	Annealing temperature	Genebank accession number	Allele Range (bp)
1	INRA005	12	CAATCTGCATGAAGTATAAATAT CTTCAGGCATACCCTACACC	55-65°C	-	189-227
2	INRA23	3	GAGTAGAGCTACAAGATAAACTTC TAACTACAGGGTGTTAGATGAACTC	55°C	X67830	195-225
3	ETH10	5	GTTCAGGACTGGCCCTGCTAACA CCTCCAGCCCACTTTCTCTTCTC	55-65°C	Z22739	207-231
4	CSSM036[B]	27	GGATAACTCAACCACACGTCTCTG AATTTAATGCACTGAGGAGCTTGG	55-65°C	U03827	162-176
5	ETH3	19	GAACCTGCCTCTCCTGCATTGG ACTCTGCCTGTGGCCAAGTAGG	55-65°C	Z22744	273-315
6	BM2113	2	GCTGCCTTCTACCAAATACCC CTTCCTGAGAGAAGCAACACC	55-60°C	M97162	122-156
7	BM1824	1	GAGCAAGGTGTTTTTCCAATC CATTCTCCAACTGCTTCCTTG	55-60°C	G18394	176-197
8	BM1818	23	AGCTGGGAATATAACCAAAGG AGTGCTTTCAAGGTCCATGC	56-60°C	G18391	248-278
9	ETH225	9	GATCACCTTGCCACTATTTCCT ACATGACAGCCAGCTGCTACT	55°C-65°C	Z14043	132-163
10	MGT4B	4	GAGCAGCTTCTTTCTTTCTCATCTT GCTCTTGGAAGCTTATTGTATAAA	55-65°C	…	129-161
11	RM067	4	TGAGTAATGCAATAGATACAGTATT GCTTTGGCCATATGAAGAGCTTT	57°C	SQ0002237	84-116
12	TGLA227	18	CGAATTCCAAATCTGTTAATTTGCT ACAGACAGAAACTCAATGAAAGCA	55-56°C		75-105
13	TGLA126	20	CTAATTTAGAATGAGAGAGGCTTCT TTGGTCTCTATTCTCTGAATATTCC	55-58°C	-	115-131
14	TGLA122		CCCTCCTCCAGGTAAATCAGC	55-58°C	-	

		21	AATCACATGGCAAATAAGTACATAC			136-189
15	TGLA53	16	GCTTTCAGAAATAGTTTGCATTCA ATCTTCACATGATATTACAGCAGA	55°C	-	315-369
16	SPS115	15	AAAGTGACACAACAGCTTCTCCAG AACGAGTGTCCTAGTTTGGCTGTG	55-60°C	FJ828564	234-264
17	CSSM022[B]	5	TCTCTCTAATGGAGTTGGTTTTTG ATATCCCACTGAGGATAAGAATTC	55-60°C	U03806	200-213
18	CSSM016[A]	3	GATGCAGTCTCCACTTGATTCAAA AGAGCCACTTGTTACACCCCAAAG	55-58°C		148-186
19	RME40	26	TGTTCTGTGAGCATGTGCAG CTGTTTTCAAAGAGAGGGAAGC	55-58°C	AF013092	198-254
20	TGLA293	-	GAAACTCAACCCAAGACAACTCAAG ATGACTTTATTCTCCACCTAGCAGA	55°C	-	143-191
21	AGLA232	13	CCTTTGCAAATACCTCCTGACCAG AATGGTTCTACATTTGCTAGGTGTC	54°C	-	153-188
22	BL1043	7	AGTGCCAAAAGGAAGCGC GACTTGACCGTTCCACCTG	55	X67830	89-131
23	BM203	27	GGGTGTGACATTTTGTTCCC CTGCTCGCCACTAGTCCTTC	55-60	G18500	202-233
24	TGLA057	9	GCTTTTTAATCCTCAGCTTGCTG GCTTCCAAAACTTTACAATATGTAT	55	X67830	68-109
25	TGLA263	3	CAAGTGCTGGATACTATCTGAGCA TTAAAGCATCCTCACCTATATATGC	55-60	AFCO20172 97	105-130
26	BM305	17	GGTCATGGGAGGAAATACACA GTGTCCTTTTGACTCACTGTGC	55-56°C	G18776	101-141
27	BM5004	20	TCTGGAGTGAATGTTTCTGAGG TTGTGATGAGCACCTGAAGG	55-58°C	G18524	115-156
28	BMS2047	20	GCTMTCACCYTCAACCACAT	55-58°C	G18716	

			GTTTCTTAGTAGGTGGAGATCAAGGATGC			143-193
29	BMS2742	23	GCTTCAGTTCTGCTTTTCACC CTTCAGCATCTTGATTGTTGC	58°C	G18946	127-175
30	BMS510	28	TGCTGCATGATTCTCATTCC AGCCTTCCTGTTCTCTGCTG	58-60°C	G18568	81-112
31	BMS650	19	GCTAGCATTTCCCTGGCC GTTTCTTCAGAAGCACACAGAGCCAAG	60	G18860	134-174
32	CSSM42	2	GGGAAGGTCCTAACTATGGTTGAG ACCCTCACTTCTAACTGCATTGGA	55-60	-	162-220

Appendix 4.1 Herd Book Society of Zambia Standard Code for cattle registration since 1966

Herd Book Society of Zambia Standard Code for cattle registration since 1966

Letter	year	year	year
A	1966	1985	2004
B	1967	1986	2005
C	1968	1987	2006
D	1969	1988	2007
E	1970	1989	2008
G	1971	1990	2009
H	1972	1991	2010
J	1973	1992	2011
K	1974	1993	2012
L	1975	1994	2013
N	1976	1995	2014
O	1977	1996	2015
P	1978	1997	2016
R	1979	1998	
S	1980	1999	
T	1981	2000	
U	1982	2001	
W	1983	2002	
X	1984	2003	

Source: Herd book society of Zambia 2007

Appendix 4.2: The average and standard errors of weaning weight (Kg).

YoB		Mean	SE
1995		119.4200	4.7708
1996		135.7650	4.2537
1997		138.2041	3.3768
1998		152.2139	3.3178
1999		137.1690	2.6787
2000		131.5293	2.6554
2001		141.5228	2.7656
2003		131.6969	2.7219
2004		142.5737	2.9409
2005		128.3188	3.0931
2006		135.0661	3.1003
2007		105.7034	4.1663
2008		115.0081	3.6370
2002		131.1703	3.3854
2009		117.1664	4.8422
Breed			
Angoni		119.3867	2.4862
Boran		142.2837	2.0169
Breed	Sex		
Angoni	F	114.3500	2.7080
Angoni	M	124.4235	2.6907
Boran	F	137.7434	2.1182
Boran	M	146.8239	2.1819