EVALUATION OF GENETIC DIVERSITY OF SAHIWAL CATTLE IN KENYA

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DECLARATION AND APPROVAL

DECLARATION

This thesis is my original work and has not, wholly or in part, been presented for an award of a diploma or degree in any other university known to me.

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DEDICATION

This work is dedicated to my family for their encouragement and support and Professor A. K. Kahi for his mentorship.

ABSTRACT

The Sahiwal cattle breed in Kenya is a product of a long-term upgrading program involving Sahiwal bulls and the Small East African Zebu (SEAZ) dams. It is an important animal genetic resource that play dual purpose role but information about its population structure, demographic trends and genetic diversity is lacking. The breed faces several challenges that include high risks of inbreeding, drought related challenges, competition from exotic breeds and indiscriminate crossbreeding. Therefore, the breed could be at a risk of losing genetic diversity and also increased vulnerability to extinction. The objectives of this study were to explore geographical distribution of the breed, characterize its population structure, assess its status and trends of genetic diversity and lastly to conduct a population viability analysis (PVA) of the main herd of the breed at the National Sahiwal Stud (NSS). Geographical distribution was analysed using ArcView GIS 3.2. Population structure and genetic diversity were analyzed using POPREP software system while population viability was evaluated using VORTEX version 9.98. The number of registered Sahiwal cows and bulls used for breeding annually indicated an unstable situation and even a downward trend of the breed population growth though the geographical distribution was sparse. Males stayed in the breeding herd much longer than females. Generation Interval (GI) was longer by about 3 years in males than in females. Family sizes varied widely in male pathways than in female pathways. The mean number of discrete generation equivalents traced was 2.46. The mean level of inbreeding was 0.58% for all animals and 2.23% for inbred animals while the mean additive genetic relationships (AGR) in the whole population was 0.87%. The average inbreeding for inbred animals decreased slowly at the rate of -0.0012% per annum while for the entire breed increased by 0.025% per annum. The overall population size of the NSS herd was predicted to increase at a deterministic rate of 12.5% and stochastic rate of 3.2% before any truncation due to limited carrying capacity. Female mortality prolonged generation interval for both males and females whereas male mortality had no effect on generation interval. The proportion of breeding males had no effect on deterministic growth rate but it improved genetic diversity of the herd. An increase in adult breeding females increased the viability of the NSS herd. The study revealed that the Sahiwal population is not going extinct but it is below the level required to maintain genetic diversity in the long term.

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LIST OF ABBREVIATIONS

AnGR	Animal Genetic Resources
ASALs	Arid and Semi Arid Lands
CPUs	Central Processing Units
DAD	Domestic Animal Diversity
DE	Degree of Endangerment
EBVs	Estimated Breeding Values
FAO	Food and Agriculture Organization
FMD	Foot and Mouth Disease
GDP	Gross domestic product
GPS	Global Positioning System
IUCN	International Union for the Conservation of Nature
KAGRC	Kenya Animal Genetic Resources Centre
KARI	Kenya Agricultural Research Institute
KLBO	Kenya Livestock Breeders Organization
KSB	Kenya Stud Book
MOET	Multiple Ovulation and Embryo Transfer
NDRI	National Dairy Research Institute
NSS	National Sahiwal Stud
PE	Probability of Extinction
RCCSC	Research Center for Conservation of Sahiwal Cattle
SCBS	Sahiwal Cattle Breeders Society

CHAPTER ONE

GENERAL INTRODUCTION

1.1 Background

Livestock genetic resources are an essential component to promoting world food security and contributes to the livelihoods of over a billion people (FAO), 2007a). Livestock diversity thus contributes in many ways to human survival and wellbeing (Drucker, 2001). In Kenya, they are an important part of the national economy and more importantly to resource poor farm households (Lanyasunya *et al*., 2005). As a sub-sector of agriculture, livestock production accounts for about 10% of the gross domestic product (GDP) (R.O.K, 2002). Only about one third of the total land area of Kenya is arable (R.O.K, 2007). The remaining land area is semi-arid to arid and characterized by low, unreliable and poorly distributed rainfall. In the arid and semi arid areas (ASALs), where over 60% of all farm animal genetic resources (FAnGR) are found (FAO, 2005; R.O.K, 2007), livestock contributes about 42% of the agricultural GDP, 90% of employment and 90% of family incomes. These areas are unsuitable for arable farming but have great potential for livestock production and consequently suitable for conservation of indigenous animal genetic resources (AnGR).

Animal genetic resources are crucial for sustainable economic development and food security but their genetic diversity is at an increasing loss because more breeds are facing extinction risk (Canali, 2006). The Kenya Sahiwal cattle breed is an important animal genetic resource that contributes to the livelihood of people mainly in the ASALs through efficient provision of meat and milk (Rege *et al*., 1992). The breed was introduced in Kenya from India and Pakistan in the early 1930s to upgrade the local Small East African Zebu (SEAZ) cattle for both milk and beef production under rangeland conditions (Muhuyi *et al*., 1999). Imported bulls and the best SEAZ cows from Livestock Improvement Centres were collected and brought together to initiate a breeding program that formed the National Sahiwal Stud (NSS) at Naivasha in 1962. Long-term upgrading of the selected SEAZ dams with imported Sahiwal bulls at the NSS resulted in the Kenya Sahiwal cattle breed. The breed carries unique adaptive capabilities that make it relatively competitive in terms of production and adaptation under low-input production systems (Muhuyi, 1997; Philipsson, 1999; Joshi *et al*., 2001).

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The main users of the Kenya Sahiwal cattle breed are large-scale private and government ranches and the Maasai pastoralists. Many pastoralists in Kenya use Sahiwal sires for crossbreeding with the SEAZ dams to improve growth performance and milk production (Ilatsia *et al*, 2011a). Contribution of the Sahiwal breed to adaptability is also well documented in several ecological zones of Africa (Trail and Gregory, 1981) where Sahiwals have been crossed with exotic *Bos taurus* breeds that have a high response capability for milk and beef production but lack adaptability to local conditions (Kahi, 2000). However, the population of the Kenya Sahiwal breed is relatively small compared to that of other Zebu breeds such as the SEAZ and the Boran (Ilatsia *et al*., 2011a). The EAZ is the predominant cattle breed, followed by Sahiwal and their crosses with EAZ, and unimproved Boran (MOLFD, 2006). Besides, its population is decreasing constantly due to intensive indiscriminate crossbreeding with temperate and local cattle breeds in addition to other natural calamities such as severe droughts and diseases. These factors necessitate strategic breeding and conservation interventions for sustainable use of the breed. As a prerequisite, evaluation of the current population status and possible future dynamics of the breed population is a critical step.

Endangerment risk of AnGR can be analyzed in terms of population structure, trends, geographical distribution and other breeding activities (Carson *et al*., 2009; Gutiérrez *et al*., 2003). The number of registered breeding animals constitutes the part of the population that can be monitored in terms of population structure and that can actively participate in conservation and selection programs (Alderson, 2009). Therefore, knowledge of the population structure and geographical distribution of the Kenya Sahiwal cattle breed is currently of interest. However, the information is lacking because no comprehensive baseline survey has been conducted. Without such information, major breed populations and unique characteristics they contain may decline significantly, or be lost before measures are taken to conserve them. This study evaluated population structure of the breed and provides a basis for organizing breeding structure and advancing conservation strategies for sustainable breed utilization.

1.2 Statement of the problem

Information about the Kenya Sahiwal cattle breed population structure, demographic trends and geographical distribution is not available as no comprehensive baseline survey has been conducted. Though it is a well documented contributor to livestock biodiversity and rural livelihoods in Kenya, its population is relatively small compared to that of other Zebu breeds (Ilatsia *et al*., 2011a). The breed could be facing loss of genetic diversity and extinction risk because of its decreasing population and the ongoing indiscriminate utilization in crossbreeding programs (Ilatsia, 2011). Many pastoralists in Kenya use Sahiwal sires for crossbreeding with the SEAZ dams to improve growth performance and milk production (Ilatsia *et al*, 2011a). Sahiwals have been crossed with exotic *Bos taurus* breeds that have a high response capability for milk and beef production but lack adaptability to local conditions (Kahi, 2000). Extinction of breeds causes erosion of AnGR, which is a long-term threat to ensuring food security and rural development. It also has negative impacts on the ability of livestock keepers and breeders to respond to emerging diseases and parasites and to future production challenges resulting from changes in the environment including climate change (FAO, 2007a).

1.3 Objectives

The broad objective was to contribute to the effective and sustainable management of the Sahiwal cattle breed through evaluation of the genetic diversity of the breed in Kenya. The specific objectives were:

1. To explore the geographical distribution and degree of concentration of the registered Kenya Sahiwal cattle breed.
2. To characterize the population structure and determine demographic trends of the registered Kenya Sahiwal cattle breed.
3. To determine the status and monitor trend of genetic diversity within the Kenya Sahiwal cattle breed.
4. To predict the likely future status of the main herd at the National Sahiwal Stud.

1.4 Research questions

    i.   What is the range of geographical distribution and degree of concentration of the registered Kenya Sahiwal cattle breed?

    ii.   What are the number and mean age of breeding males and females, generation interval and family size variances of the registered Kenya Sahiwal cattle breed?

    iii.   What is the status and trend of genetic diversity of the Kenya Sahiwal cattle breed?

    iv.   What is the likely future status of the Kenya Sahiwal cattle breed population?

CHAPTER TWO

LITERATURE REVIEW

2.1 The Sahiwal cattle breed

FAO (2000) defined a breed as: either a homogenous, sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species, or a homogenous group for which geographical separation from phenotypically similar groups has led to general acceptance of its separate identity. Sahiwal is a dual purpose (kept for both meat and milk) breed of zebu cattle that originated in the Sahiwal district of Pakistan, a dry region of Punjab which lies along the Indian-Pakistani border (Dahlin *et al*., 1995). They were once kept in large herds by professional herdsmen called "Junglies". However, with the introduction of irrigation to the region, they began to be kept in smaller numbers by the farmers of the region. Originally, they were bred for draft and dairy purposes, and today, the breed is recognized as the best milk producing zebu breed (Dahlin *et al*., 1995).

2.1.1 Description of the Sahiwal cattle breed

The Sahiwals are heavily built and their colour ranges from reddish brown to chestnut, a dark brownish colour is common around the hump and neck; in males the colour darkens towards the extremities (i.e. head, legs and tails), while females maintain the reddish coat colour. They have a well developed hump in the cervico-thoracic position. They have height at withers of 140 cm and 120 cm for males and females, respectively; udders are large compared to cattle of other *Bos indicus* breeds; teats are large; their ears are long and drooping. Their skin coat is generally smooth and shiny especially during hot weather conditions. Compared to other Zebu cattle breeds, Sahiwals are generally docile and of calm temperament a characteristic that allows them to be milked in the absence of the calf (Kimenye, 1978; Muhuyi *et al*., 1999; AGR, 2006).

2.1.2 Distribution of the Sahiwal cattle breed

Due to its heat tolerance, parasite resistance and high milk production, Sahiwal has been spreading from its native origin in India and Pakistan to various tropical regions and comes second to the Brahman in terms of distribution among the Zebu breeds of South Asian ancestry

(FAO, 1992; Joshi *et al*., 2001). The breed is now reported to be present in 27 countries (FAO, 2007) but is widely bred and actively conserved in Pakistan (Montgomery, Punjab region or the present day Sahiwal district), India, and Kenya (AGTR, 2006). Pakistan, India and Kenya are endowed with the majority of purebred Sahiwal cattle and have actively been involved in breeding and conservation programs. In Kenya, the high grade Sahiwals together with their crosses with other breeds are owned by the NSS whereas a few are owned by private commercial breeders (Ilatsia *et al*., 2011a).

2.1.3 Utilization of the Sahiwal cattle in the tropics

The Sahiwal cattle breed is an important national genetic resource of Pakistan. Sahiwal genetic resources are among the leading sources of milk in Pakistan coming second to buffaloes in domestic milk supply in Punjab province, which is home to nearly half of the Pakistan population (ACO, 2006; Khan *et al*., 2008; Government of Punjab, 2010). The breed is largely bred in Montgomery, Punjab region of Pakistan or the present day Sahiwal district. It is widely considered as one of the best milk producing zebu breed in Pakistan. From Pakistan, the breed has been exported to many other countries (Maule, 1990) for both cross- and pure-breeding. The population of Sahiwal cattle breed was reported to be decreasing in Pakistan as a result of crossbreeding with exotic breeds for dairying (Payne and Hodges, 1997).

Within Kenya, the main utility of the Sahiwal cattle breed is seen in crossbreeding for dual-purpose production in the middle- to lower-potential areas. Sahiwal cattle genetic resources are mainly kept by pastoralists, private and government ranches, and by a few smallholder dairy farmers for domestic milk production and revenue generation through sale of live animals and surplus milk (Muhuyi, 1997; Bebe *et al*., 2003; Roessler *et al*., 2010). The Sahiwal breed is used to upgrade the relatively well adapted SEAZ for improved milk production and growth performance under the challenging rangeland conditions (Meyn and Wilkins, 1974; Trail and Gregory, 1981; Muhuyi *et al*., 1999). The breed is mainly utilised for milk and beef production because it has relatively high milk production and growth performance compared to other Zebu cattle breeds. Its suitability for the rangelands is based on the fact that it has evolved and been reared under almost similar harsh agro-climatic conditions in its native home in the Punjab region of India and Pakistan (Trail and Gregory, 1981; Muhuyi, 1997; Muhuyi *et al*., 1999; Joshi

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et al., 2001). Sahiwal bulls and semen have been exported from Kenya to several other East and Central African countries for crossing with various local Zebu breeds for milk production as well as provision of farm power (KARI, 2004; Mulindwa *et al*., 2006; Hatungumukama and Detilleux, 2009).

In India, Sahiwals are raised by smallholder farmers, government and private nucleus farms mainly for dairy production (Joshi *et al*., 2001; Singh *et al*., 2005). Organised crossbreeding programs involving the Sahiwal and mainly European breeds have been used to develop synthetic breeds in India. For example the Karan Swiss and Frieswal have been developed through several years of crossing the Sahiwal to the Brown Swiss and Friesian breeds, respectively (Singh and Gurnani, 2004; Gaur *et al*., 2006; NDRI, 2007). The synthetic breeds have shown the advantage of combining the high production levels of the European breeds and adaptation of the Sahiwal on a sustainable basis for dairy production under smallholder production conditions (Singh and Gurnani, 2004; Gaur *et al*., 2006).

2.2 Conservation of the Sahiwal cattle genetic resources

Sahiwal genetic resources are distributed in 27 countries in Asia, Africa and the Caribbean (Joshi *et al*., 2001; FAO, 2007). Pakistan, India and Kenya are endowed with the majority of purebred Sahiwal cattle and have actively been involved in breeding and conservation programs (Ilatsia, 2011). However, other programs might have been developed in other regions but have not been reported.

2.2.1 India

In India, there is no national database indicating the population estimates of Sahiwal cattle but there exist breeding and conservation programs in the country. A pure breeding program is implemented in 12 state-owned farms receiving technical support from the National Dairy Research Institute (NDRI). The contributions of the NDRI in the breeding program mainly involve coordination of performance recording, genetic evaluation and dissemination of genetic material to the farmers (Joshi *et al*., 2001; NDRI, 2007). *In situ* conservation is mainly concentrated in the 12 government maintained herds where less than 2000 breeding animals are hosted (Joshi *et al*., 2001; Government of India, 2003). There are also a few Sahiwal herds

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maintained on a religious basis referred to as '*Gaushalas*' given that cattle are sacred in the Hindu religion (Ilatsia, 2011). There are two well maintained '*Gaushalas*' at Sirsa in Haryana and Gurudwara in Punjab, each with a herd of approximately 200 Sahiwal cows. Smallholder farmers also keep between 2-3 pure Sahiwal cows for milk production (NDRI, 2007). *Ex situ* conservation involve cryopreservation of frozen semen and embryos in national gene banks maintained by the NDRI.

2.2.2 Pakistan

Strategic breeding and conservation programs have been operational in Pakistan for the last three decades. This could be traced to previous collaborative research programs involving the FAO, the Pakistan Research Council and the Swedish University of Agricultural Sciences, which recommended the establishment of a genetic improvement and conservation program for the breed in Punjab (FAO, 1992; Dahlin *et al*., 1995). This initiative culminated in the recent establishment of the Research Centre for Conservation of Sahiwal Cattle (RCCSC) by the Punjab state government. The RCCSC has the statutory mandate to register Sahiwal cattle, carry out performance recording and genetic evaluation and to conduct strategic research, in collaboration with national and international research organisations, for genetic improvement and conservation of the breed. Currently the centre has 24 sub-centres in Punjab which host more than 11,000 registered breeding cows (RCCSC, 2007).

The RCCSC herds and other private herds form *in situ* conservation units in Pakistan. These farms are also the source of semen and embryos, which are frozen and stored for future use. Indiscriminate crossing remains a major challenge to conservation of the Sahiwal cattle breed in Pakistan (FAO, 1992; Dahlin *et al*., 1995; Government of Pakistan, 2003). To forestall this, the Pakistan government has formulated breeding policies and regulations that prohibit crossing of the Sahiwal cattle with exotic dairy cattle breeds (Government of Pakistan, 2003). The RCCSC could be regarded as a model conservation program for the Sahiwal breed in the tropics. The livestock sector strategy for the government of Punjab state has also prioritized the Sahiwal cattle breed among other indigenous livestock breeds for further genetic improvement and conservation (Government of Punjab, 2010).

2.3 The Kenya Sahiwal cattle breed

Kenya is the only country in Africa with major resources of Sahiwal cattle and serves as an important source of stock and semen for the continent (Trail and Gregory, 1981). Conservation of Sahiwal genetic resources in Kenya involve both, *in-situ* and *ex-situ* strategies. Government and privately owned nucleus herds act as *in-situ* conservation units, which produce breeding animals for the pastoral herds (Muhuyi, 1997). Pastoral herds also act as *in-situ* conservation units where Sahiwal cattle genetic resources are reared for both subsistence and commercial purposes. *Ex-situ* conservation takes place exclusively through preservation of frozen semen at the Kenya Animal Genetic Resources Centre (KAGRC) from superior bulls at the NSS (KARI, 2004). In Kenya there is no national breeding policy that governs use and development of specific livestock species and breeds. The yet to be operationalized animal breeding policy (MOLD, 2009) describes conservation measures only in general terms and gives broader recommendations with no clear or specific policies.

The Sahiwal cattle breed was introduced in Kenya in 1939 when breeding bulls were imported from India and Pakistan for upgrading the local Zebu dams for higher milk production and enhanced growth performance (Meyn and Wilkins, 1974; Trail and Gregory, 1981). In 1939, four Sahiwal bulls were imported by the Government from Pusa, India. After 1945, 60 Sahiwal bulls and 10 Sahiwal cows were imported from Jahangirabad in Pakistan. Another importation of 15 Sahiwal bulls was from Karnal in India in 1964 (Muhuyi *et al*., 1999). In addition to the ten cows imported from Pakistan, improved indigenous zebu cows were selected from livestock improvement centres and used as foundation stock in the grading up and multiplication of the Kenya Sahiwal cattle breed by systematic crossing with the imported Sahiwal bulls (Muhuyi *et al*., 1999).

In Kenya, the Sahiwal is mainly kept by ranches (government and privately owned) and the Maasai pastoralists (Roessler *et al*., 2010; Ilatsia *et al*., 2011a). The ranches act as the nucleus herds for pure Sahiwal breeding and the genetic progress is transferred to the pastoral herds through breeding bulls (Muhuyi, 1997; Ilatsia *et al*., 2011a). Kajiado, Transmara and Narok are the three geographical areas in Kenya with the highest populations of the Sahiwal genetic resources i.e. pure and crossbreeds (Ilatsia *et al*., 2011a). These areas are inhabited by the

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Maasai community who keep them as a source of livelihood. Kajiado county benefited from the initial stock of Sahiwal bulls that were imported from India and Pakistan by the British colonial government in the 1930s. In Transmara, Sahiwal bulls were first introduced in the late 1980s through a collaborative project between the Government of Kenya and the Germany International Technical Cooperation (Ilatsia, 2011). Narok county acquire breeding bulls from the neighbouring Kajiado district but their main source is the NSS.

2.3.1 Performance of the Kenya Sahiwal cattle breed and its crosses

The Kenya Sahiwal is principally a dual-purpose (meat and milk) breed (Mpofu and Rege, 2002). The average age at first calving varies between 30.4 and 46.7 months depending on the management level. Services per conception are about 2 and days open are 151; the calving interval is 411-437 days (Ilatsia *et al*., 2007). Birth weight of the Sahiwal was reported as 22.9kg (Mwandotto, 1994). The weaning weight of suckled Sahiwal calves is 160-180 kg, hence they compare favourably with the Boran. Mature weight of the Sahiwal cows and bulls at the NSS average at 425 kg and 500 kg, respectively (Muhuyi *et al*., 1999). The growth rate is similar to that of the Boran. Pre-weaning survival rate is about 78% and post-weaning about 96%. Milk let down problem is prevalent, as is the case in most zebu cattle. Lactation milk yield of the Sahiwal in Kenya vary from 972 to 2490 kg depending on the management level in different regimes (Ilatsia *et al*., 2007). The butter fat percentage is also indicated to vary between 3.5 and 5.3 (Muhuyi *et al*., 1999).

The Sahiwal Cattle Breeders Society (SCBS) of Kenya recognizes three categories of Sahiwal: foundation animals (have at least seven-eighths Sahiwal ancestry and have passed inspection), purebred Sahiwals (are minimally the progeny of registered animals above foundation stock and have passed inspection and weight-for-age evaluations) and pedigree Sahiwal (are minimally the progeny of registered animals above foundation stock and have passed inspection, weight-for-age, and dam's minimal lactation evaluations). The Sahiwals have been crossed with exotic breeds that have a high response capability for milk and beef production but lack adaptability to local conditions (Ilatsia *et al*., 2011b). Sahiwal, when crossed with exotic *Bos taurus* breeds, produced more milk than the indigenous *Bos indicus* cattle (Trail and Gregory, 1981). Kimenye and Russell (1975) suggested that crosses of European *Bos taurus*

breeds with Sahiwals out-yielded their purebred herdmates of either breed in both the semi-arid highlands and the hotter and more humid coastal belt. Therefore, to increase milk yield the Sahiwal cattle are being crossed with various breeds, including exotics. Results from Deloraine Estates and Cedarvale Farms in Nakuru county showed that the Sahiwal breed is superior to the Ayrshire in transmitted effects for growth rate, indicating that Sahiwal can usefully be included in programs geared towards beef production (Trail and Gregory, 1981).

2.3.2 Production systems for Sahiwal cattle breed in Kenya

Sahiwal cattle genetic resources are raised under low-input production systems by both pastoralists and ranchers, a strategy that aims to minimise the potential effects of genotype by environment interaction when breeding animals are exchanged (Ilatsia *et al*., 2011a). Their functions in low-input production systems are mainly related to family subsistence and revenue generation through sale of surplus milk and live animals. The primary breeding goals of the producers are high milk production, large body size, good fertility and adaptation to local production conditions (Roessler *et al*., 2010). The NSS is a research herd used for improvement of the breed for milk and meat production. It was established by collecting the best cows and bulls from the livestock improvement centres so as to centralize all breeding activities following growing demand for Sahiwal bulls and increased importation costs. The NSS is a member of the SCBS of Kenya and the Kenya Stud Book (KSB) (Muhuyi *et al*., 1999). The KSB is a farmers' organization under the Kenya Livestock Breeders Organization (KLBO) that provides the overall livestock registration services in the country (Kosgey *et al*., 2011). Its major objective is recording and maintaining a central national database for all registered stock with due regards to dates of birth and extended pedigree details. National pedigree recording of the Sahiwal breed in Kenya is done by the KSB in collaboration with the SCBS of Kenya.

The NSS constitutes purebred Sahiwal cattle and is the leading source of breeding stock for both pastoralists and other stud herds. Compared to other nucleus herds, the NSS keeps relatively good performance and pedigree records, which are used to support selection and management decisions (Ilatsia, 2011; Kosgey *et al*., 2011). At the NSS, young bulls averaging 9 months are weighed monthly up to 24 months. At 24 months, ten test bulls are pre-selected from a total of 75 bull calves on the basis of an index computed from the breeding value of the sire,

dam, and growth rate of the young bull. The ten bulls are maintained for 6-7 years until progeny test results are available. At the end of progeny testing period, the best two bulls out of ten in terms of milk production from their daughters are selected and eventually relocated to KAGRC for semen production. Female selection consists of eliminating 50% of heifers on the basis of first lactation milk yield and a further 50% at the end of the second lactation. The selected heifer herd is used for progeny testing of the bulls (Mpofu and Rege, 2002).

2.4 The status and trend of animal genetic resources

Over the past 50 years, available AnGR have declined considerably due to: changes in production systems, mechanization, loss of rangeland grazing resources, natural calamities, disease outbreaks, inappropriate breeding policies and practices, inappropriate introduction of exotic breeds, loss of animal keepers' security of tenure on land and access to other natural resources, changing cultural practices, the influence of population growth and urbanization, and the failure to assess the impact of these practices in terms of sustainability (FAO, 2007a). About 1350 breeds of domestic animals identified by the FAO currently face extinction in the near future (Scherf, 2000). A survey that was conducted to determine the status of cattle genetic resources of sub-Saharan Africa revealed that the continent is home to a total of 145 cattle breeds. Out of the 145 breeds, 47 (about 32%) were considered to be at risk of extinction. Of the breeds identified to be at risk of extinction, six were in the rare category, 10 were vulnerable, another 10 were endangered and 15 were in the critical category (Rege, 1999).

Extinction is an irreversible process in which identifiable populations or genetically controlled characteristics disappear. It may be at the species level, at the sub-species level, at the breed or variety level, and finally at the level of individual characteristics or genes. Over the past 15 years, about 300 of 6000 breeds of farm animals identified by the FAO have become extinct (Scherf, 2000). It is estimated that 1-2% of the described farm animal breeds go extinct per year; this is equivalent to the vanishing of one or two breeds per week (Simianer, 2005b). A total of 22 breeds previously recognised in sub-Saharan Africa have become extinct in the last century. This number excludes some populations, which have lost their individual identity due to admixtures involving two or more originally distinct breeds (Rege, 1999). According to a report by Reist-Marti *et al*. (2003), nearly half of the current cattle diversity and cattle breeds in Africa will be

lost in the next 20-50 years if conservation measures to reverse this trend are not implemented. A large loss of potentially valuable genetic diversity is represented by the large number of breeds facing extinction risk (Cunningham, 1996).

2.4.1 Genetic diversity of animal genetic resources

Genetic diversity represents the heritable variation within and between species or a collection of individuals within a species such as a breed, strain, line, herd/flock etc (Rege and Okeyo, 2006). The diversity ultimately resides in the variations in the sequence of the four base pairs which, as components of nucleic acids, constitute the genetic code. Domestic animal diversity (DAD) is the genetic variation existing among the species, breeds, strains and individuals which have been domesticated to meet human needs for food and agricultural production (Rege and Okeyo, 2006). Genetic diversity of AnGR make it possible for humans to survive in a wide range of environments, from the hot and humid tropics to arid deserts and extremely cold arctic or mountainous regions. Genetic diversity also enables livestock to adapt to diseases, parasites, wide variations in the availability and quality of food and water, and other limiting factors (FAO, 1999). Therefore, loss of genetic diversity would compromise the efforts to achieve food security, improved human nutritional status and rural development. Animal breeding aims at changing the genetic makeup of animals so that they better meet human needs. Such improvement is sought by selection within breeds or use of differences among breeds through crossbreeding, grading-up to a superior breed by repeated back-crossing, or formation of a synthetic population. Therefore, loss of variation will restrict the options available to meet unpredictable future requirements.

2.4.2 Conservation of animal genetic resources

Conservation is one of the four Strategic Priority Areas of the recently adopted Global Plan of Action for AnGR (FAO, 2007a), underlining the need for governments to address this topic in national plans for management of AnGR. The realization of the need for conservation of AnGR has been on the international agenda for some 50 years (Barker, 1994) but its translation into action has been slow. In the developed world, organizations such as the Rare Breed Survival Trust in the UK, Safeguard for Agricultural Varieties in Europe, and the American Livestock Breeds Conservancy in the United States of America have instituted effective programs

(Alderson, 1990) for the conservation of rare and endangered breeds. However, no such organizations and programs exist in the developing world.

Conservation of all livestock breeds is considered to be financially infeasible (Bennewitz *et al*., 2007) and may not be necessary. Therefore, a process of prioritizing breeds for conservation is necessary. A wide number of factors could potentially contribute to the decision regarding the priority of breeds for conservation. Reist-Marti *et al*. (2006) proposed a number of factors that contributed to priority for conservation among a group of African cattle breeds. Among these factors were the total population size of the breed and trends in population size in the previous 10 years, distribution of the breed within the country, degree or risk of indiscriminate crossbreeding, level of organization of farmers, existence of ongoing conservation schemes, political stability of the country, socio-cultural importance of the breed, and the reliability of this information. Breeds with small population sizes and large risk for extinction should generally receive greater priority in conservation programs.

2.5 Criteria and classification of endangerment status

Degree of endangerment (DE) of a breed is a measure of the likelihood that, under current circumstances and expectations, the breed will become extinct within a specified period of time (Gandini *et al*., 2004). The endangerment process is usually described by a function of downward or upward trend in the number of breeding animals or breeding herds and locations in addition to conditions, which may affect the existence of a breed (FAO, 1995). Monitoring of the DE of livestock breeds provide information on the erosion process of breed diversity and on the urgency with which conservation strategies need to be implemented. Instead of some arbitrary number of breeding animals (male and female) per breed taken from census records, the effective population size (N_e) has been proposed as the main factor for assessment of breeds for endangerment (Al-Atiyat, 2008).

There is not a consistent system for the recognition and definition of the factors which directly measure the DE of breeds of farm livestock. Many factors have been identified and detailed (Ruane, 2000), but standardized definition and measurement of the most significant factors is lacking. The procedures adopted by governmental agencies and by several non-governmental organizations employ different principles, which inhibit effective interpretation,

and in some cases propose conflicting principles for the identification and categorization of endangerment. There is therefore an urgent need to harmonize and implement an agreed system, which will give an accurate measurement of the endangered status of each breed, and permit effective and rapid exchange of information between international and national databases (Alderson, 2009).

2.5.1 A proposed model for classification

According to Alderson, (2009) a system that was established in the United Kingdom (UK) in 1975, with subsequent development and refinement, offers one model as a basis for harmonization. The principles embedded in this procedure were based initially on genetic integrity, indicated by absence of recent introgression and measured by deoxyribonucleic acid analyses and breed assignment procedures, and thereafter by degree of vulnerability from either numerical scarcity, or geographical concentration or genetic erosion. This model identified the principal factors which determine the DE, namely numerical, geographical, and genetic. It applies them to enable the classification of breeds and their categorization into five degrees of endangerment ranging from 'Critical' to 'Transitional'.

2.5.2 Indicators of endangerment status

a) Numerical scarcity

The proposed system varies from most other systems because it includes reproductive rate, alongside mating ratio and GI, as a relevant factor in the calculation of the threshold. The system persists in the use of breeding females as the numerical criterion. The maximum numbers of breeding females which allow eligibility for categorisation of endangerment are 1000 for pigs, poultry and goats, 1500 for cattle, 2000 for equines and 3000 for sheep. Using the number of breeding females as the criterion has significant limitations while using the number of female replacements would be a superior measure (Alderson, 2009; Alderson, 2010).

b) Geographical concentration

An essential aspect of breed distribution is the extent to which a breed is concentrated in a geographical area. There is a potential risk to genetic resources arising from geographical concentration (Carson *et al*., 2009). Such population of breeds or species are at particular risk if their native area is in the path of a disease epidemic and also they can be expected to experience

a higher rate of inbreeding. A breed is categorised in one of the five categories of endangerment if 75% or more of its population lies within a circle of 25 km radius. An insight into this impact of geographical isolation was gained in the UK during the foot and mouth disease (FMD) epidemic of 2001. More than 44% of the farms whose animals were slaughtered were located in the Cambrian region of the North-West of England (FMD, 2001). As a consequence, the local sheep breeds suffered disproportionate losses (Bowles *et al*., 2003).

c) Genetic erosion

Historical genetic erosion is measured by analyses of founder effect (Alderson, 1992) and ancestor effect (Boichard *et al*., 1997). Inbreeding is an indicator of expected ongoing genetic erosion, and consequently is used as the preferred criterion to measure potential loss of genetic diversity. For immediate conservation, the level of inbreeding is considered more relevant than the rate of inbreeding (Alderson, 2009).

2.6 Population Viability Analysis (PVA)

Population viability analysis is defined as the use of quantitative methods to predict the likely future status of a population or collection of populations. This process identifies the viability requirements of, and threats faced by, a species. It then assesses the rate of population decline and the risks of extinction or quasi-extinction over a defined time horizon for the population of concern (Gilpin and Soule, 1986; Boyce, 1992; Morris and Doak, 2002). It is one of the central tools for conservation, planning and evaluation of management options. Population viability analysis requires information on the demography, ecology and habitat requirements of a species (Beissinger and McCullough, 2002; Miller and Lacy, 2003). More accurate information on these parameters permits researchers to more realistically simulate alternative future population scenarios (Durant and Mace, 1994; Brook *et al*., 2000; Ellner *et al*., 2002). It was first used in the early 1980s (Shaffer, 1981), and in the past decade it has gained broad acceptance in the conservation community as a useful tool for assessing and managing 'at risk' species (Beissinger, 2002; Morris and Doak, 2002; Reed *et al*., 2002). The results of a PVA can be expressed as extinction risk, time to decline, chance for recovery, persistence time, and local and regional occupancy rate (Akçakaya, 2000 and Beissinger and McCullough, 2001).

CHAPTER THREE

GEOGRAPHICAL DISTRIBUTION AND CONCENTRATION OF THE KENYA SAHIWAL CATTLE BREED

3.1 Introduction

The extent to which a breed is concentrated in a geographical location is an important aspect of its distribution. Concentration of a major part of the breed population in a restricted geographical area or in a few herds would usually place it at greater risk to extinction due to the consequences of catastrophic events such as disease outbreak, climatic and/or political upheavals (Carson *et al*., 2009). Decreased native area is therefore one of the indicators of breeds' endangerment status and awareness of their geographical distribution is a prerequisite for sustainable management of farm animal genetic resources. Extinction of Blue Albion cattle in 1967 and losing more than 50% of British Milksheep population in 2001 through foot and mouth disease (FMD) outbreak in UK are some cases of the vulnerability of geographically concentrated breeds (Carson *et al*., 2009). Information about a breed' native area and its geographical concentration may therefore be applied to undertake primary conservation actions, to predict its probability of extinction and to conduct other complementary studies for programming conservation (Lacy, 1993; Bennewitz and Meuwissen, 2005; Al-Atiyat, 2008).

According to a study by Ilatsia (2011), Pakistan, India and Kenya are the only countries endowed with majority of purebred Sahiwal cattle and have been involved in breeding and conservation of the breed. In Kenya, the high grade Sahiwals are mainly owned by the National Sahiwal Stud (NSS) in Naivasha whereas a few high grade Sahiwals and their crosses are owned by private commercial breeders (Ilatsia *et al*., 2011a) which serve as the nucleus herds/conservation nuclei. Kajiado, Transmara and Narok are the three geographical areas in Kenya with the highest populations of the Sahiwal genetic resources i.e. pure and crossbreeds (Ilatsia *et al*, 2011a). Kajiado is one of the areas that benefited from the initial stock of Sahiwal bulls that were imported from India and Pakistan by the British colonial government in the 1930s for upgrading the small East African Zebu (SEAZ).

In Transmara, Sahiwal bulls were first introduced in the late 1980s for upgrading the local SEAZ for both milk and growth. This was through a collaborative project between the

ministry of agriculture and livestock development and the Germany International Technical Cooperation (Ilatsia, 2011). The NSS has been the main source of breeding bulls to farmers in Narok county but they also acquire breeding bulls from the neighbouring Kajiado county. In Kenya, there exists no national database showing the breed specific population figures. However, there are at least 18 ranch herds, which host approximately 7,000 purebred Sahiwal cattle with about 1500 breeding cows (KARI, 2004). Some unpublished reports by field livestock extension officers in the pastoral areas estimate the Sahiwal population at 50,000 with about 170,000 Sahiwal x Zebu crossbreds (MOLFD, 2006).

The population of the Kenya Sahiwal cattle breed has been reported to be shrinking and relatively small compared to that of other Zebu breeds such as the SEAZ and the Boran (Ilatsia, 2011). In addition to lack of a national database, the Kenya Sahiwal cattle breed has been reported to face challenges such as inbreeding, uncontrolled crossbreeding and droughts (Ilatsia, 2011). Furthermore, its geographical distribution has not been published and therefore the extent of its geographical concentration is unknown. Decreasing of population size, breeding herds and locations; indiscriminate crossbreeding; low effective population size and presence of threatening factors of survival are indicators of imminent danger of breed extinction (Scherf, 1995; Simon, 1999). Since geographical concentration alone could represent a considerable risk of extinction to a breed, in this Chapter, the geographical distribution of the major herds of the Kenya Sahiwal cattle breed is explored and the degree of concentration and geographical endangerment status of the breed is determined. The spatial information is important in making decision of conservation and sustainable management of the breed.

3.2 Methodology

3.2.1 Data collection

Data were collected through a close collaboration with the Kenya Stud Book (KSB). The KSB was approached to enable identify farms and/or ranches that hold Sahiwal genetic resources. Another review was conducted on field data collection report by Ilatsia (2011). The survey identified a total of fifteen herds that formed the basis of this study. This was followed by a visit to the farms. Each farm was assigned a reference number, and its herd size and Global

Positioning System (GPS) coordinates were recorded in an Excel database. The survey data are summarized in Table 3.1.

Table 3.1: Global positioning system coordinates and herd sizes of the major farms that hold Sahiwal cattle breed in Kenya

	HERD NAME	HERD SIZE(f)	x	fx	y	fy	SUB/COUNTY
H1	National Sahiwal Stud	1,224	-0.713	-872.614	36.422	44,580.1718	Naivasha
H2	Elkarama ranch	900	0.128	115.173	36.900	33,210.0909	Laikipia
H3	Ole Sentu ranch	306	1.237	378.664	35.196	10,769.9546	Transmara
H4	Ole Naishu/Kamwaki	238	0.187	44.486	36.680	8,729.9564	Laikipia
H5	Ilkerin Loita	433	1.279	553.681	35.420	15,336.7647	Narok
H6	Keiyan farm	450	-1.208	-543.680	34.489	15,519.8709	Transmara
H7	Doleraine Estates	180	-0.197	-35.534	35.924	6,466.2334	Nakuru
H8	Oloodo farm	333	-1.686	-561.456	36.840	12,267.6694	Kajiado
H9	Tunai farm	314	-1.390	-436.482	35.352	11,100.6542	Transmara
H10	KARI Transmara	60	-0.994	-59.653	34.879	2,092.7170	Transmara
H11	KARI Perkerra	90	0.469	42.173	35.994	3,239.4980	Baringo
H12	KARI Lanet	58	-0.270	-15.674	36.126	2,095.3269	Nakuru
H13	OCC (Olekejuado County Council)	195	-1.929	-376.175	36.810	7,177.9867	Kajiado
H14	Ole Ntutu farms	21	-1.306	-27.416	35.668	749.0370	Narok
H15	Narok PTC	58	-1.093	-63.403	35.888	2,081.4857	Narok
	Weighted mean centre			-0.382		36.09412	Nakuru

X is the easting

Y is the northing

3.2.2 Data Analysis

Descriptive statistics of the herd sizes were analysed using Ms Excel. ArcView GIS 3.2 (http://www.esri.com) was used to compute the extent of geographical distribution and concentration of the breed. A geo-referenced map of Kenya divided into provinces was loaded into the software. A table of the herd identity and their coordinates consisting of an easting (X-axis) and northing (Y-axis) was also loaded and the herds were mapped in their respective provinces. Another geo-referenced map consisting of former districts was loaded to display the herds in their respective counties or sub-counties.

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The coordinates were then used to calculate the weighted mean centre of the breed population following the equation below:

$$\overline{X}_{wc} = \frac{\sum f_i X_i}{\sum f_i} \qquad \text{and} \qquad \overline{Y}_{wc} = \frac{\sum f_i Y_i}{\sum f_i} \qquad [1]$$

Whereby: f = herd size (number of cattle per herd)

Wc = weighted mean centre of population

X = easting

Y = northing   (Carson *et al.*, 2009)

The weighted mean centre was loaded on the districts map and the standard distance tool of the software was used to draw circles of 25km and 50km radii in order to determine how the breed population is concentrated around the mean center. The cumulative total number of cattle within each radius was calculated to determine the percentage of the animals from the weighted mean centre. A system that applies three criteria (numerical, geographical and genetic) which was established in the UK in 1975 to enable the classification of breeds and their categorisation into five degrees of endangerment (Table 3.2) was used to classify the breed. A breed is classified in one of the endangerment categories shown in Table 3.2 if 75% or more of its population lies within a circle of 25 km radius.

Table 3.2: Definitions of categories of geographical endangerment for livestock breeds

Category		Geographical concentration*
1	Critical	12.5
2	Endangered	15
3	Vulnerable	17.5
4	At risk	20
5	Transitional	25

*Maximum radius of circle (km) containing 75% of the breed population

Source: Carson *et al.*, 2009

3.2.3 Assumptions and limitations

i.   Animal registrations was assumed to be sufficiently indicative of the overall numbers of purebred animals contributing to the breed genetic divesity.

ii. Geographical mapping considered only herds with registered animals.

iii. Data on geographical distribution of the breed in Kenya is limited and not up to date

iv.   Sahiwal crossbreeds were not considered as part of the breed population in the analysis

3.3 Results and discussion

3.3.1 Herd sizes

The total number of animals considered in the analysis was 4860. The study revealed that the number of animals per herd is highly variable ranging between 21 and 1224 animals. Mean herd size was 324 animals. Figure 3.1 illustrates the herd sizes of the farms/ranches used in this study. The variable herd sizes revealed that the number of herds does not give enough information about a breed population size and structure. The big variation in herd sizes requires to be improved since it increases the risk of breed endangerment through the high possibility of termination of any one herd (especially the small herds).
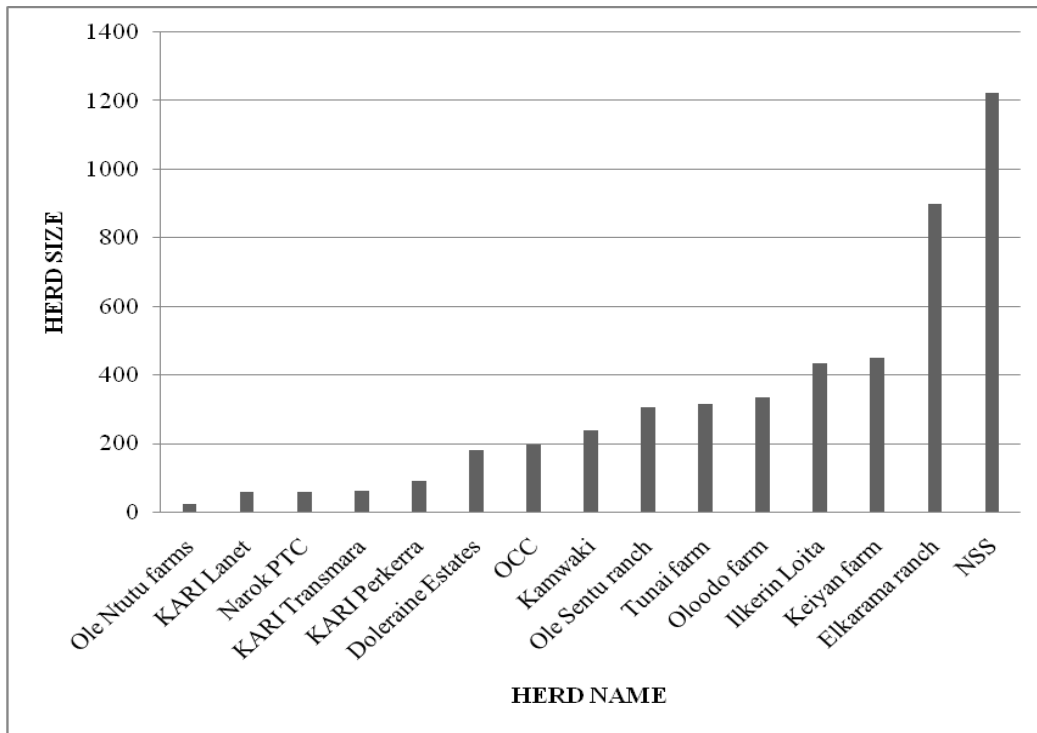
Figure 3.1: Herd sizes of the Kenya Sahiwal cattle breed in the fifteen farms/ranches in Kenya

Small herds face the risk of increased inbreeding thus inbreeding depression and ease of termination in case of a catastrophic event (Webb, 2014). Crosses of pure Sahiwal with exotic breeds have been reported to outperform pure Sahiwal (Thorpe *et al*., 1993) and therefore uncontrolled introgression may also lead to depletion of pure Sahiwal genetic resources in some

of the herds. Some of the farms identified from KSB such as Marula Estates in Naivasha and Kilifi plantations at the coast no longer keep Sahiwal breed.

3.3.2 Geographical distribution

Geographical distribution of the Kenya Sahiwal cattle breed in the fifteen herds at the former province level is shown in Figure 3.2. The herds are confined in five counties of the former Rift Valley province only with Narok county holding the largest number of herds (seven) and the highest breed population. The weighted mean center of the breed (Table 3.1) is located in (-0.382, 36.094).
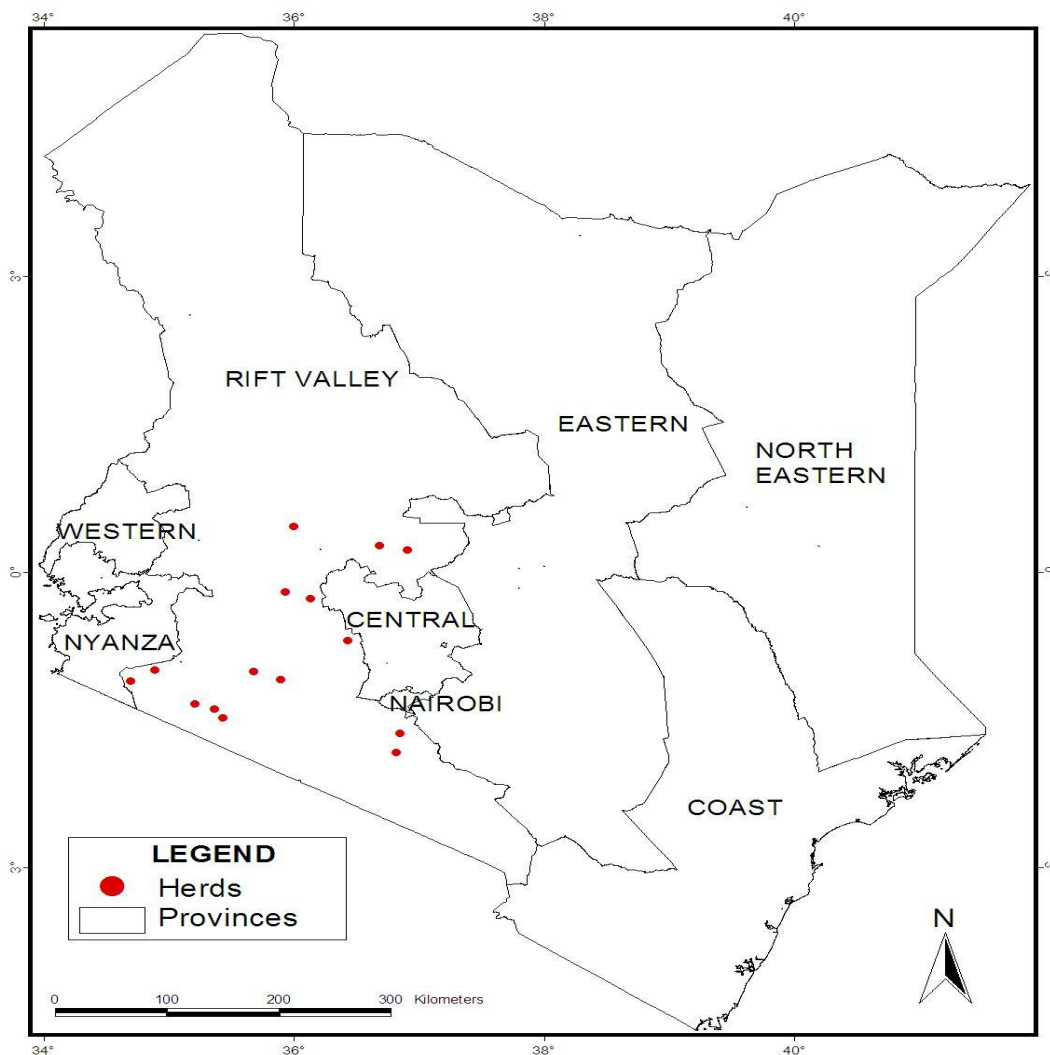
Figure 3.2: Distribution of the Kenya Sahiwal cattle breed in the former Kenya provinces

3.3.3 Geographical concentration

The circled areas show 25km and 50km radii buffer regions (Figure 3.3). The map shows that the breed is highly dispersed since only 1.2% of the breed population is located within a circle of 25km radius from the population mean center. Extending the buffer region to 50km radius, only 28.0% of the breed population lay within the buffer area. A similar study was carried out for Markhoz goat and it was found that the breed was geographically isolated since 77% of its population lay within a radius of 7km (Bahmani *et al*., 2011). Carson *et al*., (2009) evaluated the geographical concentration of twelve commercially farmed UK sheep breed. For ten of the twelve breeds analysed, up to 95% of each breed's numbers lay within a radial distance of less than 65 km from the mean centre of the breed. Six of the breeds had up to 95% of their numbers within a radius less than 50 km.
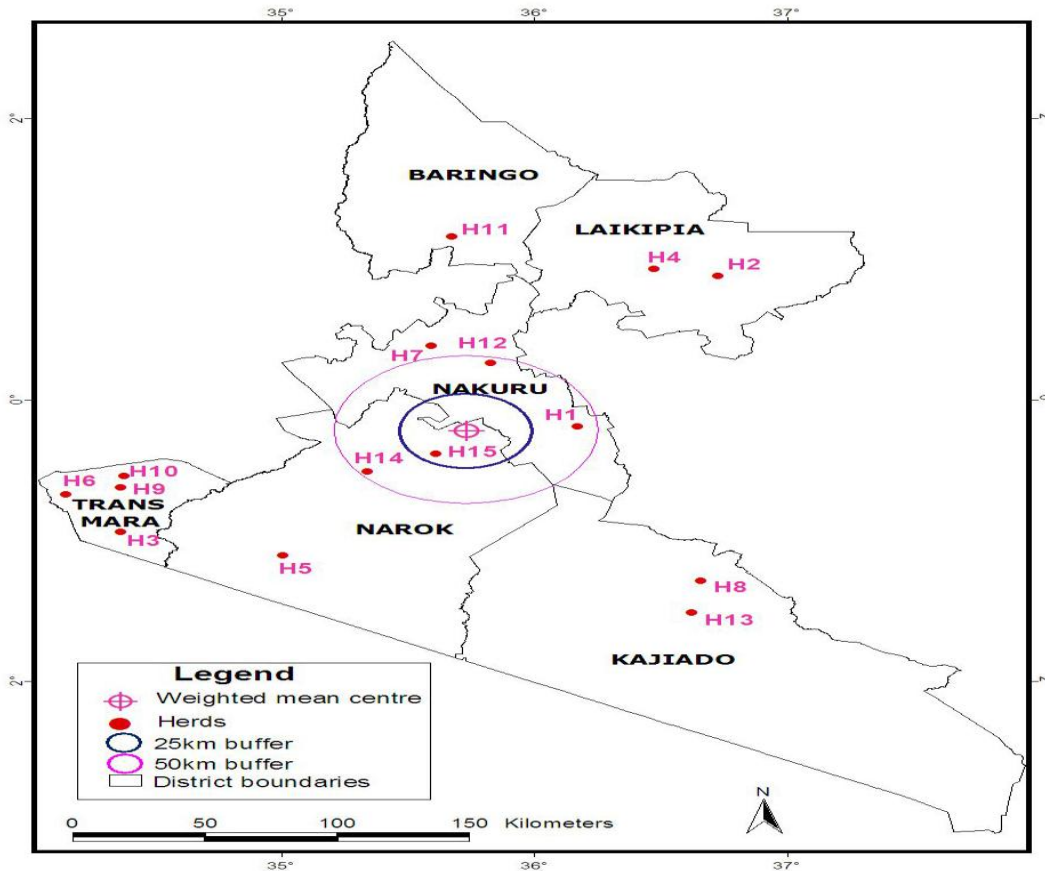
Figure 3.3: Geographical concentration of the Kenya Sahiwal cattle breed within 25km and 50km radii from the population mean center

Decreased native area is one of the indicators of endangerment. A system that applies three criteria (numerical, geographical and genetic) was established in the UK in 1975 to enable the classification of breeds and their categorisation into five degrees of endangerment ranging from 'Critical' to 'Transitional' (Table 3.2). A breed is classified in any of these categories if 75% or more of its population lies within a circle of 25 km radius. The loss of genetic resources during the FMD outbreak in UK in 2001 provided a guide to the validity of the proposed threshold for geographical concentration (Alderson, 2009). The Kenya Sahiwal cattle breed does not fall under any of the five categories and thus it is not geographically threatened by the risk of extinction.

Though the system fulfils the fundamental requirements for endangered breeds, it is amenable to further refinement to assist in effective monitoring of the ongoing introgression which continues to threaten some breeds that are not classified as endangered (such as the Kenya Sahiwal). Limited geographical distribution makes a breed vulnerable because the breed is at a particular risk in the event of a catastrophe such as a disease epidemic. The Blue Albion cattle from UK explains the vulnerability of geographically isolated and concentrated breeds. The breed went extinct in 1967 during FMD outbreak which was concentrated in its home county of Cheshire. Elsewhere, the geographically isolated British Milksheep lost >50% of its population in 2001 due to FMD outbreak while five other breeds (Cheviot, Herdwick, Hill Radnor, Rough Fell, Whitefaced Woodland) lost 25-50% of their population (Carson *et al*., 2009).

The impact of climate change is expected to heighten the vulnerability of livestock breeds to such extinctions. The direct effects include higher temperatures and changing rainfall patterns, which could translate into increased spread of existing vector-borne diseases and macro-parasites, accompanied by the emergence and circulation of new diseases. Changes in rainfall patterns will result in increased frequency of prolonged droughts thus aggravating the losses of AnGR (Rowlinson, 2008). Climate change is also expected to reinforce the existing factors that affect livestock production systems thus causing change in livestock production systems (FAO, 2007b; Thornton *et al*., 2008). Increasing human population and increased demand for livestock products is also driving livestock production towards intensification. Livestock production systems are intensifying whereby farmers are adopting high yielding breeds. Majority of Sahiwal

keepers have resolved to cross the breed with other exotic breeds and zebus so as to improve on growth rate and milk production (Muhuyi, 1997).

3.4 Conclusion

Considering the threats faced by the breed ranging from climate change to indiscriminate crossbreeding, it would be crucial to constitute more conservation nuclei in many parts of the country and expand the existing ones. Some of the conservation nuclei can be based in government research centres and institutions. This would reduce vulnerability of the breed as a result of a wider geographical cover and increased population size thus offering protection in the event of a catastrophe. The information gathered in this study can be adopted to establish a national database which will be updated after every few years to monitor breed population trend. However, additional information need to be included in the database such as age categories, number of purebred males, number of purebred females, number of females for breeding purebred replacements and for crossbreeding.

CHAPTER FOUR

POPULATION STRUCTURE AND DEMOGRAPHIC TRENDS OF THE REGISTERED SAHIWAL CATTLE BREED IN KENYA

4.1 Introduction

The Sahiwal cattle breed in Kenya is a product of a long-term upgrading program involving Sahiwal bulls and the Small East African Zebu (SEAZ) dams to improve milk production and growth performance under low input production systems (Muhuyi *et al*., 1999). Due to its heat tolerance, parasite tolerance and high milk production, Sahiwal has been exported to other Asian countries as well as Africa and the Caribbean but Pakistan, India and Kenya are endowed with the majority of purebred Sahiwal genetic resources (FAO, 1992; Joshi *et al*., 2001; FAO, 2007). The main users of the breed in Kenya are large-scale private and government ranches and the Maasai pastoralists (Ilatsia *et al*., 2011a). Though the breed is an important animal genetic resource that play dual purpose role, its population is relatively small compared to that of other Zebu breeds such as the SEAZ and the Boran (Ilatsia, 2011). This factor necessitates strategic breeding and conservation interventions for sustainable use of the breed genetic resources. Ilatsia (2011) reviewed some of the options for breed improvement and conservation strategies for the breed in the tropics and recommended studies to document the diversity of the breed and breeding organization structures supported by stakeholders.

Previous studies on the Sahiwal breed have mainly concentrated on documenting their performance levels under different production systems (Muhuyi *et al*., 2000; Karimi *et al*., 2005; Ilatsia *et al*., 2007). Recently, Ilatsia *et al*., (2011b) evaluated the suitability of various breeding schemes for genetic improvement and conservation of Sahiwal cattle genetic resources in Kenya. When designing conservation and genetic improvement strategies, both short term and long term implications of selection decisions have to be considered. High genetic gain and economic returns are mostly desired; however maintenance of genetic diversity is crucial in the long run (Bijma *et al*., 2001). The Sahiwal cattle breeding program in Kenya is characterized by small herds where a few bulls are used in mating (Ilatsia *et al*, 2011a). In such cases, outstanding bulls will often have numerous female descendants, and the same bulls are likely to sire many sons that will eventually enter the breeding cycle. Breeding opportunities may be limited if the

available bulls are closely related to a large proportion of the female population (Ilatsia *et al.*, 2007). Under such circumstances, it may become increasingly challenging to maintain given levels of effective population size and control inbreeding depression (Falconer and Mackay, 1996). Dahlin *et al.*, (1995) described the genetic diversity of the Sahiwal breed in Pakistan through systematic evaluation of pedigree information and recommended the need to integrate herds for better utilization of breeding animals and broaden the genetic base for selection.

Some simple population parameters have an important impact on the genetic variability of a population such that studies on population structure may elucidate important factors that affect the genetic evolution of populations (Valera *et al.*, 2005). Knowledge of population structure combined with information on genetic change can guide future management actions that promote genetic improvement of breeds (Malhado *et al.*, 2010). Therefore, knowledge on the population structure of the Kenya Sahiwal is currently of interest. It will provide information on the levels at which conservation measures are considered urgent for this breed in tropics, as well as provide a basis for utilization of available breeding animals in order to achieve desired genetic gain and variability. In this Chapter, the demographic trends are explored and the population structure of the breed characterized by estimating the number and age of breeding males and females, generation interval (GI) and family sizes using pedigree information of animals registered between 1949 and 2008.

4.2 Materials and Methods

4.2.1 Data source

Pedigree data used in this study were collected from the NSS and the KSB. The NSS is a research herd used for development of appropriate husbandry and breeding practices for cattle keepers mostly in the southern rangelands of Kenya. The stud constitutes purebred Sahiwal cattle and is the leading source of breeding stock for both pastoralists and other stud herds. Compared to other nucleus herds, the NSS keeps relatively good performance and pedigree records, which are used to support selection and management decisions (Ilatsia, 2011). The pedigree data collected at the NSS were corroborated with additional records from the KSB. The KSB is a farmers' organization under the Kenya Livestock Breeders Organization (KLBO) that provides the overall livestock registration services in the country. Its major objective is recording and

maintaining a central national database for all registered stock. Data kept include dates of birth and extended pedigree details.

4.2.2 Description of the pedigree data

Pedigree data consisted of unique identification of all animals and information on the sire, dam, birth date and sex. A total of 19,592 pedigree data available for animals born between 1949 and 2008 were used in this study. The total number of individuals evaluated was 517 sires and 6,259 dams, of which 6,776 individuals had progeny while 12,816 had no progeny. The total number of animals registered with both parents unknown was 1,353 (founders). Of the total number of founders, 21 had no progeny while 243 were sires with 7,074 offspring and 1,089 were dams with 1,823 offspring. Non-founders were 18,239; 274 sires with 10,059 offspring and 5,170 dams with 16,037 offspring. 16,754 non-founders had both the sire and dam known, while 1,106 and 379 had information only on dam and sire, respectively. The POPREP software (Groenveld *et al*., 2009) was used to characterize the population structure of the Kenya Sahiwal cattle breed. POPREP is a web-based application tool for analysis of pedigree information. Sahiwal pedigree file was converted from Ms Excel to notepad format conforming database for uploading, evaluation and report generation.

4.2.3 Data analysis

The input file format {ASCII (American Standard Code for Information Interchange), five pipe delimited data columns, date format (YYYY-MM-DD), sex encoding (1=male, 2=female)} and the consistency of the pedigree was verified. These are parents older than offspring and animals showing up only as sire or dam depending on their sex and pedigree loops. In the web interface, the email address and name of the breed were specified and pedigree file was then uploaded. After computation of population structure parameters, a typeset report was generated containing text that describes definition, computation and meaning of the parameters (Groeneveld, *et al*., 2009).

a) Breeding males and females

The number of breeding males and females used over the years and those whose offspring were selected to become parents in the next generations were identified and computed

by POPREP on annual basis. They were identified through birth records of their offspring. The number of breeding animals used over time was described by counts broken down by year.

b) Age structure of parents and generation intervals

The Age of the identified breeding males and females per year was computed. A total of fifteen (15) age groups (2, 3, 4... to 15, ≥16) were identified and the percent number of parents in each age group was calculated. Parents greater or equal to 16 years of age were grouped together in ≥16 years age group. To test the variation of age of parents with time, average age of parents for every two years was further computed from 1971 to 2008. Years between 1949 and 1970 were omitted in estimating average age of parents because breeding animals used during this period were base population whose birth dates were unknown.

In the calculation of GI, an offspring was considered selected if it had produced at least one progeny. The GI along the four selection pathways: sire to son (SS), sire to daughter (SD), dam to son (MS), and dam to daughter (MD) were computed from records of birth dates of registered animals in each year and the birth dates of their sires and dams following POPREP (Groeneveld, *et al*., 2009):

  i.   All animals born in a given year were considered (subset 1)
 ii.   Animals in subset 1 that became parents in the later years were identified (subset 2)
iii.   The parents of animals in subset 2 were identified (subset 3)
 iv.   The GI was calculated as the average age of the animals in subset 3 at the birth of their offspring in subset 2.

Furthermore, GI was calculated separately for the males and females. Population GI for the years between 1967 and 2004 were averaged to obtain pooled GI for the entire population of the breed.

c) Family sizes

Maximum, average and variance of family sizes were calculated because these are indicative of population structure (Marquez *et al*., 2009). The number of offspring produced by sires and dams, and the number of selected offspring (those used as parents in the next generation) per sire and dam were quantified.

4.2.4 Assumptions and limitations

i. Animal registrations are sufficiently indicative of the overall numbers of purebred animals.

ii. Only the registered animals will contribute to future genetic diversity of the breed.

iii. Pedigree recording within the tropics is highly variable and inconsistent. Farms considered in this study were not an exception.

4.3 Results and Discussion

4.3.1 Breeding males and females

Figure 4.4 shows the total number of bulls used for breeding in the breed population between 1949 and 2008 and bulls whose offspring were selected for breeding in subsequent generations. The average number of bulls used for breeding every year was consistently higher than the average number whose offspring were selected in subsequent generations i.e. 23.73 ± 11.95 *vs* 16.86 ± 9.23. There was a steady increase in the number of breeding bulls up to the year 1965 after which a drop was observed. The highest number (57) was recorded in 1969 after which it changed inconsistently downward to only 8 bulls in 2008. The continuous increase at the initial stages can be attributed to the management of the NSS which focused on expanding Sahiwal base population. The small number of bulls recorded in 2008 could be due to incompleteness of the pedigree records at that time.
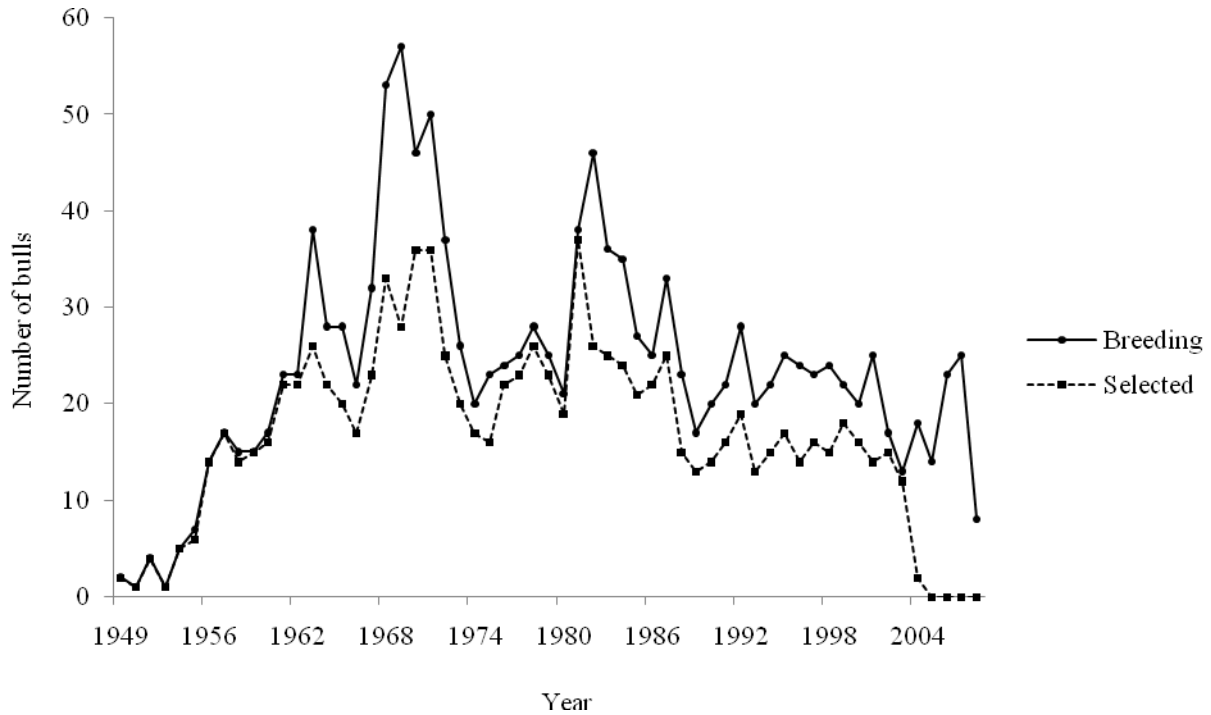
Figure 4.4: Number of breeding bulls registered in the herdbook by year

Figure 4.5 shows the evolution of cows and calves through breeding (number of dams that produced offspring) and selected (number of dams whose offspring were selected) every year of the studied period. The average number of females used annually for breeding between 1949 and 2008 was 294. The number of females used for breeding every year increased steadily until 1968 where a maximum of 727 dams was recorded, however there was negative trend thereafter. The number of dams with selected offspring remained (87.32) lower than the total number of females used for breeding. The increase in the number of breeding cows in the earlier years point to the fact that at the initial stage of the breeding program management could have focused on increasing the breeding cows to attain certain desirable population. The earlier years were also characterized with good herd management where the herd was provided with the suitable husbandry support necessary for survival (Meyn and Wilkins, 1974; Muhuyi, 1997).
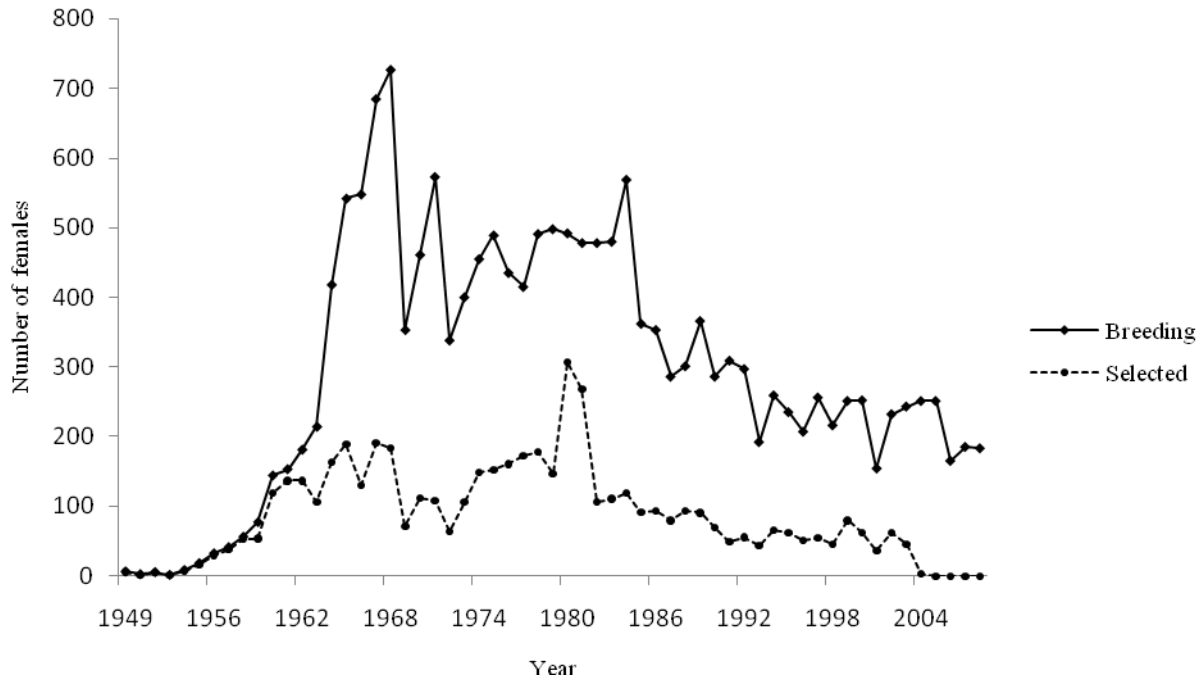
Figure 4.5: Number of cows registered in the herdbook by year

Figure 4.6 illustrates the polygynous mating system of the breed since a smaller number of males than females was used for breeding every year. In breeding programs, fewer males are often used compared to females given that intensity of selection is usually high for males than for females (Falconer and Mackay, 1996). In the current study progeny testing at NSS allows for a few proven bulls to be used on a large proportion of females.
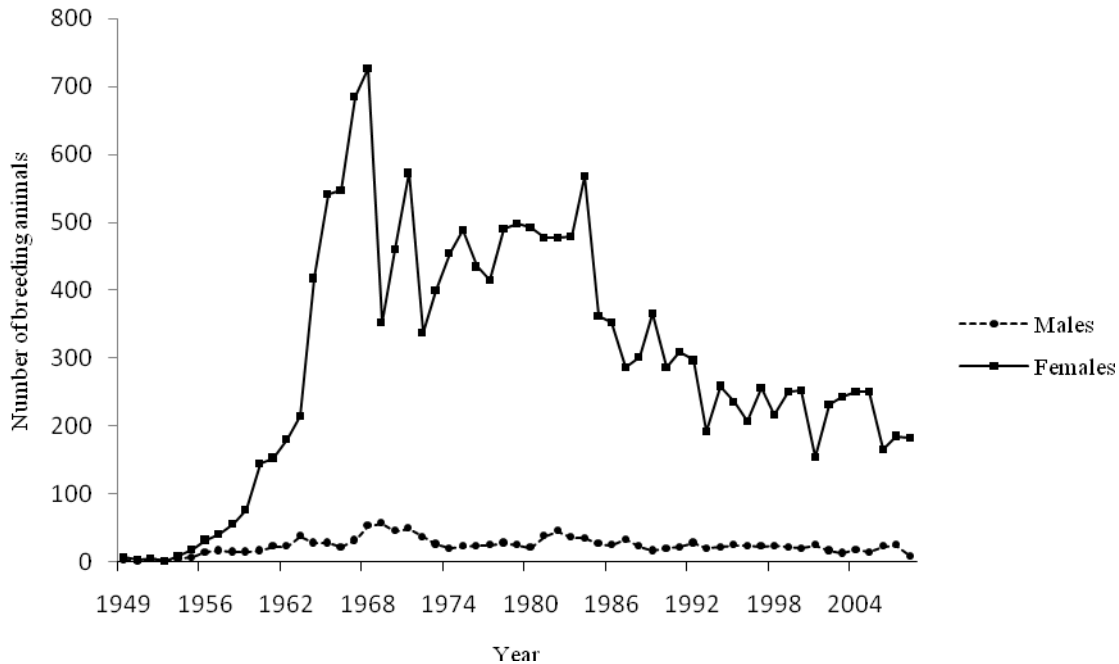
Figure 4.6: Comparison of the number of registered breeding bulls and cows used annually

Breeding population size is the main criteria in the FAO warning system to assess the DE of breeds (FAO, 1995; FAO, 2000). Number of breeding females and males define the thresholds of three categories of endangerment: critical, endangered and not at risk. With actively managed breeds, two additional categories are used, i.e. critical maintained and endangered maintained (Gandini *et al*., 2004). A breed is critical when the total number of breeding females is less than 100 or the total number of breeding males is less than or equal to five (FAO, 2000). A breed is endangered if the total number of breeding females is between 100 and 1000 or the total number of breeding males is less than or equal to 20 and greater than five. A breed is not at risk if the total number of breeding females and males is greater than 1000 and 20, respectively. Currently, the number of registered Sahiwal cows and bulls used for breeding in Kenya annually seems to indicate an unstable situation and even a downward trend of the breed population growth (see Figure 4.6).

In 2008, the number of registered breeding males and females were 8 and 183, respectively. This scenario clearly indicates that the Sahiwal cattle breed in Kenya is vulnerable to forces that could endanger its continued existence. According to Gandini *et al*. (2004) if the

current breed status is left unattended to, then the risk and probability of drifting towards extinction becomes even high. A breed is considered extinct when it is no longer possible to recreate the breed population and extinction is absolute when there are no breeding males (semen), breeding females (oocytes), nor embryos remaining (FAO, 1999). In order to integrate the existing herds and broaden the genetic base of the breed in the country, Ilatsia *et al*., (2011b) recommended a shift from the current closed nucleus breeding scheme to a more inclusive and broad open nucleus scheme so as to accommodate Sahiwal gene pools from the more diverse pastoral herds. According to his study, the Sahiwal cattle genetic resources from the pastoral herds are more genetically diverse owing to the fact that they are products of a long-term upgrading program with the SEAZ. In addition, a study on Sahiwal cattle breeding and conservation programs in tropics (Ilatsia, 2011) recommended exchange of gene pools between India, Pakistan and Kenya so as to increase the effective breeding population.

Livestock recording is not only an essential component of traceability, disease control and good farm management, but also contributes to securing access to markets for higher quality and geographical identifiable products (Hoffmann *et al*., 2011). In some countries, evolution of the number of registered breeding animals has been used to assess the stability and population growth of cattle breeds (Carolino and Gama, 2008). In the absence of sound data about total breed numbers in Australia, Rare Breeds Trust of Australia used animal registrations as the indicative measure of breed numbers. This assumes that animal registrations are sufficiently indicative of the overall numbers of purebred animals (RBTA, 2006). Al-Atiyat (2008) used the number of registered males and females of the Jordan indigenous cattle breed to declare the breed as endangered and at risk of extinction.

Several constraints have been identified that limit the adoption and practice of livestock recording in developing countries (ICAR, 2010; Kosgey *et al*., 2011) thus it has remained scarce and of low quality. Annual registration of female replacements has been proposed to be a more accurate indicative measure of a breed's variability or numerical status. It records the actual number of young animals qualified to join the breeding herd and indicates the future trend in population size. Annual registration of female replacements also accounts for breeding females that are not registered or do not produce purebred progeny, and for eligible young stock that is

not registered. This system relies on the principle that only registered animals will contribute to future generations of the breed, and the data can be accessed with relative ease from registration documents (Alderson, 2009). If countries adopt this same measure, then comparisons across countries and total global populations will become easier to monitor.

4.3.2 Age structure of parents

The age structure of breeding males and females (of 17,983 calves born over the period of 1949 to 2008) is presented in Figure 4.7. The number of animals used for breeding at different age groups varied between males and females in the breed population. The results indicate that bulls were used more at a later age for breeding when compared to cows. Majority of cows started reproduction at the age of two years. The average age of sires used for breeding was (8.2 years) higher than the average age of dams (5.3 years) used for breeding.
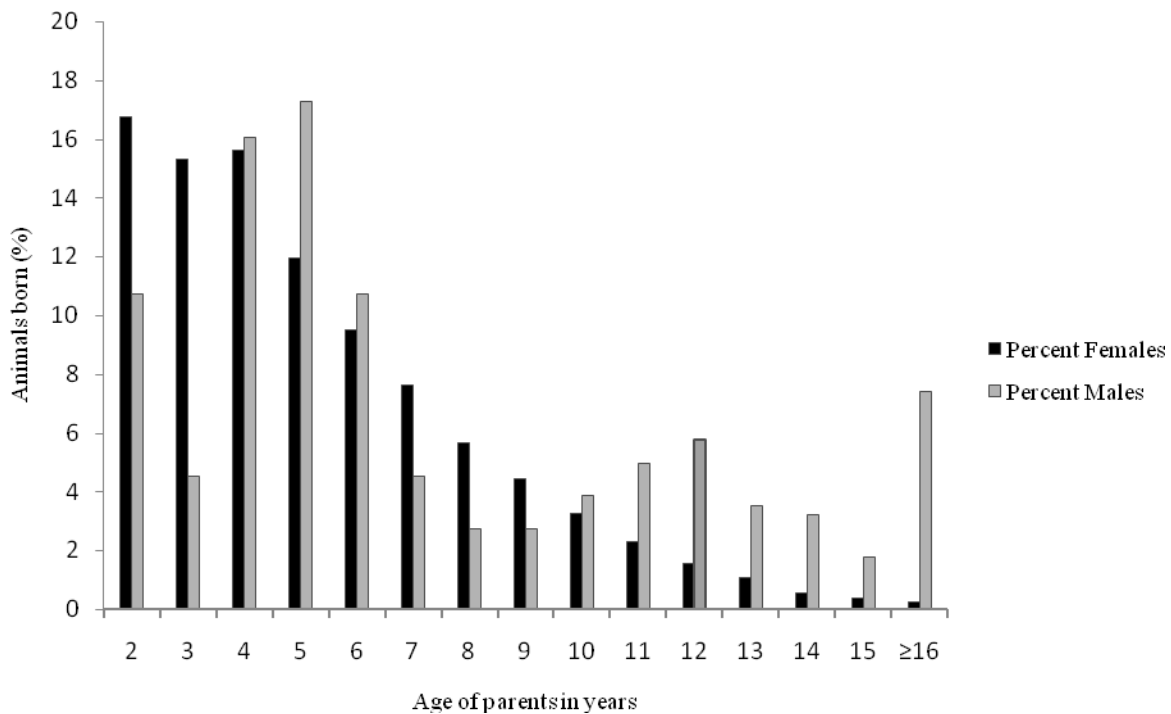
Figure 4.7: Age distribution of parents of calves in the Sahiwal cattle breed of Kenya

Results of this study indicate a tendency to use older bulls and cows as the average age of males and females used for breeding increased steadily over the years. Average age of breeding

bulls remained higher than that of cows from 1972 to 2008 (see Figure 4.8). Old bulls were used more intensively than old cows. For instance, only 6.22% calves were born by cows above 10 years of age while bulls of the same age sired 26.68% calves, only 0.25% calves were born by cows in the age group ≥16 years but the number of calves from bulls of the same age group was higher at 7.42% confirming intensive use of older bulls in the breeding herds. Long retention of breeding bulls within the herds is due to shortage of breeding bulls for replacement as reported by Ilatsia *et al*., (2011a). The older age of breeding males than females is attributed to the progeny testing program at the NSS which implies that proven bulls are only available when they are between 8-10 years of age. In the progeny testing program, final cow selection is done at the end of second lactation implying that cows are introduced into the breeding herd earlier than proven bulls therefore contributing to the lower average age of breeding females.
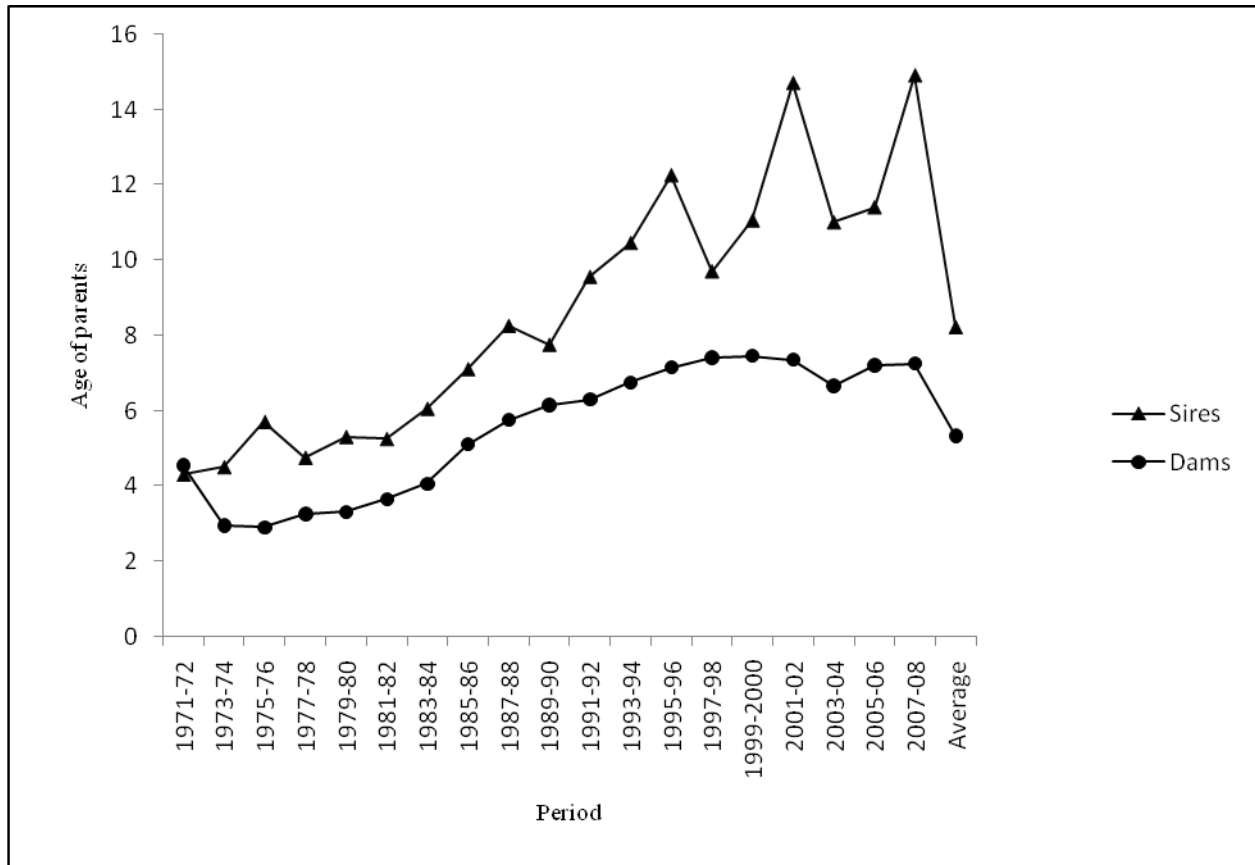
Figure 4.8: Average age of parents used for breeding over the studied period

4.3.3 Generation Intervals

Generation intervals for males, females, entire breed population and the four selection pathways are presented in Table 4.3. The average estimated GI ranged between 5.0 and 8.7 years. The resulting mean GI for the entire breed population was about 6.3 years.

Table 4.3: Average generation intervals for males, females, entire breed population and the four selection pathways

Pathway	Number of individuals	Average GI (yrs)
Sire-son (SS)	118	8.7
Sire-daughter(SD)	2135	8.1
Dam-son (MS)	180	5.8
Dam-daughter (MD)	2899	5.0
Males	2253	8.2
Females	3079	5.1
Population	3202	6.3

When GI was evaluated for the 4 paths of selection, it was about 3 years longer in the sire pathways. The age of the sire at the birth of its son was higher than that observed for other paths (sire-daughter, dam-son and dam-daughter). A similar analysis was conducted for the NSS herd by Muasya *et al*., (2011) and revealed longer GI in the sire pathways than in dam pathways. The average results were comparable to those reported for the South African cattle breeds and Brazillian Zebu i.e. 6.7, 6.0 and 6.56 years for Drakensbergers, Nguni, and Gyr Mocho respectively (Filho et al., 2010; Maiwashe et al., 2006). Longer GI in male than female pathways was in agreement with the findings of Reis Filho et al., (2010) for Gyr dairy cattle. However, the female pathways in the Gyr cattle had longer GI. Other studies have reported longer GI in females than in males for example in Alentejana cattle breed (Carolino and Gama, 2008).

The GI for sire lines was longer than the recommended 7 years for SS and 8 years for SD (Van Tassell and Van Vleck, 1991). Within the Kenya Sahiwal breed, fertility and survival traits are treated as secondary traits (after production traits) and therefore given less emphasis particularly in the selection process (Ilatsia *et al*., 2007). Poor reproductive performance of the breed is one of the factors contributing to prolonged GI through late age at first calving, extended calving intervals and more services per conception (Ilatsia *et al*., 2007). The long GI in the sire lines can be explained by the 8-10 years progeny testing scheme and the continuous use of

genetically superior bulls for a long period without replacement. Aggravating the situation is the high pre-weaning mortality rates which were reported to be higher in males than females (Muhuyi *et al*., 1999).
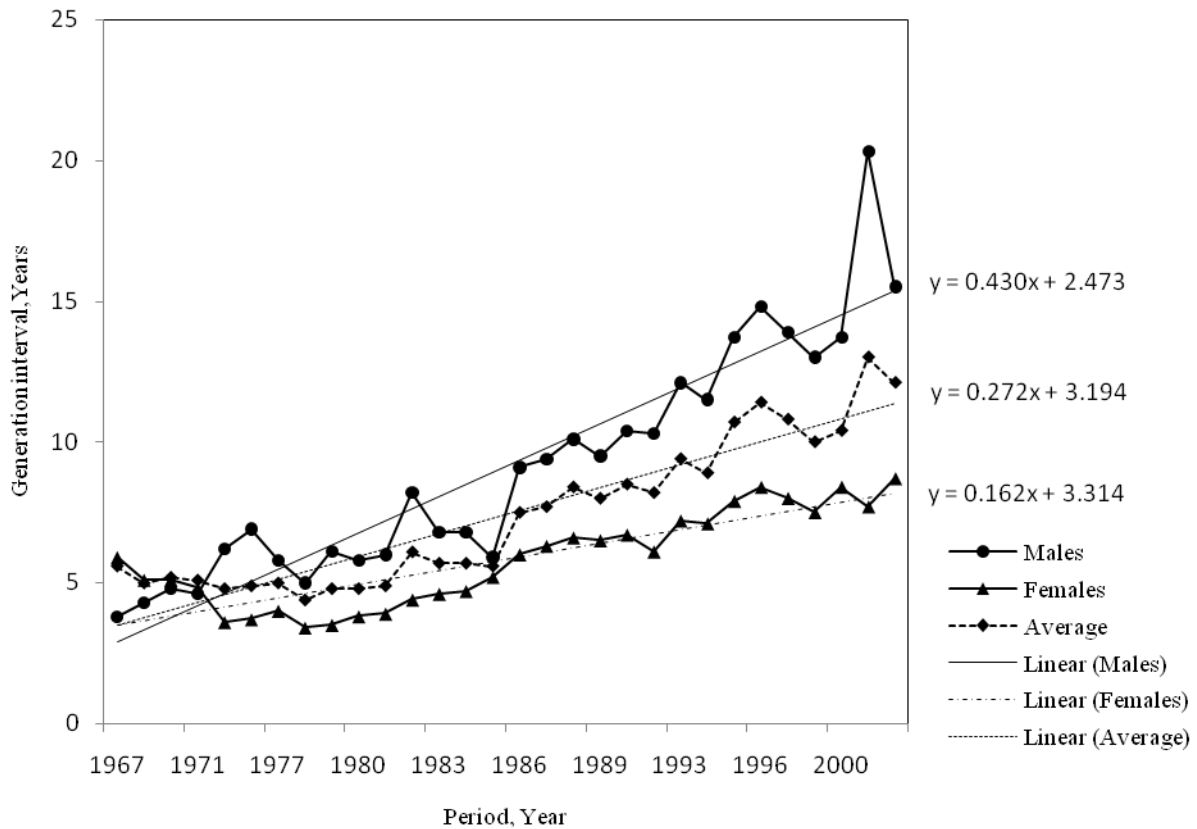
Figure 4.9: Generation interval of the Sahiwal breed in Kenya between 1967 and 2004

Figure 4.9 shows the continuous increase of average GI of the males, females and entire breed population (average) with time. There was a steady increase in GI for both breeding males and females over the years. The increase in GI with time indicates that Sahiwal cattle breeders have been using older proven sires rather than young newly proven sires as SS and SD over time. Optimization of GI is of fundamental importance for genetic improvement programs in cattle breeds since a reduction in the rate of genetic progress is the main consequence of a long GI. The shorter the GI, the rapid is the genetic gain in a population (Filho *et al*., 2010). Furthermore, these pathways contribute more to genetic gain because they are the main means used to transfer

genetic progress between nucleus herds and the only means of transferring genetic progress to the pastoral herds through breeding bulls (Ilatsia *et al*, 2011a).

When optimizing GI of a breeding program, a dilemma often arises on whether young animals should be selected or older animals. Selecting young animals is good for achieving a short GI but usually have less accurate estimated breeding values (EBVs). Older animals have generally more accurate EBV but selecting them would lead to longer GI (James, 1987; Van Arendonk and Bijma, 2002). Shorter GI is reachable, as demonstrated by the experimental herd at the Animal Science Experimental Station of Sertaozinho SP in Brazil, where the SS intervals were 3.66 and 3.74 years for Nelore and Guzerat breeds, respectively (Reis Filho *et al*., 2010). To optimize GI in the Sahiwal breed of Kenya, selection index can be replaced with Best Linear Unbiased Prediction (BLUP) for selecting males meant for progeny testing. In an optimal situation, BLUP-EBVs optimize the proportion of the very best young bulls with no progeny test and the very best progeny tested bulls (James, 1987). Continuous use of prominent sires for many years in the breed should also be avoided hence encouraging use of evaluated young bulls (i.e. encourage fast sire substitution).

There is more potential in reducing GI of sire lines because fewer males than females are required for breeding. Only the very best breeding animals should be kept for another breeding season while the others can be replaced by new and young breeding stock. In addition to faster genetic progress, young bull schemes have lower costs and are simpler to run than old bull schemes that use progeny-tested bulls (Mpofu and Rege, 2002). With the current advanced reproductive technologies such as artificial insemination (AI) and multiple ovulation and embryo transfer (MOET), it is possible to introduce new and young Sahiwal breeding stock from other countries through semen and embryos. Generation interval is to a large extent influenced by reproductive traits; although these traits have low heritability, progress to reduce GI can be achieved through environmental management (Ilatsia *et al*., 2007).

Proper management of breeding cows and critical evaluation of the male component of reproduction during selection of breeding bulls are contributory factors to realizing shorter GI (Ilatsia *et al*., 2007). Considering that the Sahiwal is mainly kept in ASALs, it would be

appropriate to provide breeding cows with supplemental feed during dry seasons, late gestation and early lactation stages. This would have positive impacts in reducing calving interval and minimizing pre-weaning mortality rate. Breeding season can also be altered such that animals are bred during optimal weather conditions since this may increase conception rates and minimize chances of abortion. In addition, good management practices will minimize loss of promising breeding animals.

4.3.4 Family sizes

In order to obtain the average family sizes in male and female pathways, the average number of offspring per sire and dam were quantified and presented in Figures 4.10 and 4.11 respectively. Family sizes showed large variations in male parents (35.12 ± 26.16) than in female parents (3.25 ± 0.61). Family size refers to the number of offspring of an individual that become breeding individuals in the next generation (Falconer and Mackay, 1996). Family sizes are indicative of population structure and reflect mating decisions made by breeders (Marquez *et al*., 2009). Large variances in family sizes indicate that not all animals contribute their genes equally to subsequent generations of the population because some animals are used very intensively, whereas others are not (Falconer and Mackay, 1996).

Figure 4.10 shows that majority of cows in the Sahiwal breed population had only one offspring followed by those with two offsprings. The average number of progeny per cow was 3.25 ± 0.61while the cow with the highest number of offspring had 13 calves. At the NSS female selection consist of eliminating 50% of heifers on the basis of first lactation milk yield and a further 50% at the end of the second lactation (Mpofu and Rege, 2002). This explains why most of the dams had only up to two offsprings. Early elimination of females is important because it encourgaes introduction of new-born individuals which on average are better genetically than older females and consequently reduces GI of dam lines.
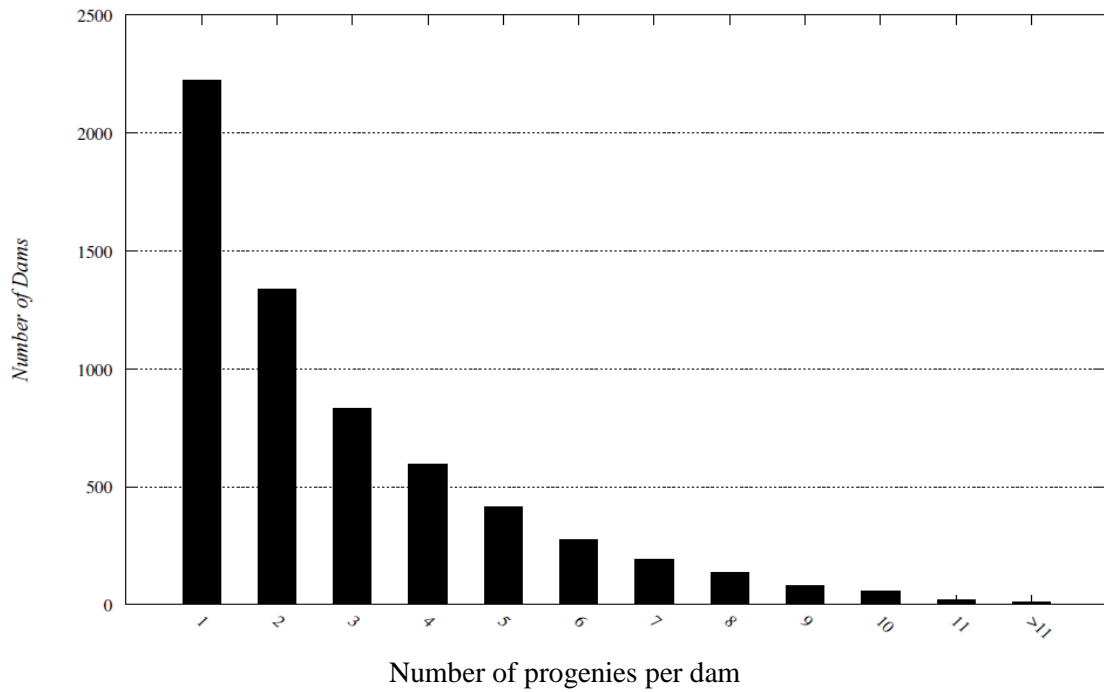
Figure 4.10: Number of progenies per dam of the registered Kenya Sahiwal breed

Number of progenies per sire
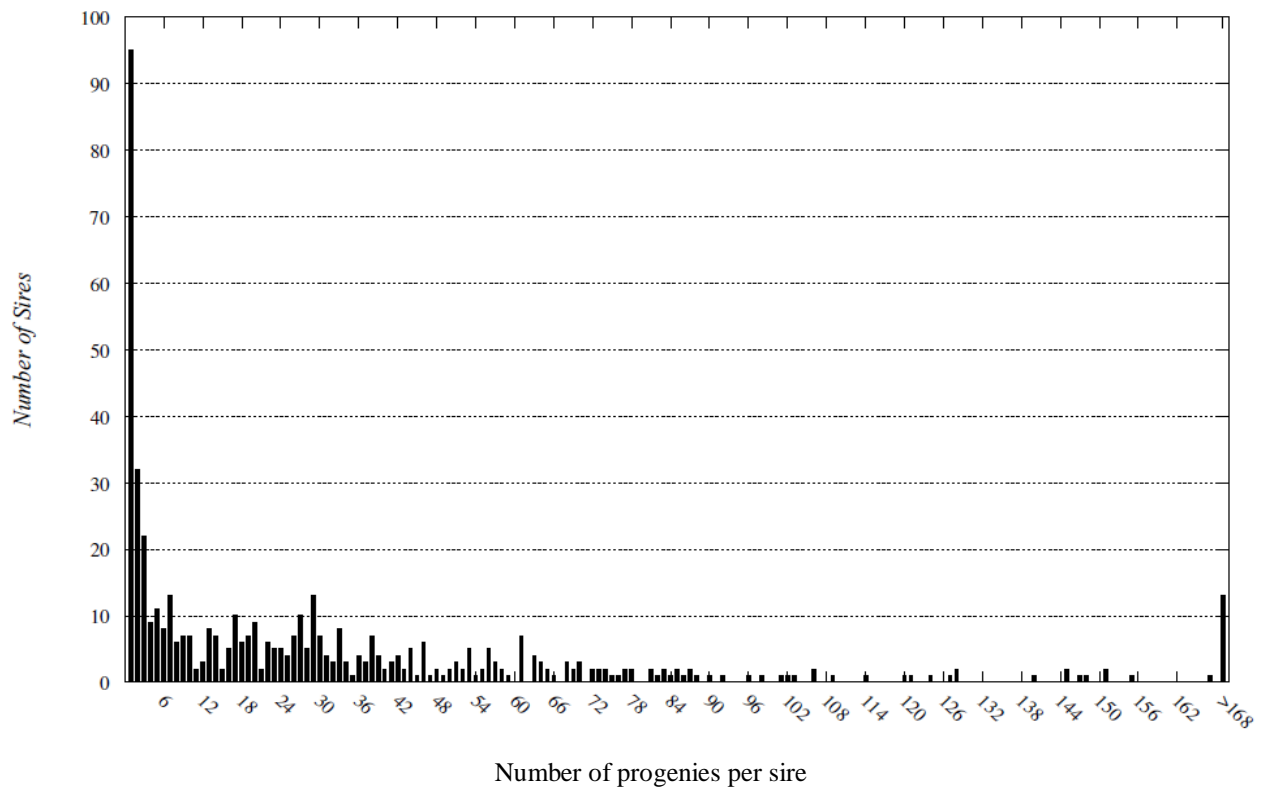
Figure 4.11: Number of progenies per sire of the registered Kenya Sahiwal breed

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Figure 4.11 quantifies the number of offspring per sire in the breed population and shows a wide variation of sire usage. About 96 bulls used for breeding had only one calf while only less than fifteen bulls had more than 168 calves each. Three sires were identified to be the more prominent in the pedigree records having the highest number of offspring. Sire ID number 149 had the highest number of offspring (322 calves). The Sahiwal breeding program in Kenya is characterized by deliberate allocation of cows to only a few prominent sires within herds. In some of the Sahiwal herds, only one bull is selected and allowed to graze together with the breeding cows throughout the year or within a particular breeding period. The selected bulls enter into the breeding herds of the breed and continue to be used leaving many offspring and resulting in large family size variances within the male pathways.

The consequence of increased variation in family sizes is an increase in the rate of inbreeding and the reduction in the *Ne* (Frankham *et al*., 2002). Relatedness between individuals also increases and thus the probability of matings between related animals is high. The variance of family size can be minimized as the number of offspring becomes almost equal for all parents. A sound management plan should therefore reduce the differential contributions of individuals to the next generations. The success and sustainability of the breeding and conservation programs for the Sahiwal cattle breed in Kenya will thus depend on the technical quality of the selection process and on the breeding organization.

4.4 Conclusion

The number of registered Sahiwal bulls and cows used for breeding has not reached the critical level for breed endangerment but the annual trend indicated a downward trend. The study identified a trend towards use of older bulls and cows leading to long generation intervals particularly in the sire pathways. The Sahiwal breeding program was characterized by deliberate allocation of cows to only a few prominent sires within herds leading to large family size variations. According to this study there is need to initiate strategies that will increase the number of registered breeding animals to above threshold for breed self-sustainability and maintenance of genetic diversity.

CHAPTER FIVE

PEDIGREE ANALYSIS TO MONITOR TRENDS AND RISKS ASSOCIATED WITH GENETIC EROSION OF THE SAHIWAL CATTLE BREED IN KENYA

5.1 Introduction

Animal genetic resources contribute to the livelihoods of over a billion people and thus form an essential component for world food security (Anderson, 2003). They contribute to satisfying human needs by providing meat, milk, eggs, draught power, manure and other resources for economic development (FAO, 2011). Over the past years, available AnGR have declined considerably due to: changes in production systems, loss of rangeland grazing resources, natural calamities, disease outbreaks, inappropriate breeding policies and practices, changing cultural practices, the influence of population growth and urbanization, and the failure to assess the impact of practices in terms of sustainability (FAO, 2007a). Considering their importance, the continuing loss of AnGR would therefore compromise efforts to achieve food security, improve human nutritional status and rural development.

An important aspect of AnGR is their genetic diversity which can be divided into within-breed and between-breed diversity. It has made it possible for humans to survive in a wide range of environments, from the hot and humid tropics to arid deserts and extremely cold mountainous regions. Genetic diversity also enables livestock to adapt to diseases, parasites, wide variations in the availability and quality of food and water, and other limiting factors. For instance, animals such as the Yak have made it possible for human communities to inhabit harsh areas where production of crops is virtually impossible (FAO, 1999). Maintaining the diversity of AnGR is therefore essential to enable farmers, pastoralists and animal breeders to meet current and future production challenges resulting from changes in the environment, including climate change (FAO, 2007).

One of the major targets of conservation programs is to maintain a high level of genetic diversity (Bijma *et al*., 2001). As a first step, the status of genetic diversity within a given population needs to be assessed because its understanding ensures sustainable use and development of AnGR (Lacy, 1995; Barker, 2001; Fernandez *et al*., 2001). Pedigree information

through pedigree analysis has been used in monitoring genetic diversity of different domesticated animal species including pigs (Fernandez *et al*., 2002; Melka and Schenkel, 2010), dogs (Hamann *et al*., 2003; Cole *et al*., 2004), sheep (Goyache *et al*., 2003; Alvarez *et al*., 2008) and horses (Sevinga *et al*., 2004). It has been successfully applied in the analysis of genetic diversity of cattle breeds e.g. Brazilian Zebu (Faria *et al*, 2009), South African dairy cattle (Maiwashe *et al*., 2006), Italian beef cattle (Riccardo *et al*., 2006), and Irish dairy and beef cattle (Mc Parland *et al*., 2007). Muasya *et al* (2011) evaluated the population structure of the Sahiwal population at KARI Naivasha through pedigree analysis and revealed important genetic variability parameters for the breed.

Genetic diversity has been defined as the variety of alleles and genotypes present in a population and is reflected in morphological, physiological and behavioural differences between individuals and populations (Frankham *et al*., 2002). Traditionally genetic diversity in populations of domestic breeds is assessed by quantifying demographic parameters under pedigree analysis (Mokhtari *et al*., 2013). The parameters include effective population size, inbreeding and founder representation in a population (Lacy, 1995; Boichard *et al*., 1997). The effective population size is the size of an ideal population that has the same rate of inbreeding as the real population under consideration with its own complicated pattern of variance in family size, sex ratio, etc (Frankham *et al*., 2002). Inbreeding coefficient is a measurement of the genetic relatedness of the sire and dam. It gives a measurement of the total percentage of variable gene pairs that are expected to be homozygous due to inheritance from ancestors common to the sire and dam. It also gives the chance that any single gene pair can be homozygous (Gutierrez *et al*., 2003).

A preliminary evaluation of pedigree information for the Sahiwal breed in Kenya was recently undertaken (Muasya *et al*., 2011), however, the study considered the NSS herd population only and overlooked the effect of animals registered from other nucleus herds on the overall genetic diversity. In this Chapter, the trend of genetic diversity within the Kenya Sahiwal breed is monitored by quantifying the depth of known pedigree, amount of inbreeding, effective population size (*Ne*), and average relatedness (AR) based on pedigree data so as to provide baseline information to advance conservation strategies for the breed.

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5.2 Materials and method

5.2.1 Data source

Pedigree data for this study were sourced from the NSS and the KSB. The pedigree files consisted of unique identification of all animals, for each animal the sire, dam, birth date and sex. A total of 19,592 pedigree data available for animals born between 1949 and 2008 were used in this study. The NSS constituted a total of 19,286 pedigree records while 11 other herds constituted 306 records.

5.2.2 Data analysis

Pedigree file for the Kenya Sahiwal breed was uploaded to POPREP (Groeneveld, *et al.*, 2009). The total number of individuals evaluated was 19,592 (517 sires and 6,259 dams), 6,776 had progeny while 12,816 had no progeny. The total number of animals registered with both parents unknown was 1,353(founders). From the total number of founders, only 21 had no progeny while 243 were sires with 7,074 offspring and 1,089 were dams with 1,823 offspring. Non-founders were 18,239: 274 sires with 10,059 offspring and 5,170 dams with 16,037 offspring. 16,754 non-founders had known sire and dam, 1,106 had only dam known and 379 had only sire known. Animals with an unknown sire, dam or both were considered to be the base population.

a) Pedigree Completeness

Pedigree completeness is the extent to which an individual's ancestry is known to some defined generation in the past. To assess the quality of the pedigree data used to estimate inbreeding and relatedness, a measure of pedigree completeness was calculated on a per year basis. The more complete the knowledge of an individual's ancestry, the higher the pedigree completeness and the more reliable is its estimate of inbreeding level (MacCluer *et al.*, 1983). The method proposed by MacCluer *et al.*, (1983) was used to measure pedigree completeness index (PCI) of the breed. This index summarizes the proportion of known ancestors for a given number of generations:

$$I_d = \frac{4 I_{d\,pat} I_{d\,mat}}{I_{d\,pat} + I_{d\,mat}}$$

[2]

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where: I_d is the pedigree completeness index, I_{dpat} and I_{dmat} are contributions from paternal and maternal lines respectively. The contributions are computed as:

$$I_{dk} = \frac{1}{d} \sum_{i=1}^{d} a_i \qquad k=pat, \ mat \qquad [3]$$

where: *k*-paternal *(pat)* or maternal line *(mat)* of an individual

a_i is the proportion of known ancestors in generation *i*

d is the number of generations considered in the calculation of the pedigree completeness

Six ancestor generations (*d*=6) were considered in this study. The average PCI of the animals in the pedigree data was calculated for the six generations. CFC software package was used to compute maximum and average generation equivalents and also to trace the longest ancestral path in the pedigree. Generation equivalents were estimated in each breed by averaging the sum of $(1/2)^n$, where *n* is the number of generations separating an individual from each known ancestor (Sargolzaei *et al*., 2006).

b) Inbreeding

Inbreeding coefficients (*F*) for each animal in the pedigree were computed using the algorithm of Meuwissen and Luo (1992) in the POPREP software package (Groeneveld, *et al*., 2009). The algorithm uses the Cholesky factor of the relationship matrix to calculate inbreeding in large populations of animals. Each row of this factor is built by tracing the entire pedigree of each individual and the *F* is then obtained from the elements of this row and from the inbreeding coefficients of the ancestors (Meuwissen and Luo, 1992). Average annual *F* was computed from 1960 to 2008 to investigate trends and rates of change in inbreeding. Minimum, maximum and standard deviations for the average inbreeding coefficients were also calculated. The rate of inbreeding was estimated by the method described in Falconer and Mackay (1996) as:

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}} \qquad [4]$$

where: ΔF is the rate of inbreeding per generation

F_t is the average inbreeding of offspring

F_{t-1} is the average inbreeding of the offspring parent

The number of inbred animals was quantified and expressed as percentage according to their level of inbreeding. The inbred animals were assigned to six different inbreeding classes as: 1=0-5%, 2=5-10%, 3=10-15%, 4=15-20%, 5=21-25% and 6=25-30%. Furthermore, the level of inbreeding for inbred animals (i.e. animals with $F>0$) by year of birth was determined. The annual rate of inbreeding was estimated by fitting a linear regression of annual average inbreeding level on years through the time period from 1960 to 2008. Inbreeding for animals with birth year before 1960 were not taken into the account in analyses because no information about their inbreeding was known and no inbred animal had been recorded.

c) Effective Population Size

POPREP calculated the *Ne* using two methods:

i. Effective population size based on the rate of inbreeding as in (Falconer and Mackay, 1996):

$$Ne = \frac{1}{2\Delta F_y L}$$

where: *ΔF* is the annual rate of inbreeding and *L* is the generation interval.

ii. Effective population size based on the number of parents (Falconer and Mackay, 1996) was used:

$$Ne = \frac{4N_m N_f}{N_m + N_f} * .7$$ [5]

where: N_m and N_f are the number of male and female parents, respectively.

The factor .7 account for mass selection as proposed by Caballero (1994). The formula refers to the number of breeding males and females in a population with discrete generations. A generation was identified as those animals born in the time span of one GI window which ends in the reporting year. The number of years per generation window were obtained from the calculation of generation interval reported in chapter 4. Effective population size per year was also calculated to monitor its trend over the studied period.

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d) Average Relatedness and additive genetic relationships

Average relatedness of an individual can be interpreted as the representation of the animal in the whole pedigree (Malhado *et al*., 2010). The AR within and between groups was computed using CFC computer program following the indirect method of Colleau (2002). It was calculated as follows (Gutierrez and Goyache, 2005):

c' = (1/n) 1'A   [6]

Where: A is the numerator relationship matrix of size n × n and 1 is a vector of ones (1 × n)

Average additive genetic relationship (AGR) among individuals in a group (e.g. animals born in a given year) was calculated as the average inbreeding of the progeny of all possible matings among the individuals. The AGRs were computed using the PEDIG Fortran Package (Boichard, 2002). Two steps were followed to calculate the rate of AGR (Δf) per generation i.e. for animals born in a given year and a generation earlier:

Firstly, the GI for animals born in a given year was calculated as the average age of their parents when they were born.

Secondly, the GI was subtracted from the year of birth of the current cohort to obtain the year of birth of the cohort born a generation earlier. Thus, the rate of AGR is (Groeneveld, et al., 2009):

$$\Delta f = \frac{f_t - f_{t-1}}{1 - f_{t-1}}$$ [7]

where: f_t and f_{t-1} are the average AGRs of the cohort born in generation t (or the current year) and the cohort born a generation earlier respectively. When computing f, the cohort is split into the group of males and females. Then, the AGR is computed for every male "mated" to each female and averaged over the cohort.

5.2.3 Assumptions and limitations
   i.   Animal registrations are sufficiently indicative of the overall numbers of purebred animals.

ii. Only the registered animals will contribute to future genetic diversity of the breed.

iii. Pedigree recording within the tropics is highly variable and inconsistent. Farms considered in this study were not an exception.

5.3 Results and discussion

5.3.1 Pedigree Completeness

Pedigree completeness for animals born in the last ten years decreased with increase in generation depth from 1st to 6th generation (Table 5.4). This implies that animals in older generations were founders with no sire and dam records. The longest ancestral path in the pedigree consisted of 16 generations separating the individual from its furthest ancestor. The furthest generations in which all ancestors were known averaged to 2.46 whereas the maximum was 6.41 complete generations (Sargolzaei and Iwaisaki, 2004).

Table 3.4: Pedigree completeness index, maximum and average number of generation equivalents for the Kenya Sahiwal breed

Parameter	Value
Average pedigree completeness index (%) for:	
1st generation	75.7
2nd generation	73.8
3rd generation	69.9
4th generation	64.7
5th generation	58.3
6th generation	51.4
Longest ancestral path traced	16
Maximum generation equivalents	6.41
Average generation equivalents	2.46

Figure 5.12 shows pedigree completeness for pedigree depth of 1 to 6 generations by year of birth, between 1956 and 2008. Pedigree completeness for generations 2 to 6 increased over time from 1956 and then declined from 2003 onwards. Pedigree completeness for generation 1 decreased over time from 100% in 1956 to 76.3% in 2008. Lower estimates of pedigree completeness were obtained for NSS population by Muasya et al. (2011). The completeness of pedigree information has an effect on the estimates of inbreeding level within a breed whereby a large fraction of missing parents causes underestimation of inbreeding levels (Cassell *et al*., 2003; Faria *et al*., 2009). Pedigree completeness of the Kenya Sahiwal was comparable to that reported for the Spanish beef cattle breeds which ranged between 0.81 and 2.97 generation equivalents (Gutierrez *et al*., 2003). Van der Westhuizen (2009) reported higher pedigree

completeness 85% completeness for 3 generation pedigrees in the Bonsmara breed. There does not seem to be a specified level of pedigree completeness recommended in the literature to make conclusive decisions about inbreeding or other population parameters (Steyn *et al*., 2012).
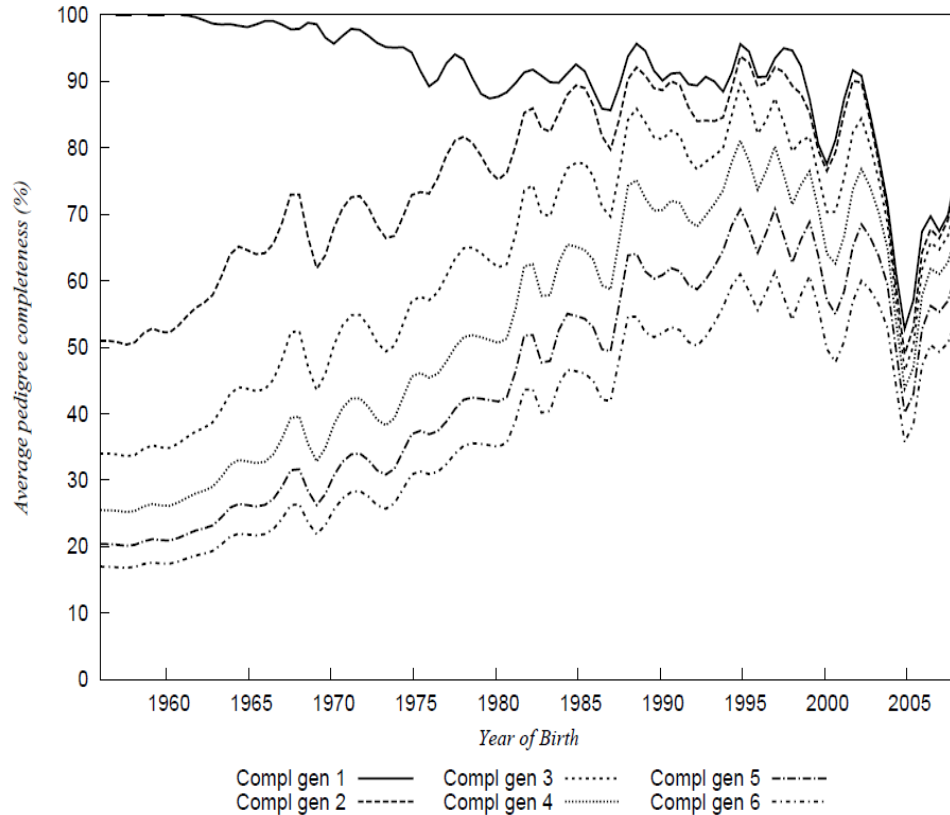
Figure 5.12: The trend of average pedigree completeness of the Kenya Sahiwal cattle breed for 1 to 6 generations

5.3.2 Inbreeding

a) Number of inbred animals

Figure 5.13 shows annual trend of the total number of registered and inbred animals in the Kenya Sahiwal cattle for the period between 1960 and 2008. The total number of inbred animals recorded annually increased over time from one animal in 1960 to 221 animals in 1984 and then generally increased until 2008 (Figure 5.13). The number of inbred animals remained lower than the total number of animals registered over the studied period. The total number of animals decreased over the years while the proportion of inbred animals increased with about 73.12% of calves born in 2008 inbred (Figure 5.13). A total of 4,656 (23.76%) animals in the

entire breed population were inbred. The shrinking breed population and increase in the number of inbred animals may result most of the animals in the breed population being closely related thus limiting choices of mating. Inbreeding level will also accumulate over time leading to intensively inbred animals and consequently economic losses due to inbreeding depression (Weigel and Lin, 2002), unless counteractive measures are introduced and implemented on time.
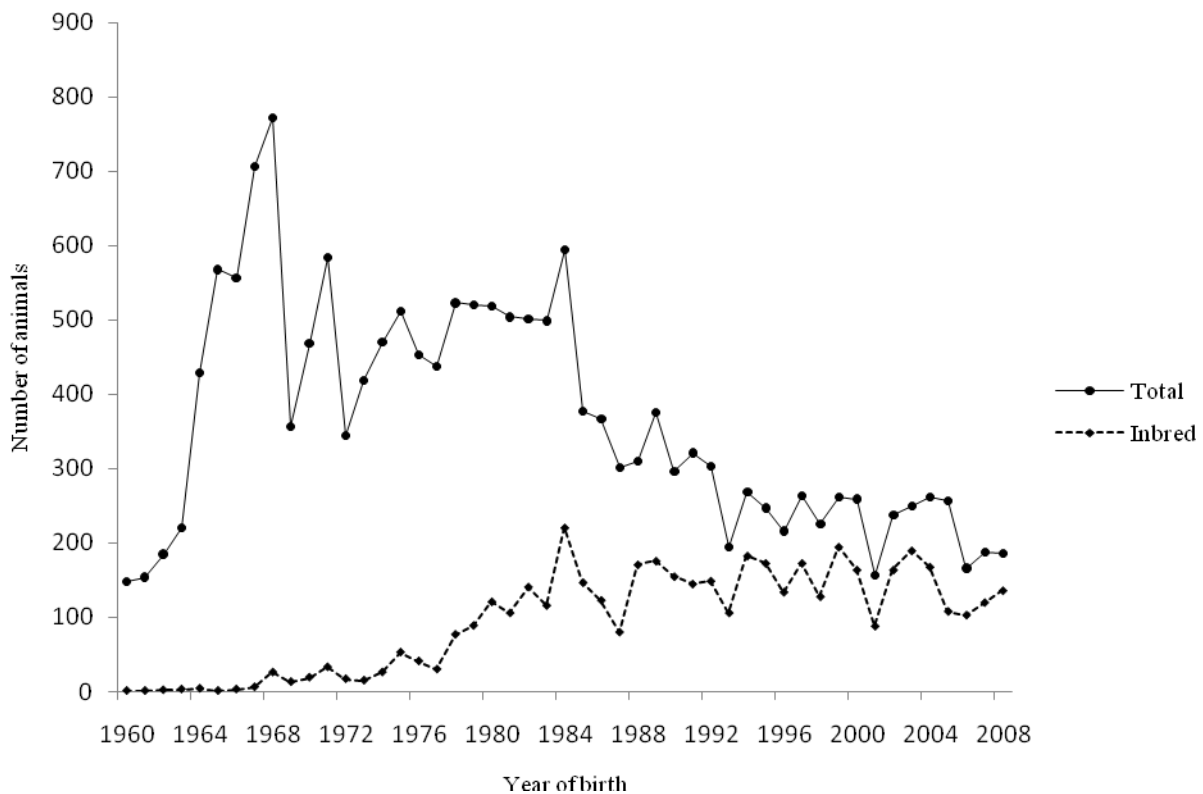
Figure 5.12: Annual trend of the total number of registered and inbred animals in the Kenya Sahiwal cattle breed

b) Distribution of animals by year and inbreeding level

The trend of inbreeding in the breed from 1968 to 2008 is shown in Figure 5.14. There was a decrease in the average F of inbred animals as the number of inbred animals increased over the years. The average F of the total population showed a gradual increase over time due to the increasing proportion of inbred animals. Although the inbreeding level of inbred animals decreased over time, the number of inbred animals increased over the studied period and a large proportion of the breed population was inbred by the year 2008. In 1960's when the closed herd

breeding scheme for the Kenya Sahiwal breed was drawn up and implemented, inbreeding level of the breed was high suggesting that some of the founders were already inbred. In 1978, following reports of declining performance of the breed, mating of related animals was avoided leading to a decline in the F from 1980 (Mpofu and Rege, 2002). The minimum F for individual animals was zero while the maximum was 26.56%. The average annual level of inbreeding was 0.58% for all animals and 2.23% for inbred animals. The variation between F of all animals and inbred animals suggest presence of highly inbred animals within the breed.
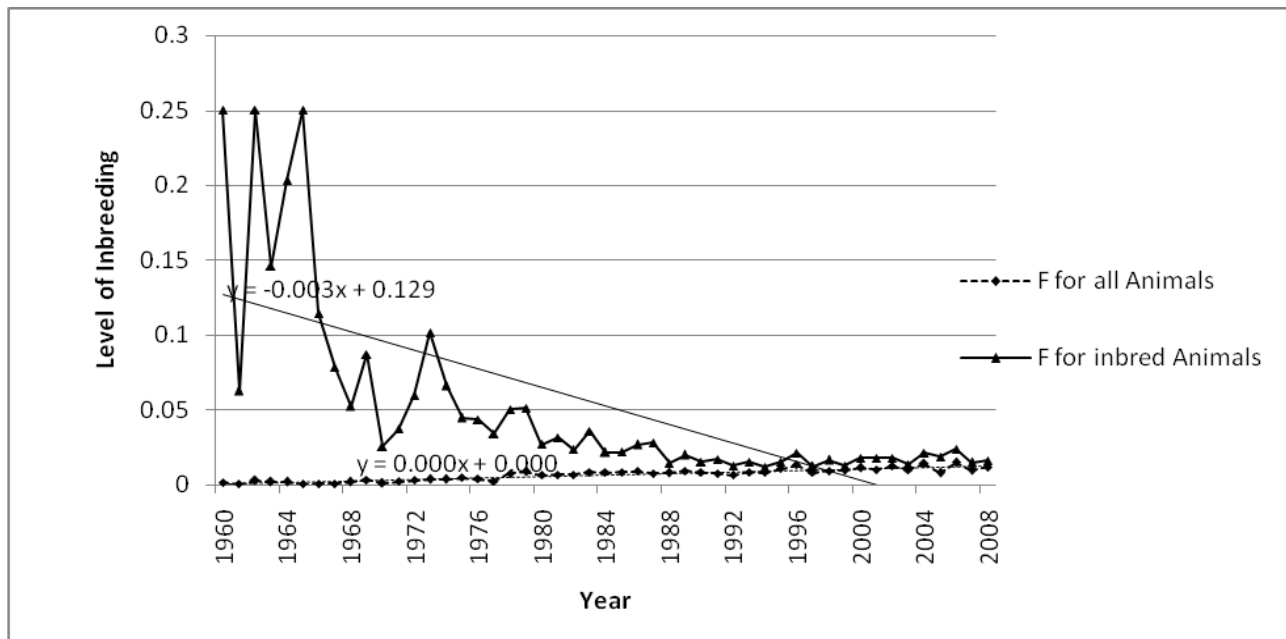
Figure 5.13: Average annual inbreeding coefficient of the registered and inbred animals

The trend of inbreeding was analysed and illustrated for males and females seperately (Figure 5.15). No inbred sire was recorded in the pedigree until 1983 whereas inbred dams were recorded from 1964. On average, sires had a higher inbreeding coefficient than dams i.e. 0.79% vs 0.55%. Inbreeding level of the dams showed a gradual increase with time at a rate of 1.90% per annum. The average inbreeding of sires was more inconsistent than of dams but it increased at a faster rate of 2.90%. The inconsistencies observed in inbreeding can be attributed to the occassional importation of semen from bulls in other countries. For instance, inbreeding level of sires dropped abruptly from 1.22% in 1991 to 0.06% in 1993 following importation of 1000 doses of semen in 1991(Muasya *et al*., 2011).
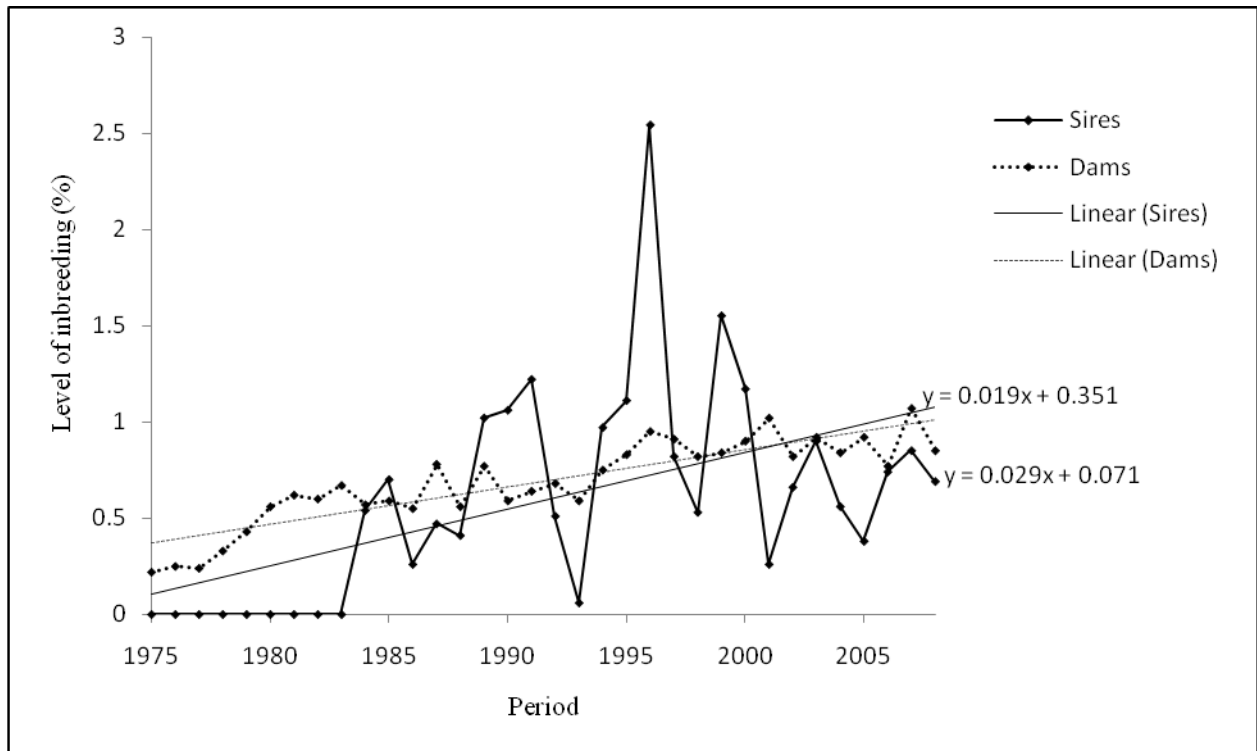
Figure 5.14: Average inbreeding level of sires and dams used for breeding between 1975 and 2008

A wide range of inbreeding level was reported in the breed with about 87.24% of the inbred animals having 0%<F≤5% while 0.26% had 25%<F ≤30% (Figure 5.16). Increased inbreeding results in impaired survival, health, vigor, and reproductive efficiency and also generates increased frequency of animals affected by genetic defects (Thompson *et al*., 2000a). Losses in milk production, decreased lactation length and increased age at first calving were reported in some dairy cattle when inbreeding level reached 10% (Thompson *et al*., 2000b). Livestock breeds are categorized in one of the endangerment categories established in the UK if their inbreeding level is projected to reach 10% and above within 25 years (Caraviello, 2004; Alderson, 2009). The average inbreeding level of the breed can be considered low because it has not reached 10%. High pre-weaning mortality rates and reduced reproductive efficiency reported in the Kenyan Sahiwal cattle breed (Ilatsia *et al*., 2007) may be an outcome of the intensively inbred individuals within the breed. The high proportion of inbred animals and increasing inbreeding level over time is a threat to the genetic diversity of the breed in the long term.
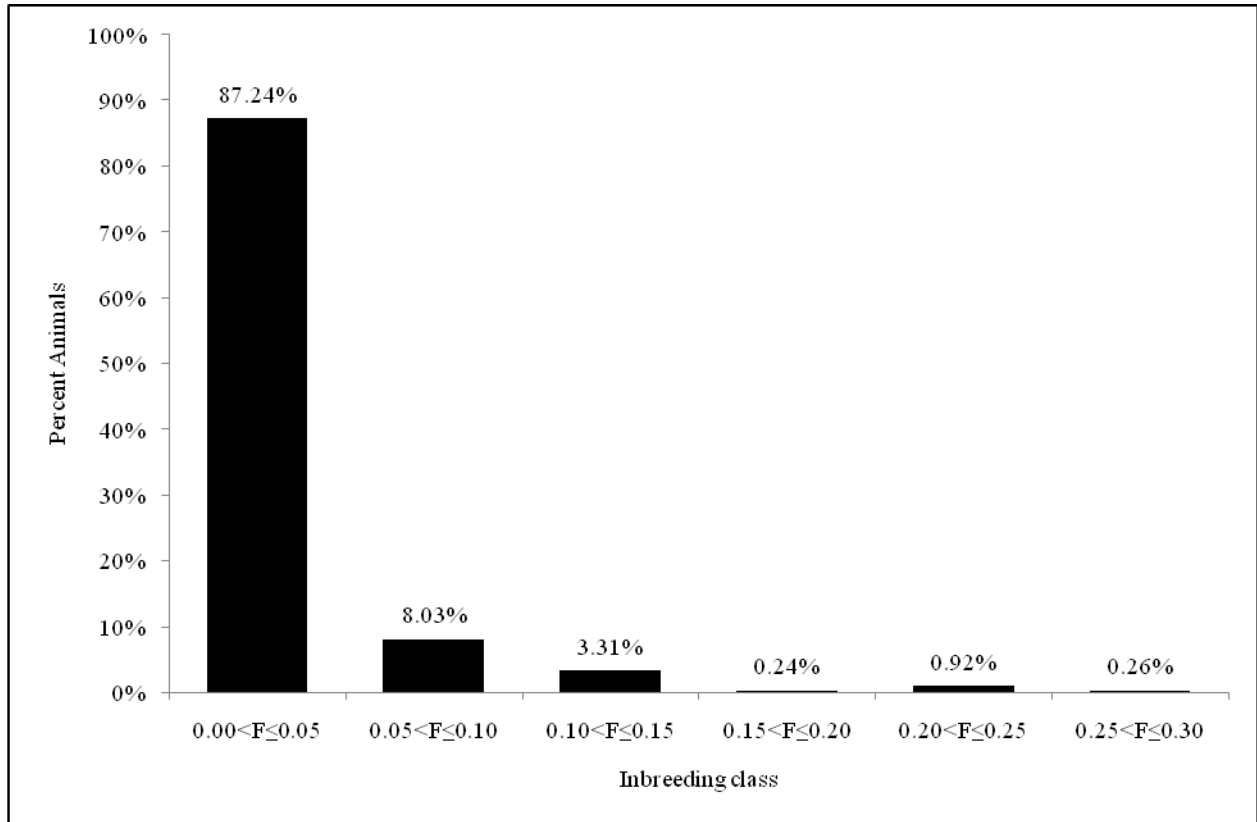
Figure 5.16: Distribution of inbred animals according to their inbreeding classes

c) Rate of inbreeding

The annual rate of inbreeding from 1960 to 2008 is shown in Figure 5.17. It changed inconsistently throughout the studied period, but the maximum annual rate of inbreeding of 0.71% was estimated in 2006. The inbreeding coefficients of animals are very sensitive to the quality of available pedigree information and thus absolute *F* levels provide less information for comparative purposes than the average rate of increase per generation or per annum (Stranden and Kantanen, 2009). A large fraction of missing parents in a pedigree may cause under-estimation of the inbreeding level and the associated losses arising from inbreeding while more complete pedigree gives more accurate inbreeding estimates (Lutaaya *et al*., 1999).
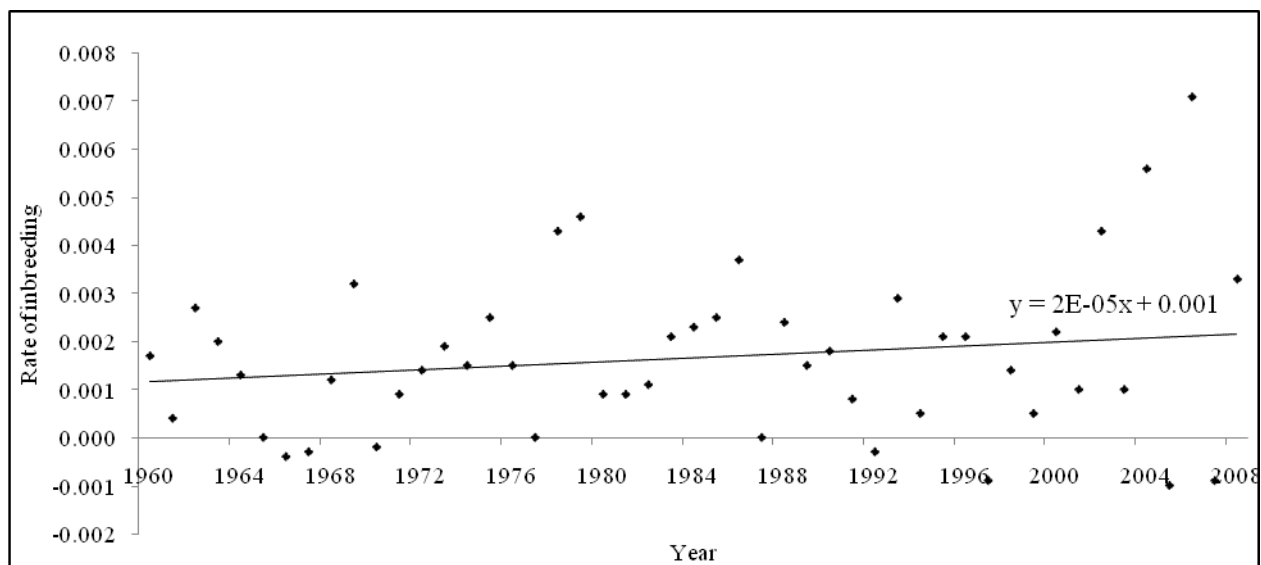
Figure 5.17: Annual rate of inbreeding of the registered Sahiwal breed population in Kenya

Regression of the rate of inbreeding on year of birth of animals born between 1960 and 2008 resulted in an estimated rate of inbreeding of 0.025% per year which represents rate of inbreeding of 0.158% per generation for the breed. Rate of inbreeding for inbred animals decreased at -0.0012% per year thus -0.0075% per generation. A higher level of annual rate of increase was reported by Muasya *et al*. (2011) for the NSS herd. The level of inbreeding in this study is lower than inbreeding levels reported in cattle breeds in the United States of America and Portugal (Cleveland *et al*., 2005; Carolino and Gama, 2008) but greater than levels reported for cattle breeds in Spain (Gutierrez *et al*., 2003), South Africa (Maiwashe *et al*., 2006) and Ireland (Mc Parland *et al*., 2007). The decreasing rate of inbreeding of inbred animals in the Kenya Sahiwal breed is similar though not as steep as that of Irish Angus (-0.02) reported by Mc Parland *et al*. (2007).

To maintain fitness within breeds, the rate of increase in inbreeding should not exceed 1% per generation (FAO, 1998). Mc Parland *et al*. (2007) reported a rate of inbreeding of 1.68% per generation for the Kerry breed, which exceeds the recommended maximum level. The average increase in the rate of inbreeding for the Kenya Sahiwal breed is below the recommended critical level of 1% per generation suggested for animal breeding programs (FAO, 1998). To avoid the problem of inbreeding within the nucleus herds of the Sahiwal breed in Kenya, the herds should be opened to allow for movements of registered bulls from other herds

into the nucleus and encourage cooperation among nucleus herds through exchange of bulls and/or cows as suggested by Ilatsia *et al*., (2011a). In order to optimize inbreeding level and rate, there is need to revise the Sahiwal breeding program in Kenya particularly allocating dams to sires. Computerized mating program at the NSS would help balance genetic progress and inbreeding depression and consequently control inbreeding.

5.3.3 Effective Population Size

The trend of *Ne* based on rate of inbreeding (ΔF) and the number of parents per generation from 1970 to 2008 is shown in Figure 5.18. Estimates of *Ne* varied among different years considered (1970 to 2008) and also between the two methods used for estimation. The *Ne* estimates based on ΔF ranged between 70 and 1,000 with a mean of 335 animals. The *Ne* estimates based on the number of parents ranged between 188 and 576 with a mean of 339 animals. Effective population size increased with decrease in ΔF but when ΔF equaled zero (indicating no change between consecutive generations), *Ne* was not considered because it was infinite. Regression of *Ne* on year of birth of the registered animals showed a decline in *Ne* when both methods were considered (Figure 5.18). The rate of decline was faster when *Ne* was estimated using the number of parents.
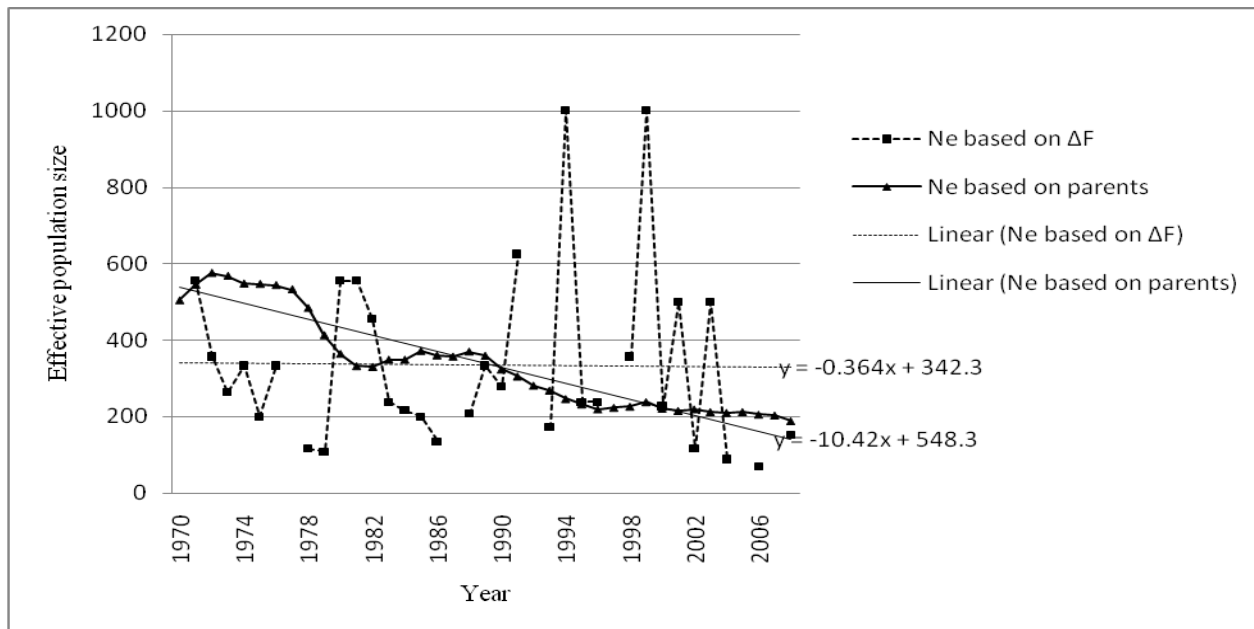
Figure 5.18: The trend of *Ne* based on ΔF and number of parents for the Kenya Sahiwal cattle breed from 1970 to 2006

Effective population size can be used as a measure of genetic diversity within populations, with large values indicating more variability and small values indicating less genetic variability (Maiwashe *et al*., 2006). Effective population size is also preferred for the assessment of risk status within breeds (FAO, 1992; Gandini *et al*., 2004). Effective population size of 50 to 100 animals will take into account the effects of inbreeding, mutation and genetic drift, and thus minimizing the loss of genetic variability and decrease in population fitness (Meuwissen, 1999). However, to sustain the genetic diversity and evolutionary potential of a population for several generations, *Ne* of 500 is essential (Frankham *et al*., 2002). The *Ne* estimated using both methods were within the limit recommended by FAO (1998) suggesting that the population is viable and has adequate genetic variability. However it was below the recommended level to maintain genetic diversity in the long term (Frankham *et al*., 2002).

5.3.4 Average Relatedness and additive genetic relationships

The AR among individuals in different groups of registered animals ranged between 0.07% to 1.41% (Figure 5.19). The highest AR was recorded among males while the lowest AR was recorded among the founders. AR was used to show representation of the groups in the breed pedigree. The AR coefficient complements inbreeding coefficients because they predict the average inbreeding in subsequent generations. In addition, it predicts the long-term inbreeding of a population since it takes into account the percentage of the complete pedigree originating from a founder at population level (Gutierrez *et al*., 2003). The higher AR of males prove that some males were overused and suggests that inbreeding is going to increase unless the breeding program is changed. Founders of this breed are under-represented (Muasya *et al*., 2011).
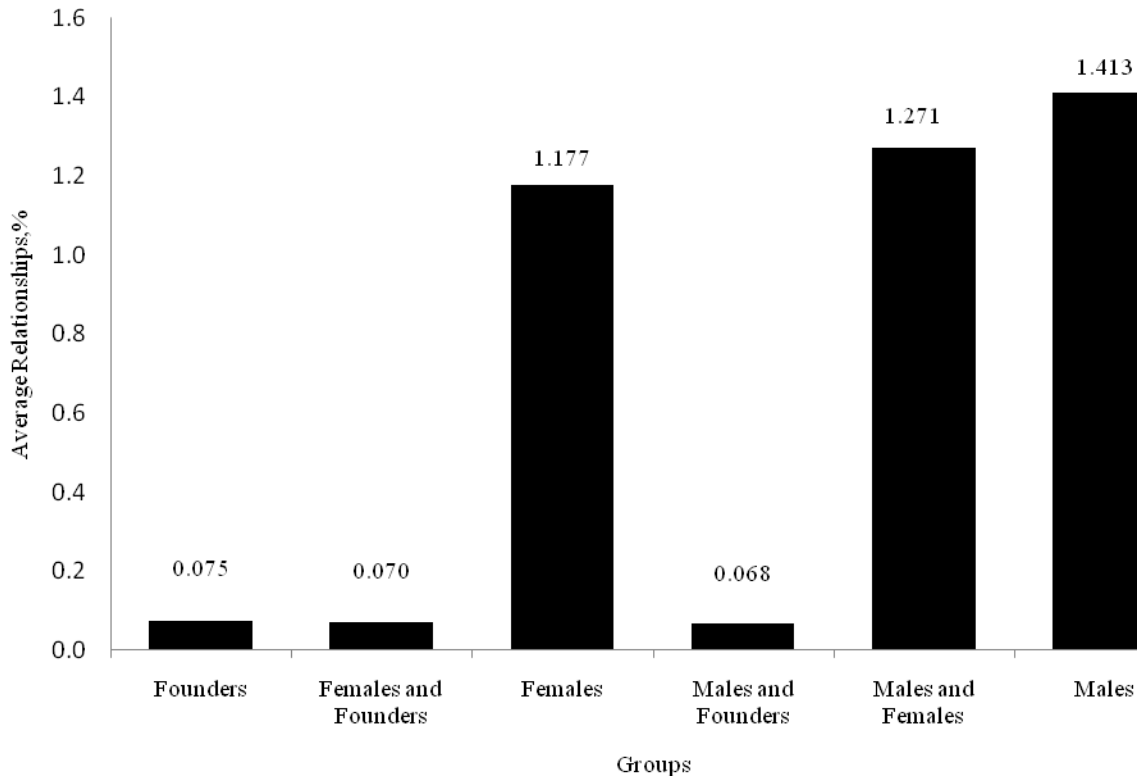
Figure 5.19: Summary of average relationships within the Kenya Sahiwal cattle breed

The average additive genetic relationships (AGR) of the whole population was 0.87%. The rate of change of the AGR (Δf) between 1963 and 2008 for the Kenya Sahiwal breed was 0.04% per year resulting in a Δf per generation of 0.3%. A graph of inbreeding and AGR per year of birth of animals in the pedigree data is presented in Figure 5.20. In this study, AGR of animals born in a given year is the average inbreeding of the progeny of all possible matings among the individuals. The two parameters showed a continuous increase over time. The AGR of the Kenya Sahiwal breed remained lower than the inbreeding level before 1988 indicating wider use of within herd mating. After 1988, AGR increased and remained higher than inbreeding level until the year 2000 owing to reports of declining performance due to inbreeding in 1978 that led to minimal use of related individuals within the breed (Boichard, 2002; Mpofu and Rege, 2002).
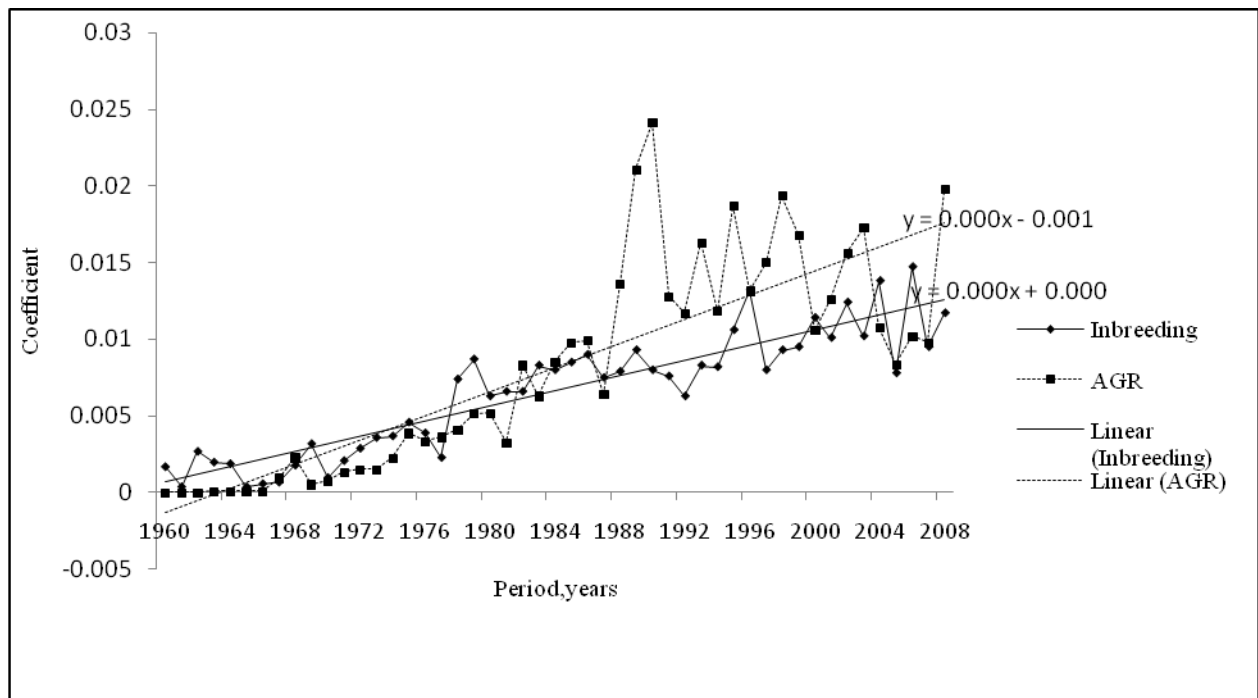
Figure 5.20: Average inbreeding coefficient and additive genetic relatedness of the Kenya Sahiwal breed

The continuous increase in AGR necessitates introduction of a strategy to control future increase in AGR while achieving genetic gain. When genetic gain is the major focus for selection of sires, the result should be substantial genetic gain in the next generation; however, an increase in the genetic relationship between the selected young bulls will also likely result (Sorensen *et al*., 2006). Closer relationships results in more inbreeding in future generations. If a small decrease in genetic gain can be accepted among the selected bulls, then the degree of relationship will be reduced in the next generation. More sires of sons will be used, leading to less of an increase in average relationship and to maintenance of more genetic variation (Sorensen *et al*., 2006). The results recommend development of an effective computerized mating program for the Sahiwal breed that will optimize genetic progress while taking inbreeding and relatedness into account.

5.4 Conclusion

The increasing number of inbred animals result in most of the animals in the breed population being closely related thus limiting choices of mating. Although mean inbreeding is

still low and its rate has not yet reached the critical level, existence of highly inbred individuals within the breed population necessitates introduction of breeding strategies to prevent further increase of inbreeding. A strategy of constraining inbreeding and maintaining genetic variability while offering opportunities for optimal genetic gain is needed. Registration of animals is a prerequisite in monitoring genetic diversity within breeds and assessing their endangerment statuses using pedigree information. Therefore comprehensive updated records are necessary in order to obtain accurate reliable estimates of genetic diversity parameters.

CHAPTER SIX

POPULATION VIABILITY ANALYSIS OF THE SAHIWAL CATTLE BREED IN KENYA

6.1 Introduction

An increasing number of livestock breeds are at a risk of extinction in the near future. This can be attributed to changes in production systems, mechanization, loss of rangeland grazing resources, droughts, floods, disease outbreaks, inappropriate breeding policies and practices, inappropriate introduction of exotic breeds, changing cultural practices, and increasing human population growth and urbanization (FAO, 2009). Over the past 15 years, about 300 of 6000 breeds of farm animals identified by the FAO have become extinct (Scherf, 2000; FAO, 2007). A field literature survey revealed that sub-Saharan Africa is home to a total of 145 cattle breeds, out which 47 (about 32%) are considered to be at risk of extinction (Rege, 1999). Already a total of 22 breeds (about 13%) previously recognised in the continent have become extinct in the last century, even though this number excludes some populations which have lost their individual identity due to admixtures involving two or more originally distinct breeds (Rege, 1999). According to Reist-Marti *et al*. (2003), nearly half of the current cattle diversity and cattle breeds in Africa will be lost in the next 20-50 years if conservation measures to reverse this trend are not developed and implemented.

Current phenomena that include climate change and rapid population growth makes conservation of livestock species that our future food supply could someday depend upon vital. They provide important benefits and have many valuable characteristics such as disease resistance, extreme climate tolerance, high milk production, and the ability to utilize poor pastures (FAO 2007). During a recent drought in Uganda, a few of the farmers who had not sold their Ankole cattle were able to move their herd to a far away water source, but the farmers with the Holstein-Friesians lost their entire herds (FAO 2007). It is therefore crucial to assess the extinction probabilities of livestock breeds whose status are not yet known so as to develop and implement management measures that would increase survival of the breeds which are already at risk. Populations with comparatively low effective population size (*Ne)* and long generation intervals are particularly vulnerable to the risk of extinction (Zachos *et al*., 2009).

Sahiwal cattle breed is one such breed with relatively small sub-populations located in Asia and Africa (Ilatsia *et al*., 2011a). In Kenya, the population of the breed is small with a relatively narrow gene pool since it was founded from a few bulls and cows. Despite the immense economic contributions of the Sahiwal breed to the livelihoods of pastoral communities, the breed faces several challenges that include high risks of inbreeding, drought related challenges, competition from exotics and indiscriminate crossbreeding (Ilatsia *et al*., 2011a; Ilatsia *et al*., 2011b). Therefore, the Kenya Sahiwal cattle breed may be vulnerable to extinction and consequently a population viability analysis (PVA) is crucial so as to form the basis for putting in place strategies that will enhance conservation and sustainable utilization. A PVA would particularly be of interest in predicting the future status of the Sahiwal population in the country based on demographic, environmental and genetic parameters.

Through PVA approach, it would be possible to assess the rate of population decline and the risks of extinction/quasi-extinction over a defined time horizon for the population of concern (Morris and Doak, 2002). Population Viability Analysis can also be used to identify the most important factors faced by a population under particular conditions. The two broad objectives of PVA in managing the rare and threatened species are to minimize their risk of extinction and to promote management conditions in which they retain their potential for evolutionary change (Akcakaya and Sjogren-Gulve, 2000). The objective of this study was thus to conduct a PVA of the main herd of the breed at the NSS so as to predict the likely future status of the breed population under the current management. A model sensitivity analysis was also carried out to determine the most important parameters influencing its viability.

6.2 Methodology

6.2.1 Data source and input requirements

The modeling exercise for PVA required a set of parameters to describe the biological characteristics and stochastic events of the herd. The input parameters for VORTEX were derived using a combination of published and unpublished data from the National Sahiwal Stud (NSS). The NSS is a research herd located at KARI Naivasha used for development of appropriate husbandry and breeding practices for Sahiwal cattle keepers. The herd was chosen because it constitutes purebred Sahiwal cattle and is the leading source of breeding stock for both

pastoralists and other nucleus herds. VORTEX Version 9.98 software package (Miller and Lacy, 2005) was used for simulations and analyses. The input parameters required for simulation of population viability were as follows:

i. *Scenario settings:* All population projections were simulated 500 times for 100 years with quasi-extinction threshold defined as a population size less than 50 individuals. The herd was simulated as single population.

ii. *Species description:* Inbreeding depression in mammal populations can be measured as the number of "lethal equivalents" contained in the genome of the population of interest. VORTEX includes the detrimental effects of inbreeding most directly through the reduced survival of offspring through their first year. Mammalian default settings of 3.14 for lethal equivalents and 50% due to recessive lethal were used. This was due to the unavailability of such data for cattle breeds (Miller and Lacy, 2005).

iii. *Labels and state variables:* Neither labels nor state variables were specified for the projections.

iv. *Dispersal:* Dispersal was not modeled since the herd was considered a single population yet dispersal takes place between populations.

v. *Reproductive system:* within the NSS herd, one bull mates with more than one cow at any single breeding season. It is easily enhanced by use of artificial insemination (AI) within the herd. Breeding system was thus specified as polygynous. VORTEX considers the age at first offspring as the age of the animal at first parturition. Sahiwal bulls are selected at 2-3 years of age either for progeny testing or for natural service in the pastoralist areas. Progeny tested bulls are only available when they are between 8-10 years of age, the expected age at which their daughters will have performance records (Muhuyi et al., 1999; Mpofu and Rege, 2002). According to Muhuyi et al.(1999), the mean age at first calving for the Sahiwal cows at NSS herd was 40 ± 3.8 months. The average age at first service for sires in all nucleus herds was reported to be 3.3 years (Ilatsia, 2011). However, at the NSS bulls are introduced in the breeding herd early. In the baseline simulation, the age at first offspring for males and females were therefore entered as 2 and 3 years, respectively because decimals were not accepted. Reproductive males and females of 20 years were identified in the pedigree records of NSS herd. An estimate of

15 years was chosen for modeling purpose to cover the difference of animals that exit reproduction early as reported by Muhuyi et al., (1999). Mean parity was set as one calf while the maximum parity was set as two calves in case of twins. The sex ratio of male:female at birth was set at 50%.

vi. *Reproductive rates and mate monopolization:* The percentage of adult breeding females and the proportion of breeding bulls in the breeding pool were calculated from the NSS breeding plan explained by Muhuyi et al., (1999).

vii. *Mortality:* VORTEX requires detailed estimates of age-sex-specific mortality rates. Survival rates in the Sahiwal herd vary with sex and age. According to NSS (2007) bulletin, pre-weaning survival rates for males and females were 78.1 ± 12.5% and 78.4 ± 10.9% respectively. Post-weaning survival rates for males and females were 95.5% and 96.4% respectively.

viii. *Catastrophes:* Catastrophes are remarkable environmental events that are outside the limits of normal environmental variation affecting reproduction and/or survival (Miller and Lacy, 2005). Natural catastrophes can be for example: floods, droughts, diseases, or similar events. These events are modeled in VORTEX by assigning an annual probability of occurrence and a pair of severity factors describing their impact on mortality (across all age-sex classes) and the proportion of females successfully breeding in a given year (Miller and Lacy, 2005). Catastrophes were not modeled due to lack of detailed information on their occurrence and how they affect the breed survival. In addition, the herd is actively managed and not prone to catastrophes.

ix. *Initial population size:* Field data by Ilatsia (2011) reported NSS herd at 1224 animals while the NSS bulletin (2007) had reported 1306 animals earlier. Because of fluctuations of herd size with time, sets of different population sizes were analyzed. Stable age distribution was specified for the simulation.

x. *Carrying capacity (K):* It was used to define the upper limit for the population size above which additional mortality is imposed randomly across all age classes. The exact estimate of K for NSS has not yet been formally established. The baseline value of K was set above the herd size at 3000 individuals.

xi.   *Harvest and supplementation:* Harvest was not considered in the baseline simulation but was evaluated in sensitivity analysis as a reduction in percent adult breeding males and females. Currently there is no importation into the NSS herd and thus it can be referred to as a closed population, therefore no supplementation was modeled.

6.2.2 Data analysis

Population viability analysis was conducted to assess extinction probabilities and to compare different management scenarios of the NSS herd using VORTEX 9.98. In order to monitor the trend of response variables with varying input parameters other simulations were run and VORTEX summary results recorded.

6.2.3 Sensitivity analysis

A sensitivity analysis was performed to investigate the parameters most sensitive to the survival of the main herd of the Kenya Sahiwal cattle breed. By using a range of possible values for the input parameters considered in sensitivity analysis, it is possible to determine what effects they have on PVA results. Each parameter was given variable levels while all other parameters were kept constant. The following parameters were considered in the sensitivity analysis: K, age at first offspring for males, mortality rate of different age classes, proportion of breeding males and females in the breeding pool, N and maximum age of reproduction. Response variables considered were mean final population size, heterozygosity and population growth rate.

The NSS herd has started a multiplication program to enable meet the increasing demand for Sahiwal by other nucleus herds (Ilatsia et al., 2011a). Therefore, the initial population size of the herd was analysed at eight different levels to evaluate the trend and effect of increasing initial population size on population growth rate, survival and final population size. The proportion of breeding bulls and adult females in the breeding pool was varied at ten levels to assess their impact on genetic diversity and population growth rate. The sensitivity analysis for age of males at first offspring was conducted to evaluate the effect of progeny testing scheme on viability of the herd. While Muhuyi et al. (1999) reported high pre-weaning mortality rates in the Kenya Sahiwal cattle breed, the trait has been for a long time treated as a secondary trait after production trait and thus its importance was assessed through sensitivity analysis. Increasing

human population and frequent droughts have effects on K of rangeland grazing resources and thus the effect of changing K on survival of the herd population was evaluated. The sensitivity index for each parameter was calculated following Pulliam et al. (1992) as:

$$S_x = (\Delta x / x) / (\Delta P / P)$$ [8]

Where:

-x is the response variable e.g. heterozygosity

-P is the examined parameter e.g. age of males at first offspring

-Δx is the change in the observed response variable

-ΔP is the change in the examined parameter

-Δx/x is the change in a response variable resulting from a change of ΔP/P in examined parameter P.

The sensitivity index was used to compare relative magnitude or importance of different input parameters analyzed on response variables. Higher index relative to the others indicates higher relative magnitude. Because a change of parameters does not affect the response variables in a linear fashion, there is no universal standard level at which P/P should be set for a sensitivity analysis (Brook and Kikkawa, 1998) but the values were set within possible levels of variation. VORTEX input parameters for the baseline simulation and range of values used for sensitivity analysis are summarized in Table 6.5. Each simulation was run for 500 iterations, running 100years with quasi-extinction threshold defined as a population size less than 50 individuals.

Table 6.5: Input values for the baseline simulation and sensitivity analysis parameters of the NSS herd

Parameter	Baseline model	Sensitivity test
Age of first offspring for males	2	2-10
Carrying capacity	3000	1500-6000
Initial population size	1200	250-3000
Maximum age of reproduction	15	9-20
Percent adult females breeding	85	5-85
Percent males successfully siring offspring	2.5	0.5-5
Percent mortality of females from age 0 to 1year	20	0-50
Percent mortality of females from age 1 to 2year	5	0-50
Percent mortality of females from age 2 to 3year	5	0-50
Percent mortality of males from age 0 to 1year	22	0-50
Percent mortality of males from age 1 to 2 year	5	0-50
Percent mortality of males from age 2 to 3 year	5	0-50

6.2.4 Assumptions and limitations

  i.   National Sahiwal Stud which is the main source of Sahiwal breeding animals in Kenya offer the best management practices for population viability.

 ii.   Population viability analysis is mainly applied in wildlife populations and its use in domestic animals is relatively new. It has certain limitations, both practical and philosophical.

iii.   VORTEX required comprehensive data some of which were not available and their effect could only be assessed through sensitivity analysis.

6.3 Results and discussion

6.3.1 Baseline simulation

VORTEX simulation results included the following:

  i.   Average of deterministic population growth rate (r_d)

 ii.   Average of stochastic population growth rate (r_s)

  NB: Population growth rate was averaged across the years simulated prior to any truncation of the population size due to the population exceeding the carrying capacity.

iii.   Probability of population extinction after 100years (PE)$_{100}$

 iv.   Average population size, averaged across all simulations

  v.   Average time to population extinction, in years T(E)

 vi.   Generation time for males and females (L $_{male}$ and L $_{female}$)

vii.   Expected heterozygosity of the extant populations (expressed as a percentage of the initial gene diversity of the population)

The aim of the baseline simulation was to assess the current management scenario at NSS to be used as a basis for conducting sensitivity tests. The results are presented in Table 6.6.

Table 6.6: Summary results for the baseline simulation of the NSS herd

Average population size after 100 years	2805
Standard deviation for N(100)	328
Deterministic population growth rate	0.125
Expected heterozygosity of the extant population	0.983
Generation time for females	7.480
Generation time for males	6.750
Probability of extinction	0
Stochastic population growth rate	0.032
Standard deviation for r_s	0.153

r_s, stochastic population growth rate; N, population size

Over the years, the population size is predicted to increase gradually after which it will be constrained by the K as illustrated in Figure 6.21. According to the results, the herd population was predicted to increase at a deterministic rate of 12.5% and stochastic growth rate of 3.2% per year before any truncation due to limited K. This observation can be attributed to the government decision in 1962 to consolidate breeding activities and develop appropriate management systems at the NSS. However, the original heterozygosity of the herd will be lost with time (Figure 6.21), an observation that can be linked to the closed nature of the NSS breeding programme (Meyn and Wilkins, 1974), where there is no exchange of genes between NSS and other existing herds (Ilatsia et al., 2011c).

The baseline simulation showed that generation length for males was shorter than for females. These results contradict results of chapter 4 of this study (Table 4.3). In this table the GI for males (8.2 years) is longer than for females (5.1 years) which is in agreement with results by Muasya et al. (2011). This contradiction could be expected because the baseline simulation ignored the influence of progeny testing which was assessed under sensitivity analysis. In addition, VORTEX program does not consider maximum breeding age for males and females separately whereas under practical conditions males stay longer in the breeding herd than females in the NSS where AI is exclusively used.
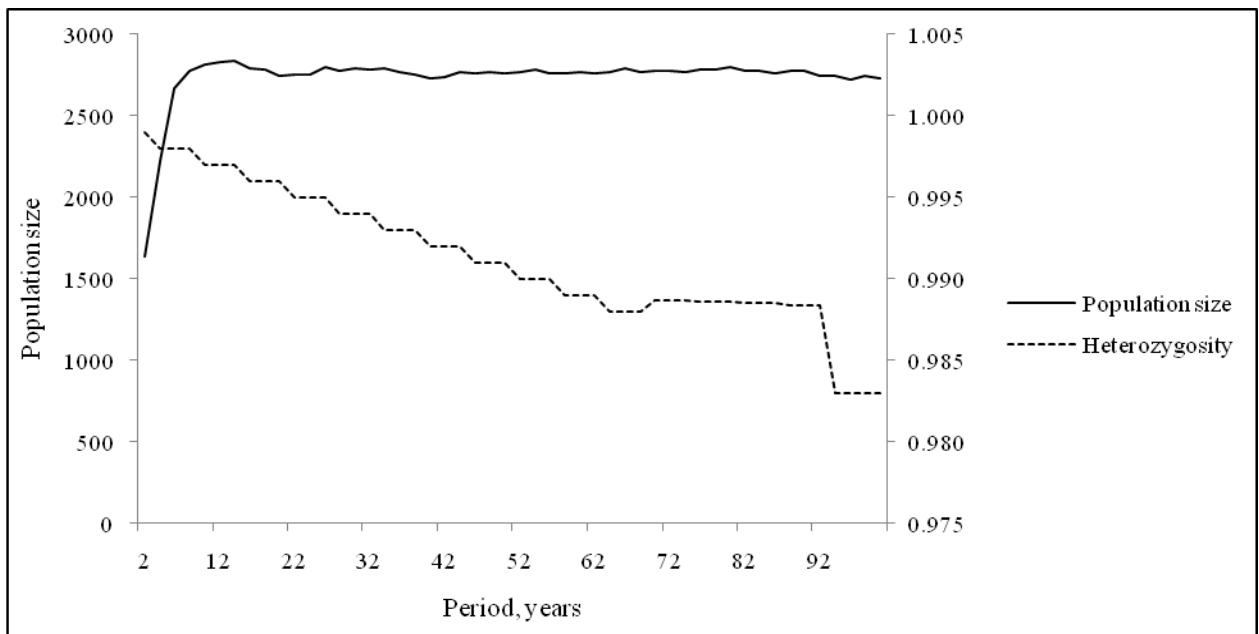

Figure 6.21: Predicted trends in population size and heterozygosity of the NSS herd in the next 100 years

6.3.2 Sensitivity test

Relative magnitude of the input variables on response variables were summarized in Table 6.7.

Table 6.7: Relative impact of sensitivity analysis on final population size, heterozygosity and population growth rate of NSS herd

Parameter	Input values	Sensitivity Index		
		Mean final N	He	Population r
Carrying capacity	1500-6000	0.7500	0.008	3.8470
Initial population size	250-3000	0.0004	0.000	0.3438
Female mortality (%)	0-50	0.0097	0.001	0.0990
Male mortality (%)	0-50	0.0037	0.001	0.0063
% breeding females	0.5-5	0.9270	0.014	0.0344
% breeding males	5-85	0.0006	0.015	0.0116
Age of first offspring for males (years)	2-10	0.0008	0.002	0.0064
Maximum breeding age (years)	9-20	0.0688	0.014	0.9160

i. *Carrying capacity (K)*

Increase in K resulted in large population size after 100 years (Table 6.7). Reducing K by half resulted in final population size decrease by 50.0% while doubling K increased the final population size by 62.7%. Carrying capacity had very minimal effect on population heterozygosity (Table 6.7). Doubling K increased heterozygosity of the population by 0.5% only while reducing K by half resulted to 1.6% loss of heterozygosity after 100years. When K is fixed to a certain number of individuals, increasing the N does not promote population growth. Instead, both deterministic and stochastic growth rates decreases so as to maintain the population size within the limit of K. According to Ilatsia *et al*. (2011a), majority of Sahiwal genetic resources are owned by pastoralists particularly the Maasai. Thousands of hectares of land traditionally owned by the Maasai pastoralists in Kenya are being lost to commercial enterprises, mining, industries and urbanization. In addition to the frequent droughts experienced in these areas, the result would be reduced K of the land. On the other hand, demand for meat and milk are increasing and consequently food insecurity will increase. Therefore, there is an urgent need for establishment of other Sahiwal holdings/ranches in protected areas if the breed is to remain viable and maintain its genetic diversity.

ii.   *Initial population size(N)*

All other factors held constant, N had no significant effect on both the final population size and genetic diversity after 100 years. This means that even when the N is small, the genetic diversity of the initial population can be conserved reasonably well if the population growth rate and the K are large enough. A recent study on the suitability of various breeding strategies for Sahiwal cattle genetic resources in Kenya (Ilatsia *et al*., 2011c) suggested close cooperation of various herds to broaden the gene pool, a conclusion that seems to be supported by the results above. Further, the parameter was of interest because nucleus farms expressed plans to expand their herds in response to the growing demand for Sahiwal breeding bulls as reported by Ilatsia *et al*. (2011a).

iii.   *Proportion of breeding animals in the breeding pool*

The proportion of males in the breeding pool had no strong effect on deterministic growth rate (Table 6.7). The simulations showed that the genetic diversity of the breed population is improved when the proportion of breeding males in the breeding pool is increased (Table 6.7). Increasing the proportion of breeding bulls by 2% increased heterozygosity of the population by 0.5%. The low percentage of breeding bulls in the NSS has no effect on population's viability but is not enough to sustain the population's genetic diversity. Muasya *et al*. (2011) reported low *Ne* for the Kenya Sahiwal cattle breed which is also an indication of low genetic variability. Apparently, generation time for both males and females are not affected by the percentage of breeding males.

An increase in adult breeding females increased the viability of the NSS measured as the mean final population size, deterministic and stochastic growth rates (Table 6.7). Reducing the proportion of adult breeding females to 30% caused a negative population growth rate and induced population extinction. Furthermore, it reduced mean final population size by 63.0% and caused loss of heterozygosity of the population. Sahiwal cattle breeding program in Kenya is characterized by small herds where a few bulls are used in mating (Ilatsia *et al*., 2011a). In such cases, outstanding bulls will often have numerous female descendants, and the same bulls are likely to sire many sons that will eventually enter the breeding cycle thus limiting the number of bulls available for mating. Expansion and close interactions of the existing breeding farms would

result in a concomitant increase in the number of available breeding bulls thus reduce over usage of only few superior bulls and reverse the decreasing genetic diversity.

iv.   *Mortality*

The sensitivity tests also revealed that changes in female mortality has strong effect on population growth rate. In contrast, male mortality (up to 50%) across all age classes has no significant impact on population growth rate (Table 6.7). When mortality rate of females of all age groups increases, both deterministic and stochastic population growth rates decrease (Figures 22 and 23). Young females aged 0 to 1 year had the greatest influence on deterministic growth rate than the other age groups whereby a unit increase in mortality of this age group reduced deterministic growth rate by 8%.
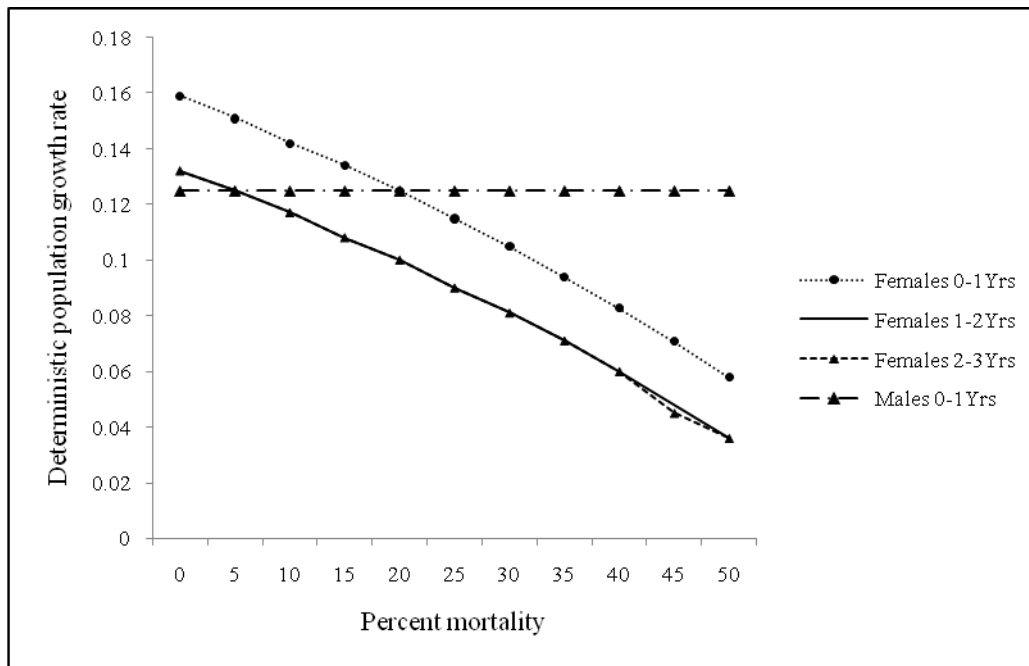
Figure 6.22: Effect of mortalities of different age groups on deterministic growth rate of the NSS herd population

71
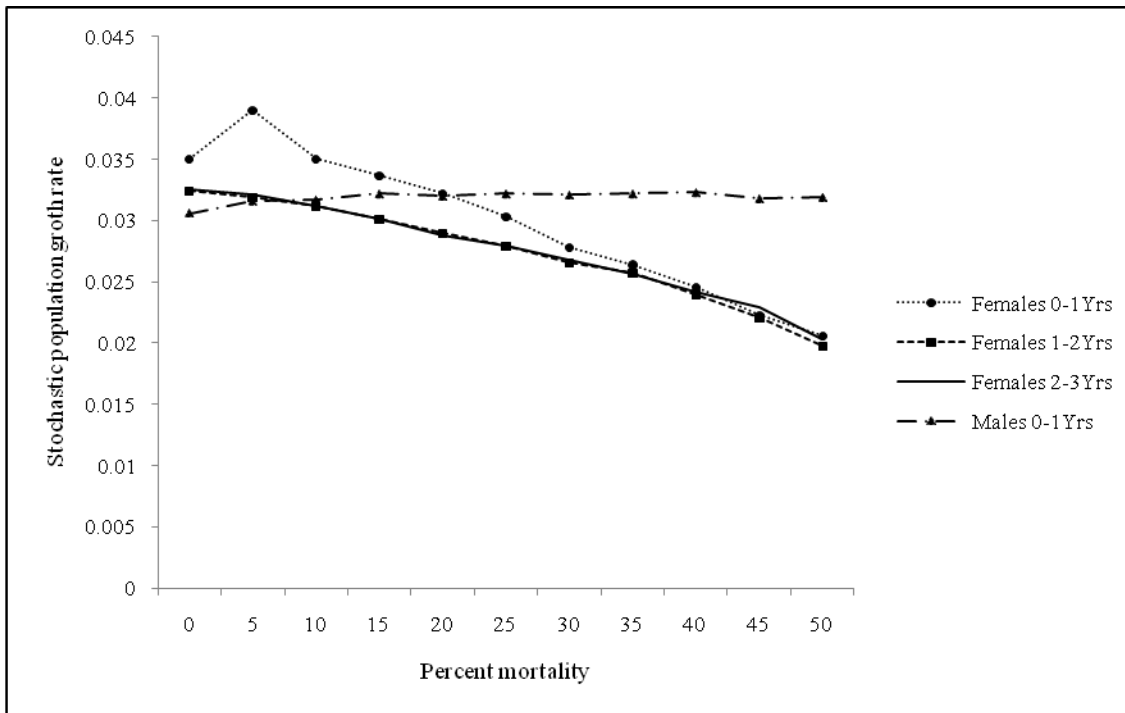
Figure 6.23: Effect of mortalities of different age groups on stochastic population growth rate

When mortality rate of females of all age groups increases, generation time for both males and females increases while mortality of males had no effect on generation length of both males and females. The reduced impact of male mortality on population viability can be attributed to the polygynous mating system of the breed. Initial genetic diversity of polygynous populations is largely conserved within the males since in this study female mortality caused no impact on expected heterozygosity after 100years whereas it was significantly influenced by male mortality. Therefore, a decrease in female mortality rate will increase the viability of breed population.

Sahiwal bulls are selected at 2-3 years of age either for progeny testing or for natural service in the pastoralist herds (Mpofu and Rege, 2002). Progeny tested bulls are only available when they are between 8-10 years of age, the expected age at which their daughters will have performance records (Muhuyi *et al.*, 1999). Increasing the age of males at first offspring has no effect on deterministic population growth rate and generation time for females. Progeny testing causes a decrease in population heterozygosity such that the population losses up to 1.65% of its initial genetic variability when the age of first offspring of males is increased to ten years. The

parameter has a significant effect on generation time for males explaining the long GIs in sire lines within the NSS herd. Increase in maximum age of reproduction promotes population growth and conserves genetic variability of the population, while prolonging the generation time for males and females. The continuous use of genetically superior bulls (through AI) for a long period without replacement at the NSS therefore contributes to the prolonged GIs of sire lines thus reduces the rate of genetic progress within the breed.
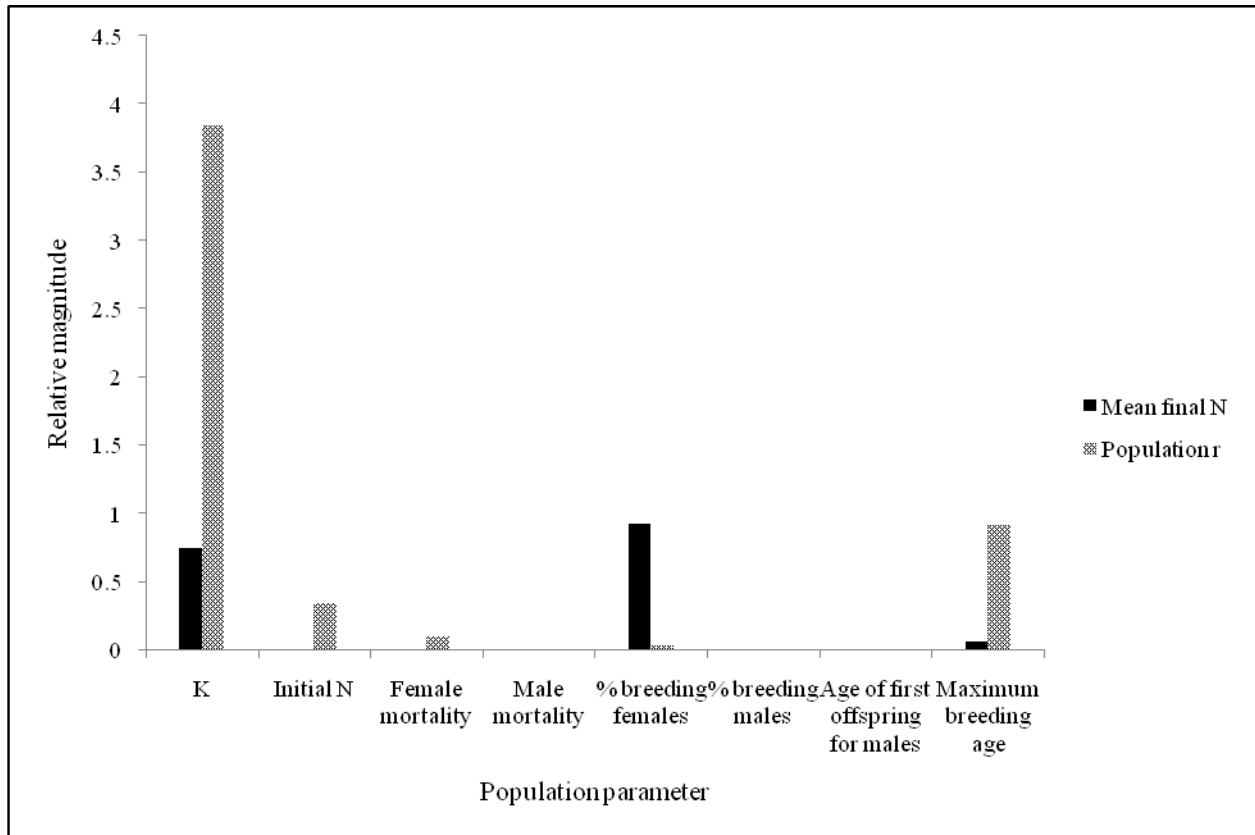
Figure 6.24: Relative magnitude of different parameters on population growth rate (r) and mean final population size of the NSS herd

From the sensitivity analysis, it is clear that the most important parameter affecting population growth is the proportion of adult breeding females in the breeding pool (Figure 24). At least 40% of the females in the population have to breed to provide a positive stochastic and deterministic growth rates and a final population size equal to or greater than the N. As the proportion of breeding females increases, the first year of extinction is postponed thus improving persistence of the breed population. Due to the polygynous nature of the bulls, their mortality has

no significant effect on population growth rate and generation time for both males and females. The results of this study are consistent with those reported by Thirstrup *et al*. (2009) on the effect of breeding males on persistence of the breed and sensitivity concerning female reproduction. Male mortality has a negative effect on population genetic diversity. Carrying capacity is the most important determinant of the final population size after the projected period (Figure 6.24). In another study, PVA on Jordan indigenous cattle showed a rapid decline following a low number of adult breeding female and feed scarcity (Al-Atiyat, 2008). In the PVA study on Przewalski horses by Slotta-Bachmayr *et al*. (2004), a sensitivity test unveiled the maximum age of reproduction and fecundity rates as being some of the most important parameters for their persistence. Therefore, PVA is useful in developing management strategies to recover and counteract declining populations. Figure 6.25 illustrates how different parameters influences population heterozygosity and shows that breeding bulls account for most of population genetic variability.
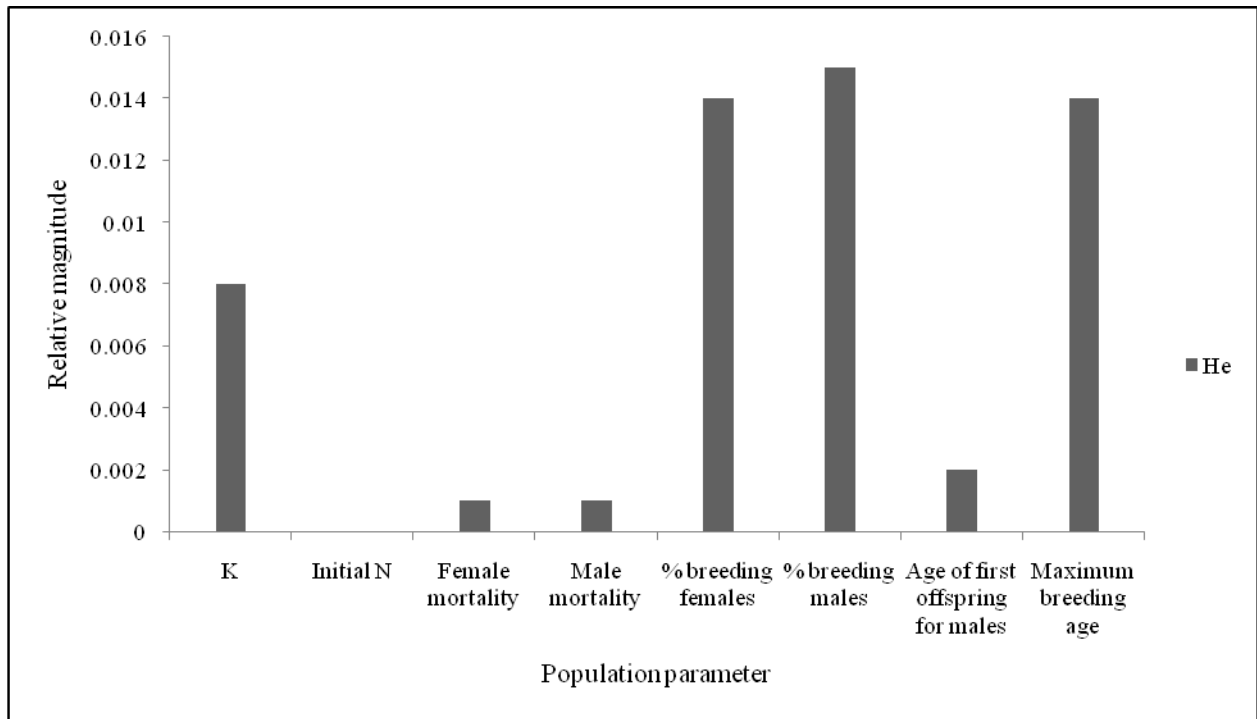
Figure 6.25: Relative magnitude of different parameters on population heterozygosity of the NSS herd

6.4 Conclusion

For the maintenance of the Sahiwal breed genetic diversity, it is important to increase the proportion of breeding males in the Sahiwal herd population. Currently, breeding bulls are the only route for improving Sahiwals in the pastoral herds. Following shortage of the breeding bulls from the nucleus herds, pastoralists are making maximum use of the available bulls and retaining them for a long time. Sensitivity test showed that post-weaning mortality rates for different age classes is paramount to the viability of the NSS population. Female survival is key in ensuring persistence of the breed and therefore needs to be considered in management and breeding strategies. The most important parameter affecting viability of the NSS population is the proportion of adult breeding females in the breeding pool. Genetic erosion of the breed can be controlled effectively through monitoring male mortality and increasing the number of breeding males. Considering that genetic variability is correlated with fitness in many cases, management actions should aim at creating conditions under which as little heterozygosity as possible will be lost in the future.

CHAPTER SEVEN

GENERAL DISCUSSION

7.1 Aim of the study

The AnGR available throughout the world are in a dramatic state of decline (FAO, 2007a). This has mainly been caused by widespread crossbreeding and the replacement of local stocks through prolonged dilution as a result of techniques that facilitate easy transfer of genetic material from one geographical region to another. The declining diversity has serious consequences for the current livestock production and future capacity to meet unforeseen challenges and opportunities (Philipsson *et al*., 2011). The motivation of this study was the increasing demand for the Kenya Sahiwal cattle breed by the pastoralists in ASALs and its continued utilization in crossbreeding with other animals both local and exotic. Information about its genetic diversity, demographic trends and geographical distribution is not available. To contribute to the effective and sustainable management of the breed, this study was designed to evaluate the population structure and monitor genetic diversity of the breed. The study involved four objectives i) to explore the geographical distribution of the major nucleus herds of the Kenya Sahiwal cattle breed, determine its degree of concentration and geographical endangerment status, ii) to characterize the population structure of the breed and explore its demographic trends, iii) to assess the status and monitor trends of genetic diversity parameters within the breed, iv) to analyze the viability of the breed population at the NSS.

7.2 Study methodology

7.2.1 Geographical concentration

Global positioning system was used to record spatial positions of the major Sahiwal herds in Kenya. ArcView GIS 3.2 mapping software (http://www.esri.com) was then used to compute the extent of geographical distribution and concentration of the Sahiwal cattle breed in Kenya. The mean center tool in toolset of the mapping software was used to compute the weighted mean center of the breed population. The standard distance tool then measured the degree to which the population is concentrated or dispersed around the mean center estimated. The tool was then used to draw buffer areas of 25km and 50km radii in order to determine how the breed population is concentrated around the mean center.

7.2.2 Population structure and genetic diversity

In this study, POPREP (Groeneveld *et al.*, 2009) was used to characterize population structure of the Kenya Sahiwal cattle breed and analyze genetic diversity parameters. POPREP is a web-based application tool for analysis of pedigree information. Input data set required were: unique identification of all animals, sire, dam of each animal, birth date and sex. Animal IDs may contain alpha numeric characters.

7.2.3 Analysis of the NSS herd viability

The viability of the NSS herd was analyzed using VORTEX 9.98 software (Miller and Lacy, 2005). It simulates deterministic and stochastic factors affecting the dynamics of a population. The software simulates a population by stepping through a series of events that describe an annual cycle of a typical sexually reproducing, diploid organism: mate selection, reproduction, mortality, increment of age by one year, migration among populations, removals, supplementation, and truncation (if necessary) to the carrying capacity. It creates a representation of each animal in its memory and follows the destiny of the animal through each year of its lifetime (Miller and Lacy, 2005). It keeps track of the sex, age, and percentage of each animal. Demographic events (birth, sex determination, mating, dispersal, and death) are modeled by determining for each animal in each year of the simulation whether any of the events occur.

7.3 Status of the Kenya Sahiwal cattle breed

Replacement of local breeds by a narrow range of high yielding breeds is a widespread consequence of the efforts to increase output (Thorntorn and Herrero, 2010). Crossbreeding of animals has been practiced widely as a means of increasing productivity of livestock breeds (Groeneveld et al., 2010). In absence of measures to ensure that the use of exotic genetic material and crossbreeding are well planned can be a serious threat to local breeds (FAO, 2006b). The *Ne* of the registered Sahiwal decreased over the years and was below the value required to maintain genetic diversity of the breed in the long term according to Frankham *et al*. (2002). This was mainly caused by use of only a few prominent sires in the breeding pool. Though the average inbreeding level of the registered Sahiwal cattle breed was considered to be low the increasing trend over time (Figure 5.17) require strategies to counteract inbreeding. When genetic gain is the major focus for selection of sires, the result should be substantial genetic gain in the next

generation; however, an increase in the genetic relationship between the selected bulls will also likely result. Closer relationships results in more inbreeding in future generations. If a small decrease in genetic gain can be accepted among the selected bulls, then the degree of relationship will be reduced in the next generation (Sorensen *et al*., 2006). Pedigree records through pedigree analysis have been used extensively to analyze population structure and genetic variability of cattle breeds. The results have been useful in development of strategies that enhance sustainable management of AnGR and maintaining their genetic diversity. Muasya *et al*. (2013) analyzed the breeding structure and genetic variability of the Holstein-Friesian dairy cattle population in Kenya and revealed weakness in the breeding program. From the study, strategies for improving the breeding program were recommended. Population parameters analyzed for the Brangus cattle in South Africa were used to construct an effective selection management for the breed (Steyn, 2012). Ivankovic *et al*. (2010) used pedigree analysis to implement a conservation program for the endangered Croatian autochthonous cattle breeds.

The Sahiwal breed is distributed to several regions in Kenya but chapter three of this study revealed that the largest population of the breed is confined within the former Rift Valley province. Geographical isolation of the breed was not identified as a threat to the population persistence since only 1.2% of its population was located within a circle of 25km radius from its population mean center. Therefore the Kenya Sahiwal cattle breed does not fall under any of the five categories of geographical endangerment defined by Alderson (2009). A previous study conducted for Markhoz goats found that the breed was geographically isolated and endangered since 77% of its population lied within a radius of 7km only (Bahmani *et al*., 2011). Most of the UK sheep breeds evaluated by Carson *et al*. (2009) were also geographically endangered.

7.5 Viability of the Kenya Sahiwal cattle breed

Population viability analysis results (Figure 6.21) showed that the population of the Sahiwal cattle at NSS is projected to increase with time after which it will be constrained by the limited carrying capacity (K). To the contrary, pedigree analysis results had indicated a downward trend in the breed population towards the last years evaluated. The projected population increase is attributed to the appropriate management systems within the herd. The problem of limited population growth due to limited K can be overcome by establishment of

more affiliate nucleus herds. As the herd population continues to grow, the original heterozygosity will be lost with time (Figure 6.21). Considering that the NSS is the main source of breeding animals for other nucleus and pastoral herds, its genetic diversity need to be conserved adequately. The proportion of breeding males in the breeding pool was observed to be the most influencial parameter on genetic diversity of the herd (Table 6.7). Expansion and close interactions of the existing breeding farms and stakeholders would result in a concomitant increase in the number of available unrelated breeding bulls and consequently increased genetic diversity.

7.6 Conclusions and recommendations

According to this study, the number of registered animals is below the threshold required for maintenance of within breed genetic diversity. Though it is not endangered lack of sustainability strategies expose the breed to high risk of population decline and increased loss of genetic diversity. Geographical distribution of the major population of the breed was found to be confined within the former Rift Valley province only thus the need to introduce and popularize the breed to other potential rangeland regions. Some of the conservation nuclei can be based in government research centres and institutions. This would reduce vulnerability of the breed as a result of a wider geographical cover and increased population size. Sahiwal breed registration from other herds except NSS was observed to be low. To allow effective monitoring of demographic trends and genetic diversity parameters, there is need for adequate and updated pedigree information. Livestock registration and recording is not only an essential component of traceability, disease control and good farm management, but also contributes to securing access to markets for higher quality and geographical identifiable products. The Sahiwal breeding program need to be reviewed so as to balance genetic progress and conservation of genetic diversity.

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