REPRODUCTIVE PERFORMANCE AND GENETIC RESPONSE TO SELECTION OF DAIRY GOATS IN KENYA FOLLOWING INCORPORATION OF REPRODUCTIVE TECHNOLOGIES AND GENOMIC SELECTION

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DECLARATION AND RECOMMENDATION

Declaration

This thesis is my original work and has not been presented previously for the award of a degree here at Egerton University or any other university.

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DEDICATION

This work is dedicated to my beloved wife Nancy Marcellino, our children; Tombe, Wani and Pitya Dominic, my loving mother Lina Denya, brothers and sisters.

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ABSTRACT

The goat industry plays a key role in provision of economic and social benefits to a significant population in Kenya. Therefore improving their performances would contribute to food security, poverty reduction and economic empowerment of resource poor rural households. Reproductive performances and estimation f response to selection are considered among the essential pillars of economic viability of dairy operations. This thesis evaluated reproductive performance and response to selection of dairy goats using reproductive technologies, genomic selection and different mating designs in Kenya. The specific objectives of the thesis were: (1) to determine the effect of breed and age on testicular and semen characteristics of dairy goat bucks, (2) to determine the effect of oestrous synchronisation protocols and type of service on reproductive performance of dairy goats, (3) to estimate response to selection in conventional and alternative dairy goat breeding programme incorporating reproductive technology and genomic selection and (4) to estimate rates of genetic gain and inbreeding in alternative dairy goats breeding programme utilising reproductive technology, genomic selection and different mating designs. The study was conducted using Toggenburg and Saanen bucks where body weight, scrotal circumference and scrotal length were measured and semen characteristics were evaluated. The does were synchronised using short (7 days) and long-term (12 days) protocols and mated using natural and artificial insemination methods. The onset and duration of oestrus, response to oestrus and conception, kidding and twining rates were evaluated. The data for testicular, semen characteristics, onset and duration of oestrus were analysed using ANOVA, while response to oestrus, conception rate and kidding rate were analysed using Chi-Square test. Deterministic and stochastic simulation models were used to evaluate response to selection under both conventional (CS) and genomic (GS) schemes utilising reproductive technologies. Breed of the bucks affected semen consistency and sperms concentration while age affected scrotal circumference and length, semen consistency, sperms concentration and motility. Synchronisation protocols and mating methods had no effect on reproductive performance parameters measured. It was found that AI-liquid semen was superior compared to AI-Frozen semen, and natural mating strategies in terms of response to selection in both conventional and genomic selection schemes. Genomic scheme outperformed conventional scheme in all the parameters measured. The mating designs significantly influenced level of inbreeding. It is concluded that short-term protocol following single fixed-time AI could be an alternative to long-term oestrous synchronisation, while adoption of artificial insemination and genomic selection optimizes response to selection in dairy goat breeding programme.

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LIST OF ABBREVIATIONS AND ACRONYMS

AI	Artificial Insemination
ANOVA	Analysis of Variance
BB	Bucks to breed Bucks
BD	Bucks to breed Does
BLUP	Best Linear Unbiased Prediction
BW	Body Weight
C^{+ve}	Conventional Positive Assortative Mating Design
CCS	Conventional Cryopreserved Semen
CIDR	Controlled Internal Drug Release Devices
CFS	Conventional AI-Fresh Semen
C^{Max}	Conventional Maximising Inbreeding Mating Design
C^{Min}	Conventional Minimising Inbreeding Mating Design
CNM	Conventional Natural Mating
C^{Rand}	Conventional Random Mating Design
CS	Conventional Scheme
C^{-ve}	Conventional Negative Assortative Mating Design
DB	Does to breed Bucks
DD	Does to breed Does
EVs	Economic Values
EBV	Estimated breeding value
FS	Frozen Semen
G^{+ve}	Genomic Positive Assortative Mating Design
GCS	Genomic Cryopreserved Semen
GLM	General Linear Model
GFS	Genomic Fresh semen
G^{Max}	Genomic Maximising Inbreeding Mating Design
G^{Min}	Genomic Minimising Inbreeding Mating Design
GNM	Genomic Natural Mating
G^{Rand}	Genomic Random Mating Design
GS	Genomic Scheme
G^{-ve}	Genomic Negative Assortative Mating Design

KES	Kenyan Shillings
Kg	Kilograms
LS	Liquid Semen
LSM	Least Square Means
LT	Long Term
LW	Daily Weight Gain
Max	Maximising Inbreeding Mating Design
Min	Minimising Inbreeding Mating Design
MW	Live Weight
MY	Milk Yield
NKW	Number of Kids Weaned
NM	Natural Mating
PGF2α	Prostaglandin F2α
QTL	quantitative trait locus
Rand	Random Mating Design
SC	Scrotal Circumference
SE	Standard Error
SL	Scrotal Length
SNP	single nucleotide polymorphism
SP	Synchronisation Protocol
SP	Short Term
-ve	Negative Assortative Mating Design
+ve	Positive Assortative Mating Design

CHAPTER ONE

INTRODUCTION

1.1 Background Information

Domestic goats (*Capra hircus*) are spread across the world with a population of one billion of which about 94% is found in Asia and Africa (Amills *et al.,* 2017; FAOSTAT, 2018). This distribution across the world and in different agro-ecological zones is due to their versatility to adapt to harsh environmental conditions and poor quality feed resources (Hegde, 2020; Kahi & Waseke, 2019). There is an increasing trend in world goat population and this has been attributed to a shift by resource poor households mainly in Asia and Africa from cattle to goat production to confront challenges associated with global warming and loss of biodiversity (Hegde, 2020).

Indigenous goats are the majority breeds of goats kept in the tropics, they have however, slow growth and milk production due to low genetic potential (Idowu & Adewumi, 2017; Msalya *et al*., 2017). Strategies used to improve their production performance include cross-breeding or total replacement with exotic dairy goat breeds such as Toggenburg, Saanen, Alpine and Angolo-Nubian to improve growth and milk production (Ahuya & Okeyo, 2006; Kahi & Wasike, 2019; Ndeke *et al.*, 2015). The performance of these exotic dairy goat breeds, however is constrained by nutrition and feeding, breeding and reproduction, diseases, climate change and underdeveloped infrastructure (Amole *et al.*, 2016; Bosman *et al.*, 2015; Mbindyo *et al.*, 2018; Ojango *et al.*, 2016).

Production and reproductive performances are considered as the essential pillars of economic viability of dairy operations (Bello *et al.,* 2012; Delgadillo & Martin, 2015). Reproductive performance is a major determinant of productivity and economic viability of goat farms (Mellado *et al.,* 2006). Most of the times however, the focus has been on the improvement of production traits and ignoring the reproductive performances. For instance, genetic selection has been concentrating on milk production at the expense of fertility traits in dairy cattle (Berry *et al.,* 2014; Butler, 2003; Pryce *et al.,* 2004). Despite the importance of reproduction in livestock breeding, much concern is still geared toward addressing issues affecting productive but not reproductive traits in dairy goats, especially in the tropics. Therefore, there is need to evaluate reproductive performance and adopt use of appropriate and effective reproductive technologies to contribute in the improvement programmes of dairy goats in the tropics.

Utilization of reproductive technologies such as artificial insemination and oestrous synchronisation could contribute significantly in the dairy goat improvement programmes. Artificial insemination (AI) has been shown to increase selection intensity, especially along the sire pathway and shortens genetic lag, while oestrous synchronisation concentrates the onset of induced oestrus and kidding, improve pregnancy and prolificacy rates (Kor *et al*., 2011). Long-term protocol with progestagens for oestrous synchronisation in goats, however, has been associated with low fertility rate (Pietroski *et al*., 2013) and therefore, short-term protocol could be an alternative. Short term protocol leads to high progesterone concentration and positively influence follicular turnover, increases the number of healthier young large follicles with the potential to ovulate and improve pregnancy rate (Menchaca & Rubianes, 2004). Therefore, adoption of short-term rather than long-term protocols have been suggested (Pietroski *et al*., 2013; Vilariño *et al*., 2011). Regardless of the synchronisation protocol adopted, AI leads to increased inbreeding levels due to use of a few superior males on entire populations (Zhang *et al*., 2015). The effect of inbreeding leads to impairment of growth, production, health, fertility and survival of animals (Van Wyk *et al*., 2009).

The negative effects of inbreeding can be counteracted by use of genomic selection. Genomic selection has been demonstrated to increase the rate of genetic gain and reduces inbreeding in different livestock species (de Roos *et al*., 2011; Forutan *et al*., 2018; Lillehammer *et al.*, 2011). It does that by more accurately capturing the Mendelian sampling variance than in the conventional method through reducing co-selection of relatives (Daetwyler *et al*., 2007). Incorporation of genomic information in selection programmes therefore, increases accuracy of selection, reduces generation interval and rate of inbreeding (Daetwyler *et al*., 2007; Liu *et al*., 2016; Van Grevenhof *et al*., 2012). Although genomic selection reduces inbreeding, mating design play a crucial role in determining the extent to which genomic selection could reduce inbreeding. Selecting appropriate mating designs reduce rates of inbreeding without compromising rates of genetic gain (Caballero *et al.,* 1996). These appropriate mating designs distribute genetic contributions of ancestors more equally across mating pairs, and this improves the genetic structures of breeding populations (Sonesson & Meuwissen, 2000). Accounting for reproductive technologies, genomic selection combined with certain mating designs, therefore, expected to increase response to selection and reduce rate of inbreeding in dairy goat breeding programmes.

1.2 Statement of the Problem

Low productive performance of indigenous goat breeds in the tropics has triggered importation of highly producing goat breeds in terms of milk and meat from the temperate areas. The exotic goat breeds, however, have low adaptability to the tropical environment, and this could affects their performance. This requires evaluation of both productive and reproductive performance to select those that can adapt well to the tropical environment. Improvement in performance of dairy goats however, is hampered by lack of proper selection and mating decisions especially, breeding soundness examination as well as low availability of breeding bucks, resulting in slow genetic progress. Use of natural mating allows superior bucks to serve only few females whereas adoption of reproductive technologies such as artificial insemination and oestrous synchronisation can increase the availability of breeding materials. The traditional long-term protocol for synchronisation of oestrus in goats, however, leads to low fertility, and therefore, short-term protocol should be evaluated as a potential alternative. In addition, the response to selection in dairy goat breeding programme incorporating reproductive technologies that have the potential to accelerate genetic gain to be evaluated. Moreover, the genetic gain and rate of inbreeding arising from using genomic selection also has not been evaluated.

1.3 Objectives

1.3.1 Broad Objective

To contribute to the improved performance of dairy goats through enhancement of their reproductive performance and response to selection using reproductive technologies and genomic selection in Kenya.

1.3.2 Specific Objectives

(i) To determine the effect of breed and age on testicular and semen characteristics of dairy goat bucks.

(ii) To determine the effect of oestrous synchronisation protocols and type of service on reproductive performance of dairy goats.

(iii) To estimate response to selection in conventional and alternative dairy goat breeding programme incorporating reproductive technology and genomic selection.

(iv) To estimate genetic gain and level of inbreeding in alternative dairy goats breeding programme utilising reproductive technology, genomic selection and different mating designs.

1.4 Research Questions

(i) What is the effect of breed and age on testicular and semen characteristics of dairy goats in Kenya?

(ii) What is the effect of oestrous synchronisation protocol and type of service on reproductive performance of dairy goats?

(iii) What is the response to selection in conventional and alternative following the incorporation of reproductive technology and genomic selection in dairy goat breeding programme?

(iv) What are the genetic gain and level of inbreeding in alternative dairy goat breeding programme utilizing reproductive technology, genomic selection and different mating designs?

1.5 Justification of the Study

Evaluation of reproductive performance would provide informed selection decision, thus leading to genetic improvement. This study provides information on the effectiveness of short-term progestagen protocol in synchronisation of oestrus and fertility in goats. Application of artificial insemination (AI) would be expected to reduce high cost of maintaining and importing breeding bucks as well as increase selection intensity and accuracy of estimated breeding values. Incorporating reproductive technology would accelerate genetic gain in breeding programmes through increasing selection intensity, reduction of generation interval, and dissemination of superior germplasm in the population. It also allow for import of semen from superior bucks with low cost compared to importing live animals and reduce cost of keeping many bucks in the farm. On the other, use of genomic selection and appropriate mating designs would counteract the negative impact associated with the use of artificial insemination such as increase rate of inbreeding.

CHAPTER TWO

LITERATURE REVIEW

2.1 Background

The contribution of livestock in reduction of poverty and malnutrition in sub-Saharan Africa is crucial. The main livestock species include cattle, sheep, goats and poultry, which provide milk, meat, hides and skin, and eggs. The population of livestock in sub-Saharan Africa is about 313.8 million cattle, 275 million sheep and 387.5 million goats (FAO, 2018). Among the sub-Saharan regions, East Africa region has a population of 54.4%, 34.2 % and 38.5 % cattle, sheep and goats, respectively (FAO, 2018). Kenya's livestock population is estimated to be 19.6 million cattle, 19.5 million sheep and 26.7 million goats (FAO, 2018). Out of the 26.7 million goats in Kenya, only 200,000 are dairy goats (Mbindyo *et al.,* 2018).

The Livestock sector in Kenya contributes about 12% of the growth domestic product (GDP), 40% of the agricultural GDP and employs 50% of the agricultural labour force (Ndeke *et al.,* 2015). Milk is the most important economic livestock product in Kenya, providing about 70% of the total gross value of livestock contribution to the agricultural sector, of which cattle and goats are the main contributors (Behnke & Muthami, 2011). Kenya is currently experiencing a growing demand for milk and dairy products driven by expanding urbanization and a rising middle class (Rademaker *et al.,* 2016). Therefore, goats especially, dairy goats as one of this agriculture sub-sector will play an increased role in improving the livelihood of the small-scale poor farmers and in the fight against food insecurity.

Goats play a significant role in the livelihood of rural population in developing countries (Kumar *et al*., 2011) especially in sub-Saharan Africa. They can be used as alternative to both beef and dairy cattle, especially by the resource-poor population for poverty reduction and improvement of family food security (Hegde, 2020). In the tropics especially in sub-Saharan Africa, dairy goats offer alternative for dairy cattle particularly in highly populated highland areas (Ahuya & Okeyo, 2006). Therefore, this chapter reviewed on the contribution of goats, their production and reproductive performance, genetic improvement and economic benefit through incorporation of reproductive technologies, genomic selection and mating designs in dairy goat breeding programme.

2.2 Contribution of Goats to Rural Population Livelihood

Goats play an important role in sustaining the livelihood of rural population in Africa, particularly in Sub-Sahara Africa of which Kenya is among them. They are kept for both

tangible benefits such as cash income, meat and milk (Hassen & Tesfaye, 2014) and intangible benefits such as insurance and cultural benefits (Tadesse *et al*., 2014). Goats are widely distributed in all types of ecological zones, mostly in the tropics and dry zones (Escareño, *et al*., 2013). They can survive well in drier tropics because of their ability to withstand dehydration and browsing habit (Desiere *et al.,* 2015). In Kenya, goats form an integral component of the livestock sector and is spread in all agro-ecological zones (Ndeke *et al*., 2015). Due to decreasing land sizes and increasing frequency of droughts, together with long-term environmental degradation, many farmers are resorting to keeping goats instead of cattle (Peacock, 2005).

2.3 Dairy Goats Sub-sector in Kenya

The dairy industry in Kenya is the most developed of the livestock sub-sectors and is comparatively among the largest in sub-Saharan Africa after South Africa (Wambugu *et al*., 2011). This sub-sector is dominated by small scale-farmers and plays an important role in the livelihoods of many farm households in rural areas of Kenya (Wambugu *et al*., 2011). Dairy provides about 70% of the total gross value of livestock contribution to the agricultural sector, of which cattle and goats are the primary contributors with 76.42 and 17 %, respectively (Behnke & Muthami, 2011). In terms of total milk per annum, cattle, sheep and goats, and camels produce 5.788, 1.293 and 0.553 billion litres of national total.

Although cattle produce large quantities of milk compared to goats, goats produce a relatively high milk yield per unit of live weight compared to cows (Atta *et al*., 2012). In Kenya, the demand of dairy goat milk is on rise because of the increasing human population and awareness of medicinal and nutritional value associated with goat milk, and also the special interest in goat milk products (Eik *et al.,* 2008; Mbindyo *et al*., 2018). Dairy goats are important source of milk with high nutritional and health benefit to humans (Kiura *et al*., 2013). Dairy goat production plays an important role in the improvement of income of the poor farmers, poverty, and hunger alleviation (Mbindyo *et al*., 2018). In Kenya dairy goats have been introduced as a poverty alleviation strategy and have increasingly become an important alternative to small-scale resource poor farmers who cannot afford dairy cattle (Ndeke *et al*., 2015). Dairy goat farming is emerging as a high-return option for Kenyan small-scale farmers (Mbindyo *et al*., 2018). This is because goats occupy small space, are easy to manage, require lower capital to acquire, are versatile feeder and have a high fecundity and short generation interval (Ndeke *et al*., 2015) and can be raised under a wide range of production systems (Amayi *et al*., 2016). Goats supply milk and meat as sources of animal protein for rural people

more than any other mammalian farm animal (Ivanović *et al*., 2016; Norris *et al.,* 2011). Their improvement for increased productivity is therefore important.

Improvement programmes are necessary to increase and sustain the productivity of dairy goats to improve livelihood of the ever increasing population (Kosgey *et al.,* 2008). Initiatives to improve livelihoods of the smallholder farmers in Kenya have centred on the use of exotic dairy goats, either for upgrading indigenous goats or as purebreds (Ogola *et al.,* 2010). The first importation of dairy goat breeds in Kenya dates back to mid-1950s, and this marks the beginning of dairy goat improvement programme in the country (Ahuye *et al.,* 2005; Ogola *et al.,* 2010). The improvement programme was initially spearheaded by the government but later on Non-Governmental Organisations joined hands with the government to continue in the improvement programme. These organisations include United Nations Development Programmes (UNDP) introduced in late 1970s and the German Development Corporation (GTZ) and FARM Africa project introduced in early 1990s (Ahuya *et al.,* 2005). The exotic goat breeds imported to Kenya are mainly Saanen, Toggenburg, Anglo Nubian, British and German Alpine (Ahuya & Okeyo, 2006; Ogola *et al.,* 2010; Ogola & Kosgey, 2012). Additionally, a dual purpose goat breed was developed called "The Kenya Dual Purpose goat" (KDPG), a four-way balanced synthetic breed from Small East African×Galla×Anglo-Nubian×Toggenburg breeds, was developed to improve performance under variable environmental conditions of low-input and low-output systems where multifunctionality, flexibility and resilience attributes are important (Bett *et al.,* 2007a; Madalena *et al.,* 2002; Scarpa *et al.,* 2003).

2.4 Nutritional and Health Benefits of Goat Milk

Chemically, milk is a complex oil-in-water emulsion containing proteins, fats, carbohydrates, and lower amounts of minerals, enzymes, cells, hormones, immunoglobulins, and vitamins (Lima *et al.,* 2018). Milk and dairy products from goats and sheep are very important for proper human nutrition, where cow milk is not readily available (Haenlein, 2001). The demand for goat milk is not only where cow milk is not available but also due to its high nutritional quality and health benefits (Clark & Mora García, 2017; Haenlein, 2004; Lopez-Aliaga *et al*., 2010; Prosser, 2021).

Nutritional Composition of Goat Milk

The physical characteristics and composition of milk vary between species. Goat milk is becoming of special interest in manufacturing food products of infants, elderly and those with special needs due to its specific composition (Ceballos *et al.,* 2009; Haenlein, 2004; Park,

2006). Goat milk composition in terms of protein, fat and mineral have been demonstrated to be higher compared to cow and human milk (Banjare *et al.,* 2017; Ceballos *et al.,* 2009; Rafiq *et al.,* 2016).

Proteins

Milk proteins are broadly divided into insoluble proteins (the casein family) and soluble proteins (whey proteins) found in lactoserum (Selvaggi *et al.,* 2014). Caseins are the major protein fraction of milk, they transport calcium phosphate in milk and thus play crucial role in bone formation and as well contribute to the requirement for amino acids (Stewart *et al.,* 1987). Whey proteins are globular molecules with a substantial content of a-helix motifs contain no phosphorus and are characterized by a high content of sulfur-containing amino acids, mainly methionine and cystine (Selvaggi *et al.,* 2014). Dairy products are a reliable source of high quality proteins, which are well balanced in amino acids (Raynal-Ljutovac *et al.,* 2008). Additionally, total protein in milk is one of the main quality criteria used to goat milk payment in many countries (Pirisi *et al*., 2007; RaynalLjutovac *et al*., 2005).

Fat

Fat content is the more variable component of milk, it changes depending on season, lactation stage, breed, genotype and feeding (Bernard *et al.,* 2009; Lima *et al.,* 2018; Nudda *et al.,* 2003). Goat milk is generally higher in medium chain, monounsaturated and polyunsaturated fatty acids (Haelein, 2017).

Carbohydrate

The main carbohydrate in milk is lactose. It is lower in goat milk compared to cow milk (Silanikove *et al.,* 2010) and synthesized in the mammary gland from glucose and galactose, where the milk protein α-lactalbumin plays an important role (Kunz *et al.,* 2000). Lactose help in intestinal absorption of calcium, magnesium and phosphorous and the utilization of vitamin D (Lad *et al.,* 2017; Schaafsma, 2008). In addition to lactose, goat milk contained other carbohydrates in small quantities such as oligosaccharides, glycopeptides, glycoproteins and nucleotides (Lad *et al.,* 2017).

Minerals and Vitamins Composition

Goat milk plays vital role of supplying minerals to people, especially where cow milk is not available. Goat milk has higher content in calcium, phosphorous, chloride, magnesium and copper compared to cow milk (Ceballos *et al.,* 2009; Krstanovic *et al.,* 2010; Lopez-Aliaga *et al.,* 2005; Turkmen, 2017). Goat milk is rich in vitamin A, thiamine, riboflavin, and niacin (Barłowska *et al.,* 2011; López-Aliaga *et al.,* 2010; Park *et al.,* 2007) with low levels of vitamin B12, vitamin E, vitamin C and vitamin D (Park *et al.,* 2007; Raynal-Ljutovac *et al.,* 2008).

Health Benefits Associated with Goat Milk

Cow milk has been associated with allergy in infants with a prevalence of about 2.5% during the first three years of life (Vita *et al.*, 2007). The easy digestibility of goat milk, its fatty acid composition, and the presence of various bioactive compounds in its constitution make goat milk potentially helpful in the treatment or even the prevention of certain medical conditions (Kompan & Komprej, 2012; Lima *et al.*, 2018; Yadav *et al.*, 2016). Habitual goat milk consumption improves mineral metabolism and increases levels of the biomarker of bone formation, which positively affects bone mineralization and turnover (Diaz-Castro *et al*., 2017). Goat milk is important in human health due to its cardiovascular benefits associated to higher content in medium chain, monounsaturated and polyunsaturated fatty acids (Haelein, 2017). Additionally, medium chain fatty acids have been found to reduce Very-Low-Density Lipoprotein lipolysis and uptake rates (Schalkwijk *et al.*, 2014). Studies have found anti-intestinal inflammatory potential of goat milk oligosaccharides in a rat model (Lara- Daddaoua *et al.*, 2006; Villoslada *et al.*, 2006). Goat milk has been reported to contain antioxidant components (Mal *et al.*, 2018). Fermented goat milk is indicated to play role in the prevention of cardiovascular diseases associated with oxidative stress and hypertension (Jirillo *et al.*, 2010; Moreno-Montoro *et al.*, 2017). This has been associated to highest total antioxidant capacity against certain radicals and some antimicrobial activity against *Escherichia coli* observed in fermented milk containing the probiotic (Ahmed *et al.*, 2015; Kerasioti *et al.*, 2016; Moreno-Montoro *et al.*, 2017). Moreover, medium-chain fatty acids (caproic, caprilic and capric acid) in goat milk reduce cholesterol by restricting its deposition and improving mobilization in tissues (Mal *et al.*, 2018; Pal *et al.*, 2017).

2.5 Factors Affecting Composition of Goat Milk

Milk composition is influenced by factors such as feed, season, breed, feeding managements, environment, stage of lactation and parity (Goetsch *et al.*, 2011; Kondyli *et al.*, 2007, 2012; Lad *et al.*, 2017; Raynal-Ljutovac *et al.*, 2008).

Nutrition and Feeding Management

The type of feed influences milk yield and composition as well as yield and quality of products (Bencini & Pulina, 1997). Differences have been observed between goats grazing on cultivated pasture and rangelands (Steinshamn *et al.*, 2014). Goats grazing on cultivated pasture have been found to have high protein and lactose content compared to those grazing on

woodland rangeland. Contrarily, goats grazing on woodland rangelands had higher fat content compared to those grazing on cultivated pasture (Steinshamn *et al.,* 2014).

Breed

Breed of goat has been shown to have an influence in milk composition (Hadaya *et al.,* 2017; Soryal *et al*., 2005; Trancoso *et al.,* 2010). The variability in milk composition can also be among individuals of the same breed, due to complex genetic polymorphism of the goat milk caseins (Lima *et al.,* 2018). Alpine goats recorded higher protein and lactose content at the start of lactation period compared to Saanen goats (Antunac *et al.,* 2001). Nubian goats milk has significantly higher fat, total protein, casein and total solids than that of Alpine goats (Soryal *et al.,* 2005). Breed also significantly affected omega 6 and omega 3 ratio in the Damascus x Alpine, Mamber x Alpine and Maber goats milk (Hadaya *et al.,* 2017). Breed of goats affected milk protein, lactose and fatty acids content with exception of fat content (Currò *et al.,* 2019; Lobo *et al.,* 2017). Breed of goats, however, has no effect on lactose content (Lobo *et al.,* 2017).

Parity and Stage of Lactation

Parity and stage of lactation affect both milk yield and composition in goats. The fat and protein content were influenced by the parity, where the first parity was significantly higher compared to the other parities (Carnicella *et al.,* 2008). Similarly, first and second parities were significantly higher in terms of lactose content in comparison to the third and fourth parities. Conversely, parity did not influence milk fat and protein contents of dairy goats (Vacca *et al.,* 2018). Stage of lactation also has been reported to affect milk composition (Currò *et al.,* 2019; Lôbo *et al.,* 2017; Strzałkowska *et al.,* 2009). Higher fat (4.53%) and protein (3.34%) were recorded at the end of lactation, whereas lower values 3.46% and 2.86% were recorded at the peak of lactation, respectively (Currò *et al.,* 2019). Kljajevic *et al.* (2018) observed significant differences among different stages of lactations on protein, fat and lactose content in goat milk. These authors reported similar trend in protein, fat and lactose content with high values during late lactation, followed by early lactation and finally mid-lactation.

Season

Previous studies have reported effect of season on goat milk composition (Midau *et al.,* 2010; Salari *et al.,* 2016). Lactose content in milk was significantly higher in spring than in summer but protein and fat content were not influenced season (Salari *et al.,* 2016). Solid non-fat content was significantly higher in dry compared to wet season and the opposite is true for calcium (Midau *et al.,* 2010). Total proteins in milk were significantly higher in late grazing season compared to early grazing season in goats (Inglingstad *et al.,* 2014).

2.6 Goat Milk Products

Milk and dairy products have always been acknowledged as an important part of human diet both in developing as well as developed nations of the world (Pal *et al.,* 2017). The nutritional and health benefits associated with consumption of goat milk have led to increased demand and consumption of goat milk products (Nguyen *et al.,* 2018). Goat milk products include soft and hard cheeses, fermented milk, yogurt, butter and butter oil, ice cream, beverage, Ghee, whey, dry whole milk, dried granulated milk, maize meal with goat milk, condensed goat milk, fruit yogurt and cultured goat cream butter (Mattiello *et al.,* 2018; Pandya & Ghodke, 2007; Park & Guo 2006ab; Ribeiro &. Ribeiro, 2010; Sagdc *et al.,* 2004). In addition, yogurt from goat milk can be mixed with some fruits or plants to improve its sensory characteristics (Costa *et al.,* 2017; Mangia *et al.,* 2014; Ranadheera *et al.,* 2012). Apart from edible products, Goat milk can be used for making lotions and creams because its fat contains capric and caprylic acids which enhance permeability in skin (Mahjour *et al*., 1993; Wongpayapkul *et al*., 2006). Recently a high volume of cosmetic products are produced from goat milk, including soaps, creams, body lotions, shampoos, hair conditioners (Ribeiro &. Ribeiro, 2010).

In Africa, goat milk products commonly consumed include fresh cheese (Iwuoha & Eke, 1996), ripened cheese (Zitoun *et al*., 2012), fermented milk (Benkerroum, 2013; Salih *et al.,* 2011) and butter (Abdelgadir *et al.,* 1998; Salih *et al.,* 2011). In Europe, especially in France there is a well-established market for cheese made from goat milk (Dubeuf *et al.,* 2004). In the United States of America, soft cheeses made up the majority of the goat milk utilization, followed by fluid milk, hard cheeses, and other products (Milani & Wendorff, 2011).

2.7 Goat Production Performance

Performance evaluation is an important aspect in livestock breeding programme. This mainly include production and reproduction performance. Different dairy goat breeds have been introduced in various parts of Kenya with different agro-ecological zones and production systems. These differences in breed, climate and production systems could influence productivity of the exotic dairy goats. Several studies were undertaken to evaluate performance parameters of these dairy goats (Ahuye *et al.,* 2003a, 2009; Bett *et al.,* 2007b; Monica *et al.,* 2014). The birth weight were 3.6, 3.2, 3.5 Kg, weaning weight were 15.3, 12.7, 12.5 Kg and average daily gain were 127, 105 and 104 Kg in 75 % Toggenburg, Toggenburg x Small East African (F1) and Toggenburg, respectively (Ahuye *et al.,* 2003b). In terms of milk production, Ahuye *et al.* (2009) reported an average daily milk yield of 1.3 Kgs in Toggenburg goats. In

another study, daily milk production was 2.6, 2.4 and 1.8 Kgs in 75 % Toggenburg, Toggenburg x Small East African (F1) and Toggenburg, respectively (Ahuye *et al.,* 2003b). Lactation length and lactation yields of 295, 316, 205, 531, 486 and 378 for 75 % Toggenburg, Toggenburg x Small East African (F1) and Toggenburg, respectively (Ahuye *et al.,* 2003). In Alpine goats, milk production was 1.54, 1.25, 1.64, 1.93 and 2.18 Kgs in local, foundation, intermediate, appendix and pedigree, respectively (Monica *et al.,* 2014). Production system also affected daily milk yield which has been reported to be 0.60, 1.30 and 2.00 Kgs for smallholder low, medium and high potential production system, respectively (Bett *et al.,* 2007b).

2.8 Factors Affecting Dairy Goat Production Performance

Dairy goat production in Kenya like any other country in sub-Saharan Africa, is influenced by a number of factors. Farming systems in these areas have evolved to cope with the formidable constraints imposed by harsh natural and economic conditions by adapting integrated crop/livestock production strategies (Escareño *et al.,* 2013). These factors include production system, breeding, Nutrition, market, diseases and security (Mbindyo *et al.,* 2018; Leroy *et al.,* 2016).

Production System: Livestock production system is defined as the farming system of interest for the study of livestock and livestock development (Otte & Chilonda, 2003). Definition of production system is one of the core important component of animal breeding goal. Knowledge on the production system is vital for understanding adaptive traits of livestock species (Otte & Chilonda, 2003). The animal production systems could be classified based on the type of resource used, on the intensity of the use of the resources, on the type of producer (nomadic, sedentary), or based on the product generated (Escareño *et al.,* 2013). Generally, goat production system is classified into extensive, semi-intensive and intensive systems (Escareño *et al.,* 2013; Peacock & Sherman, 2005). Under extensive system, goats graze freely with or without supervision on natural vegetation, typically in areas with relatively low rainfall with no external inputs. In the intensive system, animals are not allowed to graze freely and provided feeds inside their stalls. Under the semi-intensive system, animals are can graze and provided with supplementary feeding. These different types of production system could affects the performance of animals. For example, grass feeding normally results in slower growth rates due to absence of concentrate feeds and feed supplements (Webb & Erasmus, 2013). Production system also influences the quantity and composition of milk produced (Galina *et*

al., 2007; Goetsch *et al.,* 2011; Rúa *et al.,* 2017) and quality of meat (Bruce *et al.,* 2004; Frylinck *et al.,* 2013; Mancini & Hunt, 2005).

Breeding strategy: Breeding strategy refer to different ways of using parental generation (s) to generate animals of desired types (Philipsson *et al.,* 2006). Breeding strategy plays important role in livestock genetic improvement, which in turn could influence productivity. A proper breeding strategy is crucial to address both short- and long-term concerns to maintain its overall objectives, and this should state clearly whether the programme seeks to have only a pure breed, crossbreed or synthetic breed, and for which environment (Ahuya *et al.,* 2005; Ogola & Kosgey, 2012). Livestock genetic improvement is conventionally considered under the three main pathways: (i) selection between breeds, (ii) crossbreeding, and (iii) selection within breeds (Baker & Gray, 2003; Kosgey *et al.,* 2006). Majority of livestock farmers in the tropics used to commonly improve their animals genetically using within breed selection before the start of importation of exotic breeds from the temperate regions. Currently, livestock improvement in the tropics is mainly based crossbreeding of local and imported breeds. This cross breeding strategy, however, has not been successful due to improper planning (Ayalew *et al*., 2003; Kosgey *et al.,* 2006; Ogola & Kosgey, 2012) such as animosity of the genotypes with the breeding objectives and management systems (Ayalew *et al.,* 2003; Rewe *et al.,* 2002). There is need to first select the most appropriate breed or cross, and whether they can be improved further by within breed selection for successful breeding strategy (Kosgey *et al.,* 2006). Matching genotype by environment is another aspect of successful breeding strategy (Ahuya *et al.,* 2005; Bett *et al.,* 2009).

Nutrition: Seasonal fluctuation in rainfall and temperature influences the animal productivity. These seasonal effects although are experienced across all the production systems, however, it largely affects extensive and semi-intensive systems because of their reliance on natural pastures. Pastures are abundant with good nutritional quality during rainy season whereas in dry season they are insufficient with low nutritional quality (Evitayani *et al.,* 2004; Perry *et al.,* 2017). This leads to seasonal weight loss of between 20-40% at the onset of the dry season due to lack of feed supplementation during the dry season in extensive or traditional management systems in the tropics (Lamy *et al,* 2012). These seasonal weight loss affects growth (Almeida *et al.* 2006a; Kilminster *et al.* 2008) carcass quality (Almeida *et al.* 2006b; Scanlon *et al.* 2008; van Harten & Cardoso 2010) and reproduction (Almeida *et al.,* 2007; Carvalho *et al.,* 2009). The dietary concentrate level and nature of specific concentrate and forage feedstuffs influence milk production and characteristics of milk and milk products

(Álvarez *et al.*, 2007; Goetsch *et al.*, 2011). Feeding goats with different concentrate levels also affects milk yield and health (Morand-Fehr *et al.*, 2007; Tufarelli *et al.*, 2009).

Diseases: Disease is one of the major constraint affecting livestock improvement because it negatively affects production and productivity, especially in the tropics (Mwacharo & Drucker, 2005). Diseases affects all the age groups of goat and their high prevalence post a major challenge in goat production sub-sector (Tsegaye *et al.*, 2013). Average annual mortality rates in goats stand at around 10-20%, but can reach over 50% during poor seasons and disease epidemics (Mayberry *et al.*, 2018; Singh *et al.*, 2009). The common diseases affecting goats include Pneumonia, Diarrhoea, Mastitis, internal worms, Pasteurellosis, Anthrax, Dystocia, skin infection, pest des petits ruminants, orf and foot rot (Alemu *et al.*, 2019; Gizaw *et al.*, 2010; Mbindyo *et al.*, 2018; Tsegaye *et al.*, 2013). These diseases could cause negative influence on the performance of goats. Helminthes, for instance, reduces body weight and body condition in goats (Gwaze *et al.*, 2009). Additionally, pneumonia and diarrhoea were reported to cause high kids mortality (Donklin & Boyazoglu, 2004; Mbindyo *et al.*, 2018; Ramachadran *et al.*, 2006). These losses due to diseases, however, could be reduce through appropriate intervention measures. For instance, it was reported that goat mortality rates was reduced through use of better healthcare and disease management practices (Mayberry *et al.*, 2018).

Genotype by Environment Interaction Effect in Livestock: Genotype by environment interaction is a phenomenon that occurs when the relative phenotypic performance of a pair or a set of genotypes is conditioned by the environment (Bustos-Korts *et al.*, 2018). It implies that different genotypes will respond differentially to environmental changes, possibly leading to re-rankings of performance in different environments (Cardoso *et al.*, 2010; Falconer & Mackay, 1996; Lynch & Walsh, 1998). This can be interpreted that the superior animals in a given environment will not necessarily be superior in a different environment (Cardoso *et al.*, 2010). Although animals well adapted in heterogeneous environmental conditions and high performance are preferred, no single genotype can meet all these conditions and thus genotype by environment interaction is an important factor of any strategy for livestock production programmes (Buxadera & Mandonnet, 2006). Several studies have reported effect of genotype by environment in goats (Baker & Gray, 2004; Gaddour *et al.*, 2008) and other livestock species (Gourdine *et al.*, 2019; Muasya *et al.*, 2014; Wahinya *et al.*, 2020).

Market: Generally, there is a demand for goat products whether in local or export markets (Kocho *et al.*, 2011; Lamesegn, 2018). Market access and obtaining good profit margins, however, are the major challenge for low-input livestock farmers in developing countries, particularly Africa (Regge *et al.*, 2011). These are attributed to factors such as abuse

by brokers, lack of price information, access to incentive markets, poor market infrastructure and seasonality of markets (Kocho *et al.,* 2011; Marcum *et al.,* 2013; Regge *et al.,* 2011). These market challenges faced by livestock farmers could be alleviated through market standardization to improve market efficiency and profitability (Juma *et al.,* 2010; Kocho *et al.,* 2011; Musemwa *et al.,* 2007).

Socio-cultural Factors: Social-cultural practices can have either positive or negative influence on production and productivity of livestock. Livestock production and consumption of their products largely depends on cultural habits of various cultural groups. Some of the positive socio-cultural practices promoting livestock production include payment of dowry, religious and prestige (Dossa *et al.,* 2015; Nguluma *et al.,* 2020; Onzima *et al.,* 2018). On the other hand, the negative socio-cultural practices hindering livestock production for instance, are that in certain communities, youth shuns from rearing of small ruminants (Kipserem *et al.,* 2011), while in other communities women do the rearing and men do the decision making (Kinati *et al.,* 2018). In India, goat meat constitutes about 47% of the total meat consumed, since the eating of beef is taboo (Dubeuf, 2005).

2.9 Reproductive Performance in Goats

Reproduction plays central role in determining production efficiency and in genetic selection (Hansen, 2014). One of the main traits determining productivity in goats is reproductive efficiency. Reproductive performance in both male and female is very crucial, more especially in males. It is therefore, important to evaluate or assess the reproductive performance of the breeding male before mating to increase chances of high fertility rate. This makes breeding soundness examination an important tool for selecting best breeding male animal in a herd (Kennedy *et al*., 2002). Main male fertility parameters include scrotal measurements and semen characteristics. These traits can be influenced by nutrition, genotype, season and management (Bielli *et al*., 2000; Karagiannidis *et al*., 2000).

Regulation of Reproduction

Reproduction in farm animals is generally regulated by nervous and the endocrine system (Senger, 2003). These two systems work together to initiate, coordinate and regulate reproduction. Nervous system translate or transduce external stimuli into neural signals that cause change in the reproductive organs or tissues. Contrary to the neural regulation, the endocrine system depends on hormones to cause their responses. A hormone is a substance produced by a gland to acts on a remote tissue to cause change in the target tissue. Reproductive

hormones are majorly control through positive and negative feedback mechanism. These two feedback mechanisms almost control all the reproductive functions.

Puberty in Male Goats

Farm animals cannot start reproduction without reaching puberty age. Therefore, information about the onset of puberty and sexual maturation are important for good reproductive management of domestic animals (Nishimura *et al.,* 2000). Puberty can be defined as the first mount and/or ejaculation with the release of sperm in males (Delgadillo *et al.,* 2007). This period of sexual maturity can exert an important influence on the reproductive efficiency of an individual (Ahmad & Noakes, 1996). It is regulated by interactions between pituitary gonadotropins and the gonadal steroid testosterone in the male (Chakraborty *et al.,* 1989). Puberty can be influenced by several factors such as age, weight, photoperiod and breed (Delgadillo *et al.,* 2007; Deveson *et al.,* 1992; Vilakazi & Webb, 2003).

Puberty in Does

Puberty in females is defined as the age at the first expressed oestrus with ovulation but not considered sexual maturity (Bearden, 2004). The onset of puberty in does varies from 4 to 8 months and is influenced by breed, the month of birth and the presence of a male (Lea & England, 2016). Puberty can be defined as the first ovulation and/or first oestrous behaviour in females and the first mount (Delgadillo *et al.,* 2007). During the pre-pubertal age, the young female animal does not exhibit cyclic periods of sexual receptivity. Puberty is initiated by the gonadotropin releasing hormone (GnRH). As puberty approaches, pulsatile discharges of GnRH increase in frequency leading to release of high gonadotropins (follicle stimulating hormone (FSH) and luteinizing hormone (LH)) which subsequently initiate follicle growth, oocyte maturation and ovulation (Bearden, 2004).

Oestrous cycle in does

Oestrous cycle is defined as the time between periods of oestrus. In doe, oestrus period is about 21 days, however, there is individual and breed variation. This period is divided into four phases; Meteoestrus, Dioestrus, Proestrus and Oestrus.

***Pro-oestrus*:** The phase immediately preceding oestrus. It is characterised by a marked increase in activity of the reproductive system. There is follicular growth and regression of the corpus luteum of the previous cycle (in polycyclic species).

Oestrus: The period of acceptance of the male. The onset and end of the phase are the only accurately measurable points in the oestrous cycle, and hence are used as the baseline for determining cycle length. Ovulation occurs during this phase of the cycle in all domestic species with the exception of the cow, where it occurs about 12 hours after the end of oestrus.

Pro-oestrus: During this period and oestrus there is follicular growth in the absence of functional corpora lutea, the main ovarian hormones produced being oestrogens. Pro-oestrus and oestrus are frequently referred to collectively as the follicular phase of the cycle.

Dioestrus: The period of the corpus luteum. The uterine glands undergo hyperplasia and hypertrophy, the cervix becomes constricted and the secretions of the genital tract are scant and sticky; the vaginal mucosa becomes pale. The corpus luteum is fully functional during this phase, and is secreting large amounts of progesterone. The period of the oestrous cycle when there is a functional corpus luteum is sometimes referred to as the luteal phase of the cycle.

2.10 Factors Affecting Reproductive Performance in Goats

There are several factors which affect the reproductive performance in goats. These factors include breed, season, age, physiological status, nutrition and management system. These factors influence body weight, body linear measurements, scrotal circumference, testicular measurements and epididymal weight and semen characteristics in bucks (Agga *et al.*, 2011; Mekasha *et al.*, 2007).

Breed: Breed influences the reproductive performance of goats. Different breeds of bucks differ in their body weight, scrotal circumference, epididymal weight, and testicular biometry (Gemeda & Workalemahu, 2017; Maina *et al.*, 2006). Another study also observed that breed affects semen volume, sperm concentration, motile spermatozoa, progressive motility and abnormal morphology (Karagiannidis *et al.*, 2000). It has been proven that heavier breeds tend to have high body weight and testicular circumference compared lighter breeds (Belibasaki & Kouimtzis, 2000). Moreover, ejaculate volume, appearance and semen characteristics were influenced by breed (Mellado, 2016). Scrotal and semen characteristics of different goat breeds are presented in Table 2.1.

Season: Several studies have indicated effect of season on semen characteristics (Golher *et al.*, 2018; Maina *et al*., 2006; Mia *et al.*, 2013). Maina *et al*. (2006) reported that semen motility, sperm concentration, sperm abnormalities and percentage of live sperm were influenced by season, where dry season shown better than wet season (Maina *et al*., 2006). It has also been reported that the volume of ejaculates, sperm concentration, percentage of motile cells and sperm vigour are not influenced by season, but the number of sperm with normal morphology decreased in dry season (Aguiar *et al*., 2013).

Table 2. 1 Scrotal circumference and semen characteristics of selected goat breeds

Breed	**Scrotal circumference (cm)**	**Volume (ml)**	**Sperm concentration (10^6/ml)**	**Sperm Motility (%)**	**% Live sperm**	**Source**
Saanen	26.5–27.4	0.7–1.0	2780–3240	90	82–85	
Alpine	25.4–30.1	0.6–1.4	2115–3300	67–87	90	
Toggenburg	26.3	1.0–1.8	1989–2425	75–81	-	
Nubian	26.1–28.5	1.1–1.5	1770–2650	82	82	
Damascus	32.1	1.1	4519	67	-	
Zaraibi	25.9	0.8–0.98	3056–5072	65–79	82	
Majorera	26.0	1.8–2.01	3480	-	-	Mellado (2016)
Black Bengal	22.9	0.58–0.68	2797–3004	78	84–87	
Alpine	-	1.27	3610	59.88	-	
Saanen	-	1.15	3630	64.40	-	Karagiannidis *et al.* (2000)
Damascus goat	-	1.09	3690	65.14	-	
Mountain Black	-	1.21	2621	71.6	-	Kridli *et al.* (2005)
Cross Black x Damascus	-	0.88	4001	78.3	-	

Age: Body measurements, testicular traits, semen quality and quantity characteristics in farm animals are affected by age (Kabiraj *et al.*, 2011; Mahal *et al.*, 2013; Mia *et al.*, 2013). Mature bucks have been demonstrated to have heavy body weight, large scrotal circumference, higher sperm concentration, viable sperm concentration and ejaculate volume, less percentage of abnormal sperm compared to yearlings (Al-ghalban *et al.*, 2004; Mahal *et al.*, 2013; Mia *et al.*, 2013). Increase in age and body weight was associated with increase in testicular measurements in goats (Kabiraj *et al.*, 2011). Scrotal circumference strongly correlated with

age and body weight (Mukasa-Mugerwa & Ezaz, 1992). Age of bucks influences body weight and testicular measurements (Ajani *et al*., 2015; Koyuncu *et al*., 2005; Kridli *et al*., 2005) without influencing semen characteristics (Kridli *et al*., 2005). Some studies that have evaluated influence of age on scrotal and semen characteristics are presented in Table 2.2.

Table 2. 2 Scrotal and semen characteristics as affected by age in bucks

Age	**SV(ml)**	**SC (10^6)**	**MM (%)**	**LS (%)**	**NM (%)**	**Source**
9-12m	0.46	2420	79.67	88.00	91.30	Mia *et al.* (2013)
> 12-24m	0.55	2520	79.82	86.52	90.43	
> 24-36m	0.72	2760	79.56	85.11	88.70	
Yearling	0.89	2686	80.20	-	-	Kridli *et al.* (2005)
Adult	1.53	2557	62.90	-	-	
yearling	0.94	2926	63.00	-	-	Al-Ghalban *et al.*
Adult	1.13	4519	67.00	-	-	(2004)
7-9	0.40	2300	78.70	88.0	87.20	Mahal *et al.* 2013)
>9-12	0.54	2600	79.60	85.2	89.20	

*SV: semen volume, SC: semen concentration, MM: mass motility, LS: live spermatozoa, NM: normal spermatozoa

Nutrition: Reproductive performance of farm animals is largely dependent on their nutritional status (Kheradmand *et al*., 2006). Nutrition greatly affects testicular mass and in turn seminiferous tissue amounts and spermatogenic capacity in sheep and goats (Martin *et al*., 2010). Nutrition improves sperm morphology by maintaining the secretion of gonadotropins, hence the function of the testicles and the male genital tract (Martin *et al*., 2010). Nutritional supplementation improves the body weight, scrotal circumference, scrotal thickness, total scrotal weight and normal sperm cells but not sperm concentration (Almeida *et al*., 2007). Restricted feeding of goats had no effect on semen volume and sperm concentration (Wiyidono *et al*., 2017). Bucks supplemented with Guava leaves had higher scrotal circumference and scrotal length compared to those fed a control feed of Gamba and guinea grasses (Abu *et al*., 2016).

Management System: Management system can affect reproductive performance of animals. In a study by Fourie *et al*. (2004) comparing between extensive and intensive system, they found that semen colour, semen concentration, mass motility and progressive motility in favour of extensive system with exception to scrotal circumference. However, no differences were recorded in semen volume, semen pH, percentage of normal sperm, percentage of live spermatozoa and percentage of semen abnormalities. On contrary, with regards to semen abnormality, it has been reported that head, mid-piece, tail and total abnormality are higher in semen of grazing system bucks as compared to stall feeding bucks (Ramachandran & Singh, 2017). The higher sperm abnormality in the semen of grazing system bucks has been attributed to higher energy expenditure during grazing which could have led to lower nutrient availability for supply of the nutrients required for sperm production in testis and epididymal sperm maturation (Ramachandran & Singh, 2017).

Animal Effect: This is one of the factors that affects scrotal and semen characteristics of bucks. Selecting breeding bucks based on individual performance is paramount in ensuring good herd fertility. Within the same breed, individual buck has been reported to affect both the scrotal and semen characteristics. The individual variation among bucks in semen characteristics makes it necessary to perform semen evaluations on an individual basis in order to select the best males for breeding and thus optimizing reproductive performance (Karagiannidis *et al.,* 2000). Semen volume, mass motility and live sperm were influenced by individual buck effect (Sultana *et al.,* 2013). In a similar study by Sultanan *et al.* (2013), sperm concentration and normal sperm were not affected by individual variation of bucks. In another study by Pradhan *et al.* (2013), differences were recorded in semen volume and sperm concentration, however, no differences were recorded in terms of mass and progressive motility, and percentage of normal sperm. Moreover, buck effect did not affect semen volume, concentration, progressive motility and colour except mass activity (Juma, 2017).

2.11 Reproductive Technologies in Goats

Reproduction in domestic animals is under control of man and the technologies developed to facilitate that control have a major impact on the efficiency of food production (Hansen, 2014). These technologies include; artificial insemination (AI), oestrous synchronisation, multiple ovulation and embryo transfer (MOET), cryopreservation of gametes or embryos and in vitro embryo production (IVEP) applied to the multiplication of superior animals (Garcia *et al*., 2013; Gelayenew & Asebe, 2016). The application of reproductive techniques plays a major impact on the structure of breeding programmes, the rate of genetic

gain and the dissemination of superior genetic materials in the production (van Arendonk, 2011).

Artificial Insemination

Artificial insemination (AI) is the most widely used method of reproductive technologies. It enables the production of a very large number of offspring from a single elite sire and thus, play an important role in dissemination of superior genetic materials. In goat breeding, it plays an important role, especially in intensive production system, controlling reproduction to ensure production of milk and other products (Paramio & Izquierdo, 2014). The AI in goats can be done using either liquid or frozen semen, with liquid semen having higher pregnancy rate than frozen semen.

Oestrous Synchronisation

Oestrous synchronisation enhances the application of AI by bringing animals into heat more or less at the same time. There are many methods for synchronising oestrus in goats. They include use of progestagens, prostaglandins, melatonin and male effect or in combination with co-treatments. However, progestagens are among the widely used protocol for oestrous synchronisation in goats. In sheep and goats, long-term (12 to 14 d) progestagen treatments are widely used to induce and synchronize oestrus (Vinoles *et al*., 2001). Long-term progestagen treatments normally from 12 to 18 days is the most widely used protocol in small ruminants (Diskin *et al*., 2002; Vinoles *et al*., 2001). Short-term progestagen treatments is between 5 and 9 days (Pietroski *et al.*, 2013). The short term treatments sought to replace the long-term progestagen treatments that has been associated with low fertility problems. Short-term is associated with effective synchronisation of oestrus and high pregnancy rates (Souza *et al*., 2011; Vilariño *et al*., 2011; Vinoles *et al*., 2001). Significant differences exist between short-term and long-term progestagen treatments with respect to response to oestrus but fertility rate was better in short-term synchronisation treatment in ewes (Karaca *et al*., 2009). In another study, the response to oestrus, onset of oestrus and pregnancy rate were similar between short-term and long-term progestagen treatments except for the duration of oestrus (Ustuner *et al*., 2007). The response to oestrus, duration of oestrus and pregnancy rate were similar in goats treated using progestagen treatment days 6, 9, 11 and 13 (Dogan *et al*., 2016). However, the onset of oestrus was shorter for 13, 11 and 6 days compared to 9 days.

2.12 Factors Affecting Artificial Insemination in Goats

Goat artificial insemination programme is influenced by a number of factors. These factors range from animal and environmental effects.

Semen Preservation: Preservation of goat semen, especially for long term storage is a major challenge. This is because goat semen contains an enzyme called phospholipase A, secreted by the bulbo-urethral gland which interacts with egg yolk lipids or skim milk triglycerides (Pellicer-Rubio *et al.,* 1997, 1998; Sias *et al.,* 2005). The enzyme transforms phosphatidylcholines of egg yolk into lysolecithin, a toxic compound for spermatozoa, and interacts with milk proteins, such as caseins and lactoglobulin which causes deterioration of spermatozoa (Leboeuf *et al.,* 1998; Paramio & Izquierdo, 2014). Because of this, so far, there is no generally accepted optimum cryopreservation protocol for goat semen (Roof *et al.,* 2012), and this causes a problem for goat germplasm banking programme (Purdy, 2006).

Semen Deposition: Goat cervical folds or rings make passage of the insemination catheter into the uterus difficult (Paramio & Izquierdo, 2014). This can influence the movement of semen along the reproductive tract. Previous studies have reported direct correlation between depth of semen deposition and fertility (Arrebola *et al.,* 2012; Barbosa *et al.,* 2009; Salvador *et al.,* 2005). These authors noted that pregnancy increases with increased depth of semen deposition. Arrebola *et al.* (2012) observed pregnancy rate of 48 and 64 % with cervical and uterine semen deposition, respectively.

2.13 Fertility with Natural Mating and Artificial Insemination in Goats

Natural mating yields high fertility rate compared to artificial insemination (Agossou & Koluman, 2018). However, in terms of progenies produce per sire, artificial insemination surpasses natural mating. Therefore, artificial insemination is widely promoted because of its advantages over natural mating, especially in genetic improvement programmes. There are several factors affecting artificial insemination such as nutrition, breeding season, environmental conditions, parity, breed, farm, depth of semen deposition, extender composition, hormone treatment and storage time (Salvador *et al*., 2005). All these factors can affect conception rate/ kidding rate in goats artificially inseminated. The type of semen used for insemination play a crucial role in determining the conception rate. Several studies have found that cooled semen gives better results compared to frozen-thawed semen (Arrebola *et al*., 2012). Fertility studies using different mating methods are summarised in Table 2.3.

Table 2. 3 Fertility results from studies using artificial and natural mating in goats

Type of Mating	Type of semen	Fertility rate	Source
Artificial insemination	Fresh	90	Andreea *et al.* (2016)
Artificial insemination	Fresh	75-85	Luo *et al.* (2019)
Artificial insemination	Fresh	86	Paulenz *et al.* (2005)
Artificial insemination	Fresh	81 in sheep	Fornazari *et al.* (2018)
Artificial insemination	Fresh	62	Nimbkar *et al.* (2017)
Artificial insemination	Chilled	85	Andreea *et al.* (2016)
Artificial insemination	Chilled	60	Arrebola *et al.* (2014)
Artificial insemination	Chilled	72 in sheep	Fornazari *et al.* (2018)
Artificial insemination	Chilled	63,72, 82	Rajan (2010)
Artificial insemination	Cryopreserved	58	Arrebola *et al.* (2014)
Artificial insemination	Cryopreserved	54-55	Kifaro *et al.* (2007)
Artificial insemination	Cryopreserved	70	Agossou & Koluman (2018)
Artificial insemination	Cryopreserved	40-70	Kalita *et al.* (2019)
Artificial insemination	Cryopreserved	63	Nimbkar *et al.* (2017)
Natural mating	Natural mating	93	Agossou & Koluman, (2018)
Natural mating	Natural mating	84	Alemayehu *et al.* (2021)
Natural mating	Natural mating	78-80	Amnate *et al.* (2016)
Natural mating	Natural mating	80-95	Amarantidis *et al.* (2004)
Natural mating	Natural mating	88-100	Dogan *et al.* (2016)

2.14 Dairy Goat Breeding Programme

Dairy goat breeding programme has been introduced in the tropics through importation of improved dairy goats from temperate regions. The reasons being for improvement of goat milk production because the indigenous goat breeds have low milk production capacity.

Breeding Goal, Ghenotypic, Genetic and Economic Parameters

Determining the breeding goal is one of the most important elements of animal breeding programme. Animal breeding is largely concerned with selection of animals based on a well-defined breeding goal, which should fit the future farm production and market requirements

(Bett *et al.,* 2007b). In Kenya, dairy goat production system has been defined (Bett *et al.,* 2007b). The production systems are: (1) small holder low-potential (2) small holder medium potential and (3) small holder high potential.

It is crucial to consider all traits of economic importance (both production and functional traits) during development of breeding objective (Fuerst-Waltl *et al.,* 2016). Economic values estimates are required to be able to weight the traits in the breeding goal (Amer *et al.,* 2001; Bytyqi *et al*., 2015; Rewe *et al.,* 2006). The traits of economic importance in the breeding goal for dairy goats in Kenya have been identified under the three production systems (Bett *et al.,* 2007a) as presented in Table 2.5. The traits are production (milk yield, MY; 12-month sale weight, LW; consumable meat percentage, CMP) and functional (doe live weight, DoWT; number of kids weaned, NKW; kidding frequency, KF; kidding rate, KR; doe weaning rate, DoWR; doe survival rate, DoSR; post weaning survival rate, PoSR; pre-weaning survival rate, PrSR and residual feed intake of yearlings, RFIy and does RFId) traits.

Genetic and phenotypic parameter estimates are some of the input parameters needed when modelling breeding programmes. They should be population specific to minimize biasness attributed to different sample sizes, data structures and evaluation models (de Oliveira *et al*., 2018; Jembere *et al*., 2017; Ndung'u *et al.,* 2020). The genetic and phenotypic parameters used in the current study were therefore sourced from previous studies conducted in Kenya (Bett *et al.* 2007ab, 2011, 2012).

2.15 Inbreeding and Inbreeding Depression

Despite the positive attributes of using reproductive technologies in the genetic improvement programmes, they are also associated with undesirable effects of inbreeding. Inbreeding refers to the mating of related individuals (Kristensen & Sørensen, 2005) while inbreeding depression is the loss in performance, survival, fertility and vitality associated with inbreeding (Malhado *et al*., 2013). Inbreeding happens as a result of reduced number of heterozygotes and thus leading to homozygosity. Non-random mating is the most common causes of inbreeding in livestock because parents for the next generation are selected based on their performance regardless of their relationship (Nirea *et al*., 2012). There are a number of factors that contribute to accelerate inbreeding in livestock populations.

Reproductive technologies such as AI and MOET contribute to increase in inbreeding, especially if is used on a recurrent basis in a closed population (Fernandez *et al*., 2011). In AI, semen from a few best males is used on a large number of females, thus leading to inbreeding. The consequences of inbreeding include inbreeding depression, emergence of lethal

homozygous alleles and variability of genetic response (du Toit *et al*., 2012; Koenig & Simianer, 2006; Musingi *et al*., 2018). Effects of inbreeding have been reported in different species of livestock. It reduces the survival rate in South African Jersey cattle (du Toit *et al*., 2012), reduces body weight and milk yield and increases calving interval in buffaloes (Malhado *et al*., 2013). In Kenya, several studies have reported the inbreeding effects in livestock species. It has led to depression in milk yield in cattle (Musingi *et al*., 2018) and underdeveloped udder and bisexuality in goats (Marete *et al*., 2014). Given the undesirable effects of inbreeding, there is need to control/or reduce its effects by constraining the mating between the selected parents at an acceptable genetic gain.

2.16 Genomic Selection

Genomic selection is a new method of selecting the best fit animals for breeding purpose using dense panels of single nucleotide polymorphism (SNP) markers (Ibtisham *et al.*, 2017). It uses the quantitative trait locus (QTL) linked with a particular phenotypic trait and exploit them for selection purpose. In genomic selection both genotypic and phenotypic information in reference population is used to generate prediction equations of the genetic merit of individuals (de Koning, 2016). The prediction equation is developed after recording the phenotypic performance of animals in the reference population and genotyping same animals. Thereafter, the breeding values for the animals without phenotypes (selection candidates) are predicted by using the prediction equation and their genotypes only.

Genomic selection leads to reduction in the generation interval, increase in the accuracy of EBV and a reduction in costs for progeny testing (Shumbusho *et al.*, 2015; Van Grevenhof *et al.*, 2012; Wolc *et al.*, 2015). In a sheep breeding programme, it has been demonstrated that genomic selection increases genetic and economic gains (Shumbusho *et al.*, 2015). Also in Chicken, GS has proven to be superior to traditional selection (Wolc *et al.*, 2015). The GS is mostly being adopted in dairy cattle (Boichard *et al.*, 2012) where large populations of reference populations with phenotypes and genotypes are available, and also the populations with high linkage disequilibrium. It is, however, still limited in small ruminants because of expected low value, lack of recording especially in the developing countries, high cost of genotyping, low linkage disequilibrium.

Pedigree-based on Best Linear Unbiased Prediction (BLUP) estimated breeding values (EBVs) depends on pedigree information and recordings of selection candidates and relatives (Sonesson *et al*., 2012). This results in an increased rate of inbreeding per generation as selected individuals with the best breeding values are likely related and co-selected (Daetwyler *et al*.,

2007). Traditional BLUP selection increases the weight on family information, this leads to some coselection of relatives, because relatives have the same family information, and thus to more inbreeding (Meuwissen *et al.,* 2013).Genomic estimated breeding values, on the other hand are based on high-density marker data, which gives higher accuracy than pedigree-based BLUP-EBVs. This is because genetic markers provide a more accurate relationship matrix than pedigree (Goddard, 2009; VanRaden, 2008). Genomic information increases accuracy of estimated breeding values and improves prediction of the Mendelian sampling term. This is because GS reduces the emphasis put on family information and increases that on the individual's own merit and thus possible reduction of inbreeding (Daetwyler *et al*., 2007; Nirea *et al*., 2012). Use of GS allows for accurate estimation of within-family variance and distinguishes between family variance hence reducing rate of inbreeding (Daetwyler *et al*., 2007; Meuwissen *et al.,* 2013; Schierenbeck *et al*., 2011).

State of Genomic Selection in Small Ruminants

Genomic studies in small ruminants were first possible with the development of the 50K ovine SNP chip (Rupp *et al.,* 2016) and development of a 52K SNP chip for goats (Tosser-Klopp *et al.,* 2014). The development of these high throughput DNA technologies have attracted use of genomic selection in sheep and goat breeding programmes (Rupp *et al.,* 2016). Using these technologies, for the first time sequencing of genome was done in sheep (Jiang *et al.,* 2014) and goat (Dong *et al.,* 2013). With these technologies, many valuable traits can be measured before reproductive maturity, however, the higher cost of genotyping relative to the value of the animal is still hindering the uptake of this new technology in sheep and goat breeding (Rupp *et al.,* 2016). In goats several studies have been undertaken to assess the benefit of incorporating genomic selection in goat breeding programme (Carillier *et al.,* 2013, 2014; Mucha *et al.,* 2015; Shumbusho *et al.,* 2015). It was reported that implementation of some genomic selection strategies can add more profits than conventional selection method in small ruminant breeding programs (Shumbusho *et al.,* 2015). Accuracies of genomic estimated breeding values were increased in for milk yield, fat and protein content in dairy goats (Carillier *et al.,* 2014). Because of fewer number of reference population in these studies, still there is a room for increase in the accuracy and expected genetic gain. It was indicated that improvement in the accuracy is correlated with increase in reference population size and genomic heritability of the trait (Daetwyler *et al.,* 2012).

Role of Genomic Selection in Reducing Inbreeding

Pedigree-based on Best Linear Unbiased Prediction (BLUP) estimated breeding values (EBVs) depends on pedigree information and recordings of selection candidates and relatives

(Sonesson *et al*., 2012). This results in an increased rate of inbreeding per generation as selected individuals with the best breeding values are likely related and co-selected (Daetwyler *et al*., 2007). Traditional BLUP selection increases the weight on family information, this leads to some coselection of relatives, because relatives have the same family information, and thus to more inbreeding (Meuwissen *et al.*, 2013).

Using pedigree information for calculating the level of inbreeding usually underestimates the true inbreeding coefficient due to incomplete pedigree information, especially for distant generations (Keller *et al*., 2011). Here, truncation selection on BLUP-EBVs is used, where individuals with the highest EBVs are selected. This method of BLUP truncation selection (BTS) results in higher genetic gain but also higher rate of inbreeding due to high correlation of estimated breeding values within families (Sonesson *et al*., 2005).

Genomic estimated breeding values are based on high-density marker data across the genome which gives higher accuracy than pedigree-based BLUP-EBVs. This is because genetic markers provide a more accurate relationship matrix than pedigree (Goddard, 2009; Van Raden, 2008). Genomic information increases accuracy of estimated breeding values and improves prediction of the Mendelian sampling term, because it reduces the emphasis put on family information and increases that on the individual's own merit and thus possible reduction of inbreeding (Daetwyler *et al*., 2007; Nirea *et al*., 2012). Use of genomic selection allows for accurate estimation of within-family variance and distinguishes between family variance (Daetwyler *et al*., 2007; Nirea *et al*., 2012). The GS, which increases the amount of individual information and reduces the importance of family information, reduces inbreeding (Meuwissen *et al.*, 2013).

Factors Affecting Accuracy of Genomic Selection

The accuracy of genomic selection can be defined as the mean correlation between the true breeding value and the GEBV (Meuwissen *et al.*, 2013; Ni *et al.*, 2017). Accuracy of GBV is a critical parameter when performing GS, because it determines the accuracy of selection decisions and further is a critical parameter in optimization of the design of a breeding scheme (Ni *et al.*, 2017). Although genomic selection has proven to be the best selection method compared to the traditional selection method, however, its accuracy of predictions of breeding value (GBV) depends on the size of the reference population, relatedness of the animals in the reference population, the effective population size of the breed (DNA marker density) and the heritability of the trait (Hayes & Goddard, 2010; Liu *et al.*, 2011; Meuwissen *et al.*, 2013; Van der Werf, 2013).

Size of Reference Population

Creation of reference population is one of the important characteristic of genomic selection. This important because of dense phenotyping that occur for animals that are genetically related to the wider population to link the genotypic information with the phenotype (Rupp *et al.,* 2016). Few number of animals in the reference population could lead to low accuracy of genomic predictions. On the other hand, high accuracy of genomic prediction can be achieved with a larger reference population (Daetwyler *et al.,* 2010; Van der Werf, 2013). This author asserted that, in order to balance between merit and diversity, animals to be tested in the reference populations should be selected not only from a diverse genetic background within the breed but also from family lines that can be expected to contribute to the future gene pool in that breed. The accuracy of genomic selection can be increase with more phenotypic records available because more observations there will be per SNP allele (Hayes *et al.,* 2009).

Relatedness of the Animals in the Reference Population

Literatures have shown that genomic predictions are less strong when the animals to be predicted are not closely related to the reference population (Van der Werf, 2013). Conversely, the accuracy of genomic selection becomes high when more number of animals are closely related.

Heritability of the Trait

Heritability of a trait play important role in determining the accuracy of genomic selection. Traits with high heritability have high accuracy of selection compared to those with low heritability (Carillier *et al.,* 2013). Also in terms of number of records required, traits with high heritability will require fewer records (Hayes *et al.,* 2009). For traits of low-heritability such as fertility, a very large number of records is required in the reference population to realise high accuracies of genomic estimated breeding values in animals without phenotypes (Goddard, 2008).

DNA Marker Density

Dense marker map defines a very large number of chromosome segments and as such many effects to be estimated (Meuwissen *et al.,* 2001). Studies in the literature have reported that accuracy of genomic prediction increases with marker density (Calus *et al.,* 2008; Zhang *et al.,* 2019). The accuracy of estimating marker effects depends on the number of training animals, trait heritability, genome size, effective population size, relationships between training animals and selection candidates, number of QTLs and distribution of their effect, and the method used for GEBV estimation (Meuwissen *et al.,* 2013).

2.17 Mating Designs in Livestock Breeding

In selective breeding schemes, selection and mating are the two core steps that are involved. Selection pick animals to be used as parents and determine contribution of each parent to the next generation, while mating pairs the selected parents to produce the offspring of the next generation (Henryon *et al.,* 2009). Genomic selection only select superior animals to be parents for the next generation, however, how these selected parents are mated affects response to selection and inbreeding. Several studies have reported increase inbreeding rate following introduction of GS and they recommended that strategies to control it should be devised (Doekes *et al.,* 2018; Makanjuola *et al.,* 2020; Maltecca *et al.,* 2020). Management of genetic variability and avoidance of inbreeding, however, have become major issues in dairy industry (Colleau *et al.,* 2009). Adoption of appropriate mating design could lead to improve genetic gain and reduction in inbreeding (Henryon *et al.,* 2014; Liu *et al.,* 2017; Mwangi *et al.,* 2020) without any additional costs or practical constraints (Henryon *et al.,* 2009).

There are several mating designs used in livestock breeding programmes. They include; Random mating, assortative mating (positive and negative) and optimisation mating design (minimising and maximising inbreeding) (Sargolzaei & Schenkel, 2009). In random mating design, mating between sires and dams happens at random without any favour or restriction, while in assortative mating, sires mate to dams based on similarity (positive) or dissimilarity (negative). On the other hand, in the optimised mating design, pairs of mates are chosen so that inbreeding is minimized or maximized in the next generation. Previous studies have reported that positive assortative mating improved response to selection compared to random mating (Montenegro *et al.,* 2019; Saura *et al.,* 2017). However, assortative mating cannot control inbreeding because the relationships between the selected parents will be converted into inbreeding in later generations (Mafakheri *et al.,* 2019).

2.18 Effect of Population Size on Response to Selection

Determining the population size and particularly the nucleus population size is an important aspect in animal breeding plan. There are criteria for the choice of population size, and these criteria include: selection response, variance of selection response, inbreeding rate and costs of the breeding plan (Meuwissen, 1991). Studies have shown that increase in population size improves genetic gain (Abdel-Salam *et al.,* 2010; Karuiki *et al.,* 2014; Meuwissen, 1991). The genetic gain increased to 27% and 34% when the population size changed from 25,000 to 50,000 and from 50,000 to 100,000, respectively (Abdel-Salam *et al.,* 2010).

2.19 Conclusions

The current literature has shown that there is increasing demand for dairy goats and their products, and there is need for reproductive technologies to resolve problem of shortage of breeding bucks. The literature also indicated that reproductive efficiency in goats is affected by a number of factors including breed, age, individual animal, nutrition, season and environment. Additionally, reproductive technologies such as artificial insemination and oestrous synchronisation contribute to the genetic progress, however, they are associated with some shortcomings such as low conception rate and high rate of inbreeding. Based on the literature, there is therefore, need to evaluate reproductive performance of different exotic dairy goat breeds in the tropics considering genotype by environment interaction effects. Evaluation of alternative synchronisation protocols such as short-term protocol following single fixed-time artificial insemination with cooled semen or natural mating is still rudimentary. The literature also indicated that combination of reproductive technology and genomic selection would improve genetic gain and reduce rate of inbreeding.

CHAPTER THREE

COMPARATIVE REPRODUCTIVE PERFORMANCE OF SAANEN AND TOGGENBURG BUCKS RAISED UNDER TROPICAL ENVIRONMENT

Abstract

Dairy goats' production in Kenya is mainly based on exotic breeds. Although the productive and reproductive performances of these breeds have been evaluated in their countries of origin, such information is limited in the tropics. This affects informed decision making on breeds to keep for optimal productivity. The objective of this study was therefore to evaluate the effect of breed and age on scrotal measurements and semen characteristics of Saanen and Toggenburg bucks raised under extensive system in the tropics. The study was conducted using Toggenburg and Saanen bucks, the bucks were allocated into two different groups based on breed and age in 2x2 factorial completely randomised design. The body weight was determined using a hanging weighing scale expressed in kilograms (kg). Scrotal circumference and scrotal length were measured using metal measuring tape. Semen characteristics evaluated were volume, consistency, mass activity and progressive motility, live sperm cells, normal morphology and spermatozoa concentration. The current study found that breed of bucks had no influence on body weight, scrotal circumference, scrotal length, volume, mass activity, progressive motility, live sperm cells and sperm morphology. The study also found that Toggenburg bucks had higher semen consistency and spermatozoa concentration as compared to Saanen bucks. Therefore, it is concluded that Toggenburg bucks can produce high number of total spermatozoa and as a result higher semen doses for artificial insemination purposes. Further studies with more number of animals is recommended.

3.1 Introduction

Tropical goat breeds are well adapted to their environment in terms of traits such as disease resistance, heat resistance and ability to cope with poor quality feed (Peacock, 1996). These traits enable them to survive and be productive in their environments. However, they are considered poor producers because of low milk and meat yield. Consequently, livestock improvement programmes in the tropical zones imported temperate goat breeds such as Saanen and Toggenburg with the purpose of improving milk yield (Peacock, 1996).

In terms of performance between Saanen and Toggenburg in the temperate environment, Saanen surpasses Toggenburg in milk yield, body weight, and some reproductive performances

(Chandler *et al.*, 1988; Mellado, 2016). However, such differences might be altered when they are exposed to environments not similar to that of their place of origin, like in the tropics. It was previously reported that Toggenburg performs better than Saanen in the tropics in terms of milk production, because Toggenburg is well adapted to the tropical environment (Takahashi, 2012), especially when kept under semi-intensive conditions. However, such comparison is yet to be elucidated in reproductive performance traits such as testicular traits and semen characteristics in these goat breeds in the tropics, and particularly in Kenya.

Generally, the setback of these temperate goat breeds is their poor adaptation to tropical environment in their ability to resist the effect of heat stress and other factors such as diseases. Heat stress caused by high ambient temperature can result in decrease growth, milk production and fertility in livestock (Samal, 2013; Takahashi, 2012). Heat stress can influence fertility by affecting most reproductive functions; spermatogenesis, oocyte development, oocyte maturation, early embryonic development, foetal and placental growth and lactation in mammalian species (Hansen, 2009; Samal, 2013).

Testis is suspended in a scrotum outside the body in order to keep the temperature lower than core body temperature, which is required for normal spermatogenesis (Takahashi, 2012). Scrotal circumference and testicular consistency, size and weight, are excellent indicators of sperm production capacity and spermatogenic functions (Marai *et al*., 2008). Exposure of goats to heat stress reduces scrotal volume, testicular consistency and sperm quality (Marai *et al.*, 2004). Apart from heat stress, other factors which can influence reproduction in goats include breed, age, nutrition, individual animal and season (Noran e*t al.*, 1998).

Based on the above reasoning, breeding of goats whether using natural mating or artificial insemination requires proper selection of breeding buck and more especially when employing artificial insemination. Artificial insemination helps in increasing and disseminating genotypes of quality breeding stock, however, it success largely depends on the semen of the breeding buck. The breeding buck selection is the most critical decision for improvement of a herd (Ngoma *et al.*, 2016). As a result, breeding soundness examination of the breeding bucks is essential for a good flock fertility. It includes all aspects related to scrotal measurements and semen evaluation which are important in management practices, especially for artificial insemination in goat breeding programme.

Despite the importance of these exotic goat breeds in the tropics, comparative information on their scrotal measurements and semen characteristics is still scarce. The objective of this study was to evaluate the effect of breed and age on scrotal measurements and semen characteristics of Saanen and Toggenburg bucks raised under tropical conditions.

3.2 Materials and Methods

3.2.1 Ethical Approval

The Kenya Institute of Primate Research had approved the materials and procedures of this study under the permit No: ISERC/10/19 and National Commission of Science and Technology under the permit No: NACOSTI/P/19/76927/28821.

3.2.2 Experimental Site

This study was conducted between August and September, 2019 at the Tatton Agriculture Park (TAP), Egerton University, Njoro. Njoro is approximately within latitude 00º 19'00" S and longitudes 36º 06'00" E, and at an elevation between 2168 m and 2800 m above sea level. The site receives monthly total rainfall of 86.3 mm, and its temperature varies between minimum of 10.2 and maximum of 23.3ºC (Wangui *et al.,* 2018).

3.2.3 Experimental Animals and Design

The study was conducted using total of twelve healthy bucks. The bucks were divided into two groups, one group with six Toggenburg and the other group with six Saanen bucks. Within each group the bucks were further subdivided into two groups based on their age (one group between age of 1-2 years and the other group 3-6 years). The experimental design was Completely Randomised 2x2 factorial design.

3.2.4 Management, Housing and Feeding of Experimental Goats

The bucks were managed under semi-intensive system. They were kept in stall to protect them from direct sunlight, rains and adverse weather conditions. They were fed on natural pastures and supplemented with mineral licks for sheep and goats (NutriFarm for Animal feed supplement industry, Thessaloniki, Greece) and water was given *ad libitum* throughout the experimental period.

3.2.5 Measurement of Body Weight and Scrotal Measurements

The body weight (BW) was determined using a round spring balance scale with maximum weight 150 kilograms (Hanson Company Ltd, Maidenhead, United Kingdom). Scrotal parameters measured were: Scrotal circumference (SC) and scrotal length (SL). Both the SC and SL were measured using a flexible measuring tape in centimetres as described by Akpa *et al.* (2012). The SC was measured as the maximum dimension or largest diameter of the scrotum after pushing the testes firmly into the scrotum. The SL was measured as the

distance along the caudal surface of the scrotum to its point of attachment to the tip of the scrotum.

3.2.6 Semen Collection and Evaluation

Semen Collection: Data on semen was collected once every week for a period of 7 weeks. Semen was collected using electro-ejaculator design for small ruminants (Lane Manufacturing, Denver, Colorado, USA). The collection procedures followed was according to instructions from the company. Briefly, a buck was restrained in a standing position and the urethral opening cleaned. Then the rectal probe was lubricated with a lubricating jelly and inserted in to the rectum of a restrained buck at approximately 10 cm. After insertion of the probe, the prostate gland was massage 8 to 10 times before the control button was applied to generate power. Thereafter, the control button of the instrument was pushed for 4-6 seconds and power of 9 volts was generated and held for 5-8 seconds, and again brought to 0. This procedure was repeated after a rest period equal to the duration of electrical stimulation until ejaculation took place. During collection and examination, the semen was protected from cold shock and exposure to direct sunlight. Collecting tube was fitted to the artificial vagina to collect the semen. The temperature on the inner liners of the artificial vagina was kept between 42ºC-45ºC while that of the collecting tube was maintained between 30ºC-37ºC before semen collection to prevent cold shock to the sperm cells.

Semen Evaluation: The semen samples collected were evaluated for volume, consistency, mass activity, progressive motility, live sperm cells, concentration and normal morphology. Semen consistency, mass activity and progressive motility were evaluated as described by Steyn, (2005). The semen volume and density were determined directly from the graduated transparent tube used for semen collection. The semen consistency was ranked as watery (0), thin milky (1), milky (2), thin creamy (3), creamy (4) and thick creamy (5). The mass activity was evaluated based on the wave motion (from a scale of 0-5) by viewing a drop of undiluted semen under power magnification (10x magnification) using a phase contrast microscope (Richter Optica, Model U2, China) mounted with a camera. Progressive motility was assessed by putting a drop of diluted semen on pre-warmed glass slide (25.4x76.2mm) covered with a cover slip (22x22mm) (SailBoat Lab Co., Ltd, Zhejiang, China) and viewed under power magnification (40x) of phase contrast microscope. Semen drop was mixed in saline solution (0.9 % sodium chloride, manufactured by Abacus Parental Drugs Ltd., Kampala, Uganda). The progressive motility was evaluated as percentages from 0-100%, depending on the individual motility of the sperm. Sperm concentration was determined using

the standard procedures with an aid of Neubauer improved haemocytometer (Marienfeld Company, Lauda-Königshofen, Germany) under phase contrast microscope at magnification power of (40x). The sperm cells were counted in 5 smaller squares of improved Neubauer haemocytometer and spermatozoa concentration per one millilitre was calculated using the formula: Number of sperm cells counted in 5 smaller squares x 5 x 10^4 x dilution factor. The dilution rate of 1:200 semen to water was used. The Sperm cells morphology and percent Live/dead were evaluated using Eosin-Nigrosin (Hi-Tech Solutions, New Delhi, India). A mixture of 5µl of spermatozoa and 10µl eosin-nigrosin stains was smeared on a slide and allowed to air dry for 30 minutes, thereafter, two hundred sperm cells from different microscopic fields were examined under a contrast phase microscope (40x magnification).

3.2.7 Statistical Analyses

The effect of breed and age on body weight, scrotal measurements and semen characteristics were analysed using analysis of variance (ANOVA) with General Linear Model (GLM) of SAS (Version 9.0). Correlation analysis among body weight, scrotal measurements and semen characteristics was analysed using Pearson's product-moment procedures of SAS (Version 9.0). Differences was considered significant at $P < 0.05$. The fixed effects were breed and age, while the dependent variables were semen consistency, semen volume, mass activity, progressive motility, sperm concentration, normal morphology, body weight, scrotal circumference and scrotal length. The following model was fitted for data analysis:

$$Y_{ijk} = \mu + B_i + A_j + (B * A)_{ij} + e_{ijk} \quad 1$$

Where Y_{ij} − Observation on the dependent variables, μ −Overall mean, B_i − Fixed effect of breed, A_j – Fixed effect of age, $(B * A)_{ij}$ −Interaction effect of breed and age, e_{ijk} −Random error.

3.3 Results

The findings on the effect of breed on body weight, scrotal and semen characteristics are presented in (Table 3.1). The results showed that there was no significant difference between the two breeds in terms of body weight, scrotal measurements. The breed effect, was however, observed in semen consistency and sperm concentration. Other semen characteristics such as volume, mass activity, progressive motility, live sperm cells and normal morphology were not affected by the breed.

Table 3. 1 Effect of breed on body weight, scrotal measurements and semen characteristics of Saanen and Toggenburg dairy goats

Parameters	Breed	
	Toggenburg (LSM± SE)	**Saanen (LSM± SE)**
Body weight and scrotal measurements		
Body weight (kg)	51.00±6.31[a]	42.60±6.31[a]
Scrotal circumference (cm)	28.20±0.89 [a]	26.60±0.89 [a]
Scrotal length (cm)	11.90±0.57 [a]	10.80±0.57 [a]
Semen characteristics		
Volume (ml)	1.00±0.10 [a]	0.97±0.09 [a]
Consistency (0-5)	2.94±0.21 [a]	1.76±0.19 [b]
Mass activity (0-5)	4.02±0.16 [a]	3.69±2.87 [a]
Progressive motility (%)	79.24±3.51 [a]	74.10±2.63 [a]
Sperm concentration (x10^9/ml)	2.87±0.27 [a]	1.67±0.24 [b]
Live sperm cells (%)	86.24±2.27 [a]	87.49±1.94 [a]
Normal morphology (%)	91.24±1.04 [a]	91.08±0.95 [a]

**Means with different superscripts within the same row differ significantly at P< 0.05*

*LSM: Least Square Means

The effect of the age of bucks on body weight, scrotal and semen characteristics are presented in (Table 3.2). Age of the bucks had significant effects on body weight, scrotal and semen characteristics. There was a significant difference (P <0.05) between the young (1-2 years) and adults (3-6 years) in terms of their body weight, scrotal circumference and scrotal length. Additionally, semen consistency, mass activity, progressive motility and sperm concentration differed significantly (p <0.05) in terms of age. The semen volume, live sperm cells and normal spermatozoa morphology, were however, not affected by age of the bucks. Interaction effects between breed and age was not significant for all the variables measured.

Table 3. 2 Effect of age on body weight, scrotal measurements and semen characteristics of Toggenburg and Saanen dairy goats

Parameters	Age in years	
	Young (LSM ± SE)	**Adults (LSM ± SE)**
Body weight and scrotal measurements		
Body weight (kg)	35.20±3.27 [b]	58.40±3.27 [a]
Scrotal circumference (cm)	26.10±0.73 [b]	28.70±0.73 [a]
Scrotal length (cm)	10.30±0.35 [b]	12.40±0.35 [a]
Semen characteristics		
Volume (ml)	0.89±0.10 [a]	1.08±0.10 [a]
Consistency (0-5)	1.97±0.20 [b]	2.73±0.20 [a]
Mass activity (0-5)	3.60±0.15 [b]	4.12±0.16 [a]
Progressive motility (%)	72.05±2.73 [b]	81.30±2.78 [a]
Concentration ($x10^9$/ml)	1.85±0.25 [b]	2.70±0.26 [a]
Live sperm cells (%)	86.58±1.9 [a]	86.62±1.94 [a]
Normal morphology	90.25±0.99 [a]	92.07±1.00 [a]

**Means with different superscripts within the same row differ significantly at P< 0.05*

*LSM: Least Square Means

The correlation among body weight, scrotal and semen characteristics for the Toggenburg and Saanen dairy goat breeds are presented in (Table 3.3). The results shown that scrotal circumference, scrotal length and body weight had positive correlation among each other. Sperm concentration had a positive correlation with semen consistency, and mass activity was positively correlated with progressive motility.

Table 3. 3 Pearson's product moment correlation coefficients among body weight, scrotal measurements and semen characteristics of Saanen and Toggenburg goats

Parameters	**Correlation (r)**
Scrotal circumference and body weight	0.74*
Testicular length and body weight	0.83**
Scrotal circumference and testicular length	0.96**
Concentration and consistency	0.97**
Mass activity and progressive motility	0.95**
Volume and scrotal circumference	0.07
Volume and testicular length	0.08
Volume and body weight	0.05
Volume and sperm concentration	-0.44

**Significant*

***Highly significant*

3.4 Discussion

The current study aimed at evaluating the effect of breed and age on body weight, scrotal measurements and semen characteristics of exotic dairy goat breeds raised on extensive systems under tropical conditions. The study demonstrated that, breed did not affect the body weight and scrotal measurements. The non-difference between Toggenburg and Saanen bucks body weights was unexpected. The similarity in body weight found in this study between the two breeds could be attributed to the fact that, Toggenburg goats are more adapted to the tropical environment than the Saanen goats. However, previous studies in the temperate areas reported that Saanen are heavier than Toggenburg (Peacock, 1996). This therefore, implies that, Saanen dairy goat breeds may not be suitable for extensive production systems in the tropics.

Although factors such as breed, body weight, age and individual animals have been demonstrated to affect scrotal measurements in goats (Kridli *et al.,* 2005), breed effect was not observed in the current study (Table 3.1). This could be attributed to similar body weights of the two breeds considered in this study. Since testes is part of the body and respond to tissue growth, they would follow the same trend with body weight. This could explain the breed effects observed on scrotal circumference and length (Belibasaki & Kouimtzis, 2000; Kridli *et al.,* 2005). The high positive correlation between body weight and scrotal measurements

(scrotal circumference and length) obtained in the current study (Table 3.3) confirm this phenomenon. This study agrees with results reported by Mellado, (2016) who reported close scrotal circumference values of 26.5-27 cm and 26.3 cm in Saanen and Toggenburg bucks respectively. Additionally, another study reported scrotal circumference of 26.54 cm in Saanen bucks (Ahmed *et al.,* 1997). Moreover, it was reported in another study that breed does not influence scrotal circumference and scrotal length in bucks (Gemeda & Workalemahu, 2017).

Out of the seven semen characteristics evaluated in the current study (Table 3.1), our findings demonstrated that only semen consistency and sperm concentration were affected by breed. Our findings demonstrated that, the breed only affected semen consistency and sperm concentration with Toggenburg being superior to Saanen bucks. This may be attributed to the fact that Saanen bucks are more prone to the heat stress than Toggenburg bucks. Heat stress subsequently increase the level of cortisol and reduces testosterone level (Perez-Crespo *et al.,* 2008).

The result of this study on sperm concentration was in disagreement with the previous study reported by Chandler *et al.* (1988) in the temperate region and Mellado, (2016) which reported lower values of sperm concentration in Toggenburg bucks and higher values in Saanen goats. This differences could be attributed to different environments where these studies were conducted. The temperatures in the tropics are very high and Toggenburg is well adapted to the tropics compared to Saanen (Takahashi, 2012). It had been reported that temperature affects the process of spermatogenesis (Marai *et al.,* 2008), and thus reduces the number of spermatozoa (Perez-Crespo *et al.,* 2008; Rahman *et al*., 2016). The sperm concentration of Saanen bucks in this study was lower compared to another study reported by Ahmed *et al.* (1997) in the tropics. This difference could be attributed to higher body weights of bucks, time of buck exposure to the tropical environment and management system in their study.

Age of buck influences the body weight, scrotal circumference and scrotal length (Table 3.2). The current study found that old bucks had higher body weight, large scrotal circumference and scrotal length than the young bucks. This was indicative of the linear relationship between live body weight, scrotal circumference and age (Ahmad *et al*., 2011; Siddiqui *et al.,* 2008). The differences in body weight, scrotal circumference and scrotal length between the two age categories are attributed largely due to physiological development (Ajao *et al.,* 2014). These findings corroborate with the previous studies (Ahmad *et al.,* 2011; Kridli *et al.,* 2005; Raji *et al.,* 2008).

However, age of bucks in the current study did not influence semen volume, live sperm cells and normal morphology. These findings are in agreement with the previous study by

Tabbaa *et al.* (2006) who reported that semen volume, sperm live cells and normal morphology were not affected by age of rams. However, mass activity, progressive motility, semen consistency and sperm concentration were affected by age of bucks, where bucks between 1-2 years had lower sperm motility, consistency and sperm concentration compared to those bucks between 3-6 years of age. This was an indication that these semen characteristics improve with increasing age of bucks. In agreement with the current study, other previous studies indicated that sperm concentration increased with increasing age in bucks (Al-Ghaban *et al.,* 2004; Mahal *et al.,* 2013) and bulls (Bhakat *et al*., 2011; Murphy *et al*., 2018). Additionally, it was reported that semen motility and sperm concentration increased as the age of rams increase (Benia *et al.,* 2018). The high sperm concentration in adults bucks could be attributed to increase in activity of the hypothalamic-pituitary-testicular axis and the simultaneous growth of the testis and accessory glands with sexual maturity, which are believed to continue to develop for post-puberty (Almquist, 1978). The current findings were in disagreement with previous studies which reported that age had no influence on semen consistency, mass activity, progressive motility and sperm concentration (Kridli *et al*., 2005; Tabbaa *et al.,* 2006). The discrepancies among these studies could be attributed to factors such as age, breed, nutrition and production system.

In terms of correlations, both scrotal circumference and scrotal length were positively correlated significantly with each other and with body weight. This relationship was expected because testes are body parts that respond to tissue growth, which is observed by the improvement of body weight (Kridli *et al.,* 2005). The current study agrees with previous findings by Gemeda & Workalemahu (2017) which reported positive correlation among scrotal circumference, scrotal length and body weight. Semen volume was positively correlated but not significant with scrotal circumference, scrotal length and body weight. This finding corroborates with previous study by Kridli *et al.* (2005) who reported positive correlation of ejaculate volume with scrotal circumference and scrotal length. Additionally, the semen volume was negatively correlated but not significant with sperm concentration. This was expected because high volume of semen is associated with low semen concentration and vice versa. This is in agreement with previous studies reported negative correlation between semen volume and sperm concentration (Kridli *et al.,* 2005; Rehman *et al.,* 2016).

Sperm concentration was positively correlated and significant with the semen consistency. This was expected because high semen density is an indicator of high sperm concentration and vice versa. In agreement with the current study, Kridli *et al.* (2005) reported negative correlation between sperm concentration and semen volume. There was a positive

correlation between semen mass activity and progressive motility. This positive correlation was expected because mass activity of semen gives clear indication of how the individual sperm motility will be. This is in agreement with previous studies which found that mass activity was positively correlated with progressive motility of sperm in bucks (Kridli *et al.*, 2005; Lukusa & Lehloenya, 2017) and in bulls (Ray & Ghosh, 2013).

3.5 Conclusion

In conclusion, the current study found that the Toggenburg and Saanen bucks raised under extensive system in the tropics were similar in terms of body weight, scrotal circumference, scrotal length, volume, mass activity, progressive motility, live sperm cells and sperm morphology. The study also found that Toggenburg bucks had higher semen consistency and sperm concentration as compared to Saanen bucks. Adult bucks had significantly higher body weight, scrotal circumference and length, semen consistency, sperms motility and concentration compared to young bucks. Therefore, it is concluded that Toggenburg bucks can produce high number of total spermatozoa and as a result higher semen doses for artificial insemination purposes. Further studies with more number of animals is recommended.

CHAPTER FOUR

SHORT-TERM OESTROUS SYNCHRONISATION PROTOCOL FOLLOWING SINGLE FIXED-TIME ARTIFICIAL INSEMINATION AND NATURAL MATING AS ALTERNATIVE TO LONG-TERM PROTOCOL IN DAIRY GOATS

Abstract

The traditional long-term progestagen based oestrous synchronisation protocols normally range from 10-19 days. The long-term protocol, however, has been associated with low fertility rates. This low fertility has been linked to sub luteal serum progesterone concentrations which is associated with some abnormalities in follicular development, ovulation, oocyte health, luteal function. This study therefore, investigated the hypothesis that the use short-term synchronisation protocol following single fixed-time artificial insemination with extended cooled semen and natural mating in fertility management of dairy goats could be as good as or better than traditional long-term protocol. This was tested by designing an experiment using Toggenburg dairy goats raised under semi-intensive production system in the tropics. Twenty-eight (28) females Toggenburg dairy goats were randomly allocated to two synchronisation protocols in completely randomised design and within each synchronisation protocol the animals were further subdivided into two mating methods. Oestrus was synchronised using short (7 days) and long-term (12 days) protocols and animals mated using natural mating and AI. Onset and the duration of oestrus were monitored using two intact-aproned bucks following controlled internal drug release devices withdrawal. Non-return to oestrus method was used to determine conception rate. Onset and duration of oestrus, response to oestrus and conception rate were evaluated. Onset and duration of oestrus was analysed using analysis of variance, while response to oestrus, conception rate and kidding rate were analysed by using Chi-Square test. Generally, the two protocols realised 100% response to oestrus. Onset and duration of oestrus in short-term protocol were 31.75 hrs and 31.70 hrs, respectively, while the corresponding values for long-term protocol were 33.33 and 30.93 hrs. Synchronisation protocols did not significantly differ in onset and duration of oestrus, conception, kidding and twining rate. Similarly, the two mating methods did not differ significantly on conception, kidding and twining rates. The current study has an overall of conception rate, kidding and twinning rate of 71.42, 64.29 and 44.50%, respectively. Short-term protocol following single

fixed-time AI and natural mating therefore, can be alternative to long-term oestrous synchronisation protocol in dairy goats.

4.1 Introduction

The traditional long-term progestagen based oestrous synchronisation protocols normally range from 10-19 days (Harl, 2014; Pietroski *et al.,* 2013). The long-term protocol, however, has been associated with low fertility rates (Diskin *et al.,* 2002; Pietroski *et al.,* 2013). This low fertility has been linked to sub luteal serum progesterone concentrations which is associated with some abnormalities in follicular development, ovulation, oocyte health, luteal function (Evans *et al.,* 2001; Menchaca & Rubianes, 2001; Viñoles *et al.,* 2001). Given the above reasons and long duration of treatment for the traditional synchronisation protocol, short-term protocol have been suggested (Karaca *et al.,* 2010; Menchaca & Rubianes, 2004, 2007; Menchaca *et al.,* 2018; Viñoles *et al.,* 2001). These studies demonstrated that, the short-term protocol is associated with supraluteal levels of progesterone concentrations, which positively influence follicular turnover, increases the number of healthier young large follicles with the potential to ovulate and improve pregnancy rate.

It has been documented that fertility can be influenced depending on whether fresh, cooled or frozen semen is used. On the other hand, timing of insemination or natural mating following synchronised oestrus plays crucial role in determining the fertility of an animal. Therefore, it is important to conduct studies looking at how different types of synchronisation protocols and mating methods influence fertility.

Comparative studies have been conducted comparing short and long-term oestrous synchronisation protocols following artificial insemination (AI) and natural mating (Karaca *et al.,* 2010; Pietroski *et al.,* 2013; Ramukhithi *et al.,* 2012). In these studies, does were inseminated with fresh raw semen using cervical or laparoscopic technique either 48 hrs following CIDR removal or according to the onset of oestrus at 48 and 60 hrs following sponge removal. Use of invasive technique such as laparoscopy is not convenient especially, in routine breeding of animals by farmers. In addition, application of AI at different time intervals takes long time in performing breeding activities of animals and may cause inconvenience in terms of management. Therefore, use of single fixed-time AI could offer an alternative convenient option in breeding of goats. There are, however, no studies to the best of our knowledge comparing short and long-term synchronisation protocols following single fixed-timed AI with extended cooled semen and natural mating. We reasoned that synchronising oestrus using short-term protocol following single fixed-time artificial insemination with extended cooled

semen and natural mating could be as good as or better than long-term protocol in fertility of exotic dairy goats in the tropics. This is because short-term protocol is associated with high progesterone, which could lead to improved follicular development and health, rate of ovulation and sperm transport. We tested this hypothesis by designing an experiment comparing short and long-term oestrous synchronisation protocol following single fixed-time AI and natural mating using Toggenburg dairy goats raised under semi-intensive production system in the tropics.

4.2 Materials and Methods

4.2.1 Ethical approval

The materials and procedures of this study had been approved by Kenya Institute of Primate Research under the permit No: ISERC/10/19 and National Commission of Science and Technology under the permit No: NACOSTI/P/19/76927/28821.

4.2.2 Experimental Site

This study was conducted between August and September, 2019 at the Tatton Agriculture Park (TAP), Egerton University, Njoro. Njoro is approximately within latitude 00º 19'00" S and longitudes 36º 06'00" E, and at an elevation between 2168 m and 2800 m above sea level. The site receives monthly total rainfall of 86.3 mm, and its temperature varies between minimum of 10.2 and maximum of 23.3ºC (Wangui *et al.*, 2018).

4.2.3 Experimental Animals and Design

In this study, 28 females Toggenburg goats in their third lactation were used and allocated into two synchronisation protocols with mean initial body weight (Short-term=59.00±2.76 kg and Long-term= 58.50±2.76 kg) not significantly different in a Completely Randomized Design. Within each synchronisation protocol the animals were further subdivided into two mating methods with mean initial weight (Artificial insemination= 58.71±2.76 kg and Natural mating= 58.79±2.76 kg) not significantly different. The animals were kept under semi-intensive system on natural pastures, supplemented with commercial concentrate and mineral licks as well as water offered *ad libitum*.

4.2.4 Synchronisation of Oestrus

Two different synchronisation protocols were used; short and long-term progestagen treatment. All does in both groups were treated intravaginal with progesterone using controlled

internal drug releasing device (CIDR-G) (Pfizer, New Zealand) containing 0.3 g progesterone. The CIDR-G device was left for 7 days and 12 days for short and long-term progestagen treatment, respectively. At CIDR removal, all does in both groups were injected with 150 µg of prostaglandin F2α (PGF2α) analogue (Intervet Schering-Plough Animal Health, South Africa) and 200 IU of equine chorionic gonadotropin (eCG) (Intervet Schering-Plough Animal Health, South Africa). Literatures for this protocol includes (Fonseca *et al.,* 2005; Greyling & Van der Nest, 2000; Karaca *et al.,* 2010; Menchaca & Rubianes, 2007; Pietroski *et al.,* 2013; Romano, 2004).

4.2.5 Semen Collection and Evaluation

Semen Collection; Semen was collected using electro-ejaculator for small ruminants (Lane Manufacturing, Denver, Colorado, USA). The collection procedures followed was according to instructions from the company. Briefly, the buck was restrained in a standing position and the urethral opening cleaned. Then the rectal probe was lubricated with a lubricating jelly and inserted in to the rectum of the restrained buck to a depth of approximately 10 cm. After insertion of the probe, the prostate gland was massaged 8 to 10 times before the control button was pressed and held for 5-8 seconds to generate power. Thereafter, the control button was paused for 4-6 seconds and again the control button was pressed and held for 5-8 seconds. This procedure was repeated until ejaculation took place. During collection and examination, the semen was protected from cold shock and exposure to direct sunlight. A collecting tube was fitted to the artificial vagina to collect the semen. The temperature on the inner liners of the artificial vagina was kept between 42ºC-45ºC while that of the collecting tube was maintained between 30ºC-37ºC before semen collection to prevent cold shock.

Semen Evaluation; The semen samples collected were evaluated for volume, semen density, mass motility, progressive motility, live sperm cells, spermatozoa concentration. Semen density, mass motility and progressive motility were evaluated as described by Steyn, (2005). The semen volume and density were determined directly from the graduated transparent tube used for semen collection. The semen density was ranked as watery (0), thin milky (1), milky (2), thin creamy (3), creamy (4) and thick creamy (5). Mass motility was evaluated based on the wave motion (from a scale of 0-5) by viewing a drop of undiluted semen under power magnification (x10 magnification) using a phase contrast microscope (Richter Optica, Model U2, China) mounted with a camera. The semen mass motility with wave motion of 3 and above was used. Progressive motility was assessed by putting a drop of diluted semen on pre-warmed glass slide (25.4x 76.2mm) covered with a cover slip (22x22mm) (SailBoat

Lab Co., Ltd, Zhejiang, China) and viewed under power magnification (x40) of phase contrast microscope (Richter Optica, Model U2, China). Semen drop was mixed in saline solution (0.9 % sodium chloride, manufactured by Abacus Parental Drugs Ltd., Kampala, Uganda). The progressive motility was evaluated as percentages from 0-100%, depending on the individual motility of the sperm. Semen with progressive motility of more than 70 % was used. Sperm concentration was determined using the standard procedures with an aid of Neubauer improved haemocytometer (Marienfeld Company, Lauda-Königshofen, Germany) under phase contrast microscope at magnification power of (x40). Sperm concentration was determined using the standard procedures with an aid of an improved Neubaur haemocytometer under phase contrast microscope at magnification power of (x40). The sperm cells were counted in 5 smaller squares of improved Neubaur haemocytometer and spermatozoa concentration per one millilitre was calculated using the formula: Number of sperm cells counted in 5 smaller squares multiplied by 5, the dilution factor and the volume of haemocytometer. The dilution rate of 1:200 semen to water was used for determination of spermatozoa concentration.

Semen Extension: Semen was extended using OPTIXcell extender, a commercially available animal protein free extender (IMV Technologies, France). It was prepared as per the manufacturer's instructions. Briefly, a total of 75 ml of extender was reconstituted by mixing 25 ml of the OPTIXcell with 50 ml of distilled water at temperature of 37ºC. To prepare the 75 ml of ready to use extender, the capped 25 ml bottle of OPTIXcell and flask containing 50 ml of double distilled water were both placed in a water bath at temperature of 37ºC for a period of 10 minutes to equilibrate their temperatures. Thereafter, the bottle containing OPTIXcell was removed and wiped with paper towel and then the contents were transferred to the flask containing double distilled water, and finally the bottle rinsed. The fresh extender was kept in a refrigerator at the temperature of 4ºC and used within three hours. The semen and the extender were mixed while maintained in the water bath at a temperature of 37ºC.

4.2.6 Monitoring and Recording Parameters of Oestrus

The onset and the duration of oestrus were monitored using two aproned intact bucks with high serving capacity following CIDR withdrawal. The does were monitored for total of 72 hrs following CIDR withdrawal at 8-hour interval for the detection of onset and duration of oestrus. A doe was considered to be on oestrus when it accepted mounting by the aproned buck. In addition to the doe accepting mounting, other signs of oestrus such as frequent tail wagging, bleating, swollen vulva and mucous discharge from the vulva were used to confirm that a doe was on oestrus. A doe was considered out of oestrus when it could not stand to be mounted by

the buck after the onset of oestrus. Onset and duration of oestrus were detected as described by Romano *et al.* (2018) with few modifications. Briefly, oestrus was detected once during the first 12 hrs after CIDR removal and then every 4 hr thereafter, at 10:00, 14:00, 18:00, 22:00, 02:00, and 06:00 hr for 72 hrs.

4.2.7 Natural Mating and Artificial Insemination

Mating was done using natural mating and timed artificial insemination using diluted cooled semen. For the natural mating group, one male was mated to maximum of three (3) does following CIDR withdrawal for a period of 12 hrs. In the artificial insemination group, a speculum with a built-in light source and pipette connected to a 1 ml syringe was used to cervically inseminate the does (Steyn, 2005). A doe was restrained by putting the elevated hindquarters over a rail at a height of 80-90 cm with the head downwards and the hind legs secured by one assistant. The vulva was wiped to prevent semen contamination. The speculum was inserted into the vagina to locate the cervical opening. Then 0.4 ml of diluted semen was drawn into the pipette from the semen collection tube in a water bath at 37°C and deposited into the cervix. All does were inseminated cervically at single fixed-time of 48 hrs following CIDR withdrawal. Each doe was inseminated with 0.4 ml of extended cooled semen with sperm concentration of $500x10^6$ sperm cells.

4.2.8 Pregnancy Diagnosis

The pregnancy diagnosis was carried out using non-return to oestrus method as described by Mellado (2016) with few modifications. The does were monitored twice a day using two aproned bucks (Morning and evening) to detect does that returned to oestrus from day 16-26 following natural mating and artificial insemination. Does which did not express signs of oestrus were considered pregnant while does which exhibited signs of oestrus were considered not pregnant.

4.2.9 Evaluation of Reproductive Parameters

The following parameters were evaluated. The onset and duration of oestrus as well as the response to oestrus were evaluated as described by Romano *et al.* (2018). Briefly, oestrus onset was defined as the interval from CIDR removal to the time between the last unaccepted mount and the first accepted mount. Oestrus duration was the interval from the first to the last accepted mounts. Oestrus response was defined as the proportion of females that came on oestrus from the total number of does synchronized. The conception rate as the number of does

that conceived out of the total number of does mated multiplied by 100. Kidding rate was calculated as the number of does that kidded out of the total number of does mated multiplied by 100. Twining rate was calculated as the number of does that kidded two (2) kids per total number of does kidded. None of the does among those that kidded gave birth to more than two kids.

4.2.10 Statistical Analyses

The onset and duration of oestrus were analysed using one-way analysis of variance (ANOVA). The model fitted was:

$$Y_{ij} = \mu + SP_i + e_{ij} \quad 2$$

where: -

Y_{ij} − Observation on the dependent variables, μ −Overall mean, SP_j −Fixed effect of synchronisation protocol, e_{ij} − Random error.

Response to oestrus, conception rate, kidding rate and twining rate were analysed using Chi-Square test procedures of SAS (Version 9.0). Differences were considered significant at $P < 0.05$.

4.3 Results

Our finding confirmed the premise that, synchronising oestrus using short-term protocol following single fixed-time artificial insemination with extended cooled semen and natural mating would be as good as the traditional long-term protocol in fertility of dairy goats raised in the tropics. This was confirmed by no observable significant different between the two protocols on response to oestrus cycle, onset of oestrus, duration of oestrus, conception rate, kidding rate and twining rate when single fixed-time artificial insemination with extended cooled semen and natural mating was applied.

4.3. 1 Effect of Synchronisation Protocols on Response to Oestrus, Onset of Oestrus and Duration of Oestrus.

The mean response to oestrus (%), onset and duration of oestrus (hours) following short-term and long-term oestrous synchronisation protocols are presented in Table 4.1. There was no significant difference ($P>0.05$) between short and long-term protocol in terms of response to oestrus, duration of oestrus and onset of oestrus.

Table 4. 1 Response to oestrus, onset and duration of oestrus (LSMeans±standard error) following short-term and long-term oestrous synchronisation protocol in Toggenburg goats.

Synchronisation protocol	No of goats	Response to oestrus (%)	Onset of oestrus (hrs)	Duration of oestrus (hrs)
		NS	NS	NS
Long-term	14	100	33.33±0.86	30.93±0.54
Short-term	14	100	31.75±0.84	31.70±0.52
Overall	28	100	32.54±0.85	31.32±0.53

** NS: not significant at P >0.05*

In all the two protocols, all does showed signs of oestrus at least 28 hrs after CIDR withdrawal. More does showed oestrous signs earlier in the short-term than in long-term protocol (Figure 4.1). Additionally, at 40 hrs after CIDR withdrawal all the does in different groups showed signs of oestrus (Figure 4.1).

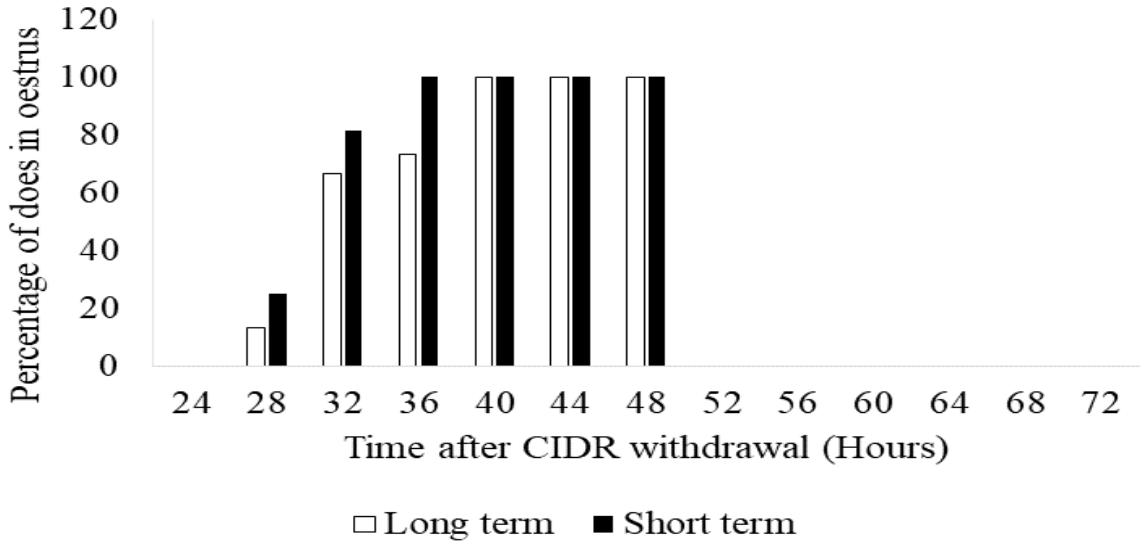

Figure 4. 1 Percentage of does on oestrus following short-term and long-term synchronisation protocols

4.3.2: Effect of Synchronisation Protocol and Mating Methods on Conception Rate, Kidding Rate and Twining Rate

The current study had an overall conception, kidding and twinning rates of 71 %, 64 and 44 %, respectively (Table 4.2). The total number of kids born were 26, and out of these, 10 were males and 16 were females. There was no significant difference between the treatment groups (Table 4.2). Additionally, kidding rate was 86 % in NM-ST compared to 57 % in each of the other three groups (AI-ST, AI-LT, NM-LT). Moreover, the twinning rate was 50% in each of AI-LT, NM-ST and NM-LT with exception of AI-ST, which had lower twining rate of 25%. When the data were pooled based on the oestrous synchronisation protocols and mating methods, no significant difference was observed between the synchronisation protocols and mating methods on conception, kidding and twinning rates.

Table 4. 2 Fertility performances following different oestrous synchronisation protocols and mating methods in Toggenburg goats

Treatments	No of goats	Conception rate (%)	Kidding rate (%)	Twining rate (%)	Number of kids born	Sex ratio	
		NS	NS	NS		Male	Female
AI-ST	7	57	57	25	5	1	4
AI-LT	7	71	57	50	6	3	3
NM-ST	7	86	86	50	9	4	5
NM-LT	7	71	57	50	6	2	4
SP							
LT	14	71	57	50	12	5	7
ST	14	71	71	40	14	5	9
MM							
NM	14	79	71	50	15	6	9
AI	14	64	57	38	11	4	7
Overall	28	71.	64	44	26	10	16

* *NS: not significant at P >0.05*

AI: Artificial insemination, **NM:** Natural mating, **ST:** Short term, **LT:** Long term, **MM:** Mating method, **SP:** Synchronisation protocol

4.4 Discussion

The findings of the current study, supported reasoning that short-term synchronization protocol could be as good as traditional long-term protocol even with single fixed-time AI with extended cooled semen and natural mating. These findings are supported by previous studies, which did not find the difference in response to oestrus, duration of oestrus and conceptions rates in goats in temperate and tropical production environments (Karaca *et al.*, 2010; Pietroski *et al.,* 2013; Ramukhithi *et al.,* 2012). The onset and duration of oestrus in the current study, however, were longer compared to those reported by Pietroski *et al.* (2013). In their study, the onset and duration of oestrus were 26.7 and 28.5 hrs in short and 25.2 and 25.2 hrs in the long-term protocol, respectively. Similarly, Karaca *et al*. (2010) reported onset of oestrus of 28.8 and 28.0 in long and short-term synchronisation protocol, respectively. Moreover, Ramukhithi *et al.* (2012) reported longer onset of oestrus (34.7 hrs vs 33.4 hrs) and duration of oestrus (37.9 hrs vs 35.2 hrs) in short and long-term synchronisation protocols, respectively, than in the current study. These differences could be attributed to different types of progestagen devices used, use of gonadotropins, breed of goats, nutrition, season and male presence (Dogan *et al.,* 2008; Orihuela, 2000). They used progestagen sponges during the non-breeding season while in the current study CIDR was used during the breeding season. These devices have different concentration levels of progesterone (Motlomelo *et al.,* 2002).

The lack of significant difference in conception rate between short and long-term synchronisation protocols found in this study concurs with previous studies in goats (Karaca *et al.,* 2010; Pietroski *et al.,* 2013) and cows (Kasimanickam *et al.,* 2015). On the contrary, to our findings Ramukhithi *et al.* (2012) reported higher pregancy rates in Boer and indigenous goats when short-term protocol was used. These differences could be attributed to differences in breed, type of progestagen and quantity of equine chorionic gonadotropin used. Although there were no significant differences between the two synchronisation protocols, short-term protocol can be a better alternative than long-term protocol. This is because short-term protocol takes few days to synchronise animals and thus reduce time spent by farmers to breed their animals. In addition, CIDR from short-term protocol can be re-used with effective oestrous synchronisation and pregnancy rate (Vilarino *et al.,* 2011).

In terms of kidding rate, there was no significant difference between short and long-term protocols. Short-term protocol, however, tended to have higher kidding rate (71 %) than in long-term protocol (57 %). This tendency could be attributed to the fact that short-term protocol achieved high progesterone concentration at the end of the synchronisation protocol, normal follicular turnover and ovulation of newly formed follicles (Menchaca & Rubianes, 2007;

Viñoles *et al.*, 2001). This study concurs with the previous finding by Karaca *et al.* (2010) who reported kidding rate of 76.5 % and 61.1 % in short and long-term protocol, respectively.

On the method of mating, regardless of oestrous synchronisation protocol, there were no differences recorded on conception rate, kidding rate and twining rate between natural mating and AI using cooled extended semen. This finding is in agreement with the previous study which reported no differences in pregnancy rate and parturition rate between natural and AI (Pietroski *et al.*, 2013). This similarity is despite the fact that in the current study single fixed-time AI was carried out 48 hrs following CIDR withdrawal irrespective of whether a doe shown signs of oestrus or not, while in the study by Pietroski *et al.* (2013), they inseminated animals at different time intervals according to signs of oestrus (48 and 60 hrs). Contrary to the current study, other studies reported significant differences on pregnancy rate between natural mating and artificial insemination with 93% and 70 %, respectively (Agossou & Koluman, 2018). This inconsistency could be attributed to different semen types and site of semen deposition used.

4.5 Conclusion

The current study confirmed that short-term protocol could replace long-term oestrous synchronisation protocol following single fixed-time AI and natural mating in dairy goats. It also demonstrated that, short and long-term oestrous synchronisation protocols have no effect on oestrous response, onset of oestrus and duration of oestrus and conception rates of dairy goats. Natural and artificial insemination methods had no effect on conception, kidding and twining rates of dairy goats.

CHAPTER FIVE

IMPROVED RESPONSE TO SELECTION IN DAIRY GOAT BREEDING PROGRAMME THROUGH REPRODUCTIVE TECHNOLOGY AND GENOMIC SELECTION IN THE TROPICS

Abstract

Reproductive technologies such as artificial insemination increases selection intensity, especially among sire and shortens genetic lag while genomic selection reduces generation interval, increases accuracy of selection and consequently leading to high rates of genetic gain. It was reasoned that, incorporating reproductive technologies and genomic selection in the current dairy goats breeding programme would generate higher response to selection compared to use of natural mating in the current conventional breeding programme. This premise was tested by deterministic simulation approach and compared to the current breeding programme where natural mating and conventional breeding programme is used in the tropics. Two breeding schemes with three breeding strategies were simulated. The first scheme was conventional breeding scheme which represented the current dairy goat-breeding programme in the tropics. An alternative scheme was genomic breeding scheme. Each scheme was evaluated with three mating strategies. The mating strategies were; natural mating, AI-Fresh semen and AI-Cryopreserved semen, with 5% of the total population in the nucleus and 95 % in the commercial. The current study found that AI-Fresh semen were superior compared to AI-Cryopreserved semen, natural mating strategies in terms of annual genetic gain, returns and profit. The AI-Fresh semen realised additional Kenya Shillings (KES) 3.00 and 3.61, 151.31 and 46.72, 148.89 and 47.81, in genetic gain, returns and profitability compared to natural mating and AI-Cryopreserved, respectively The AI-Fresh semen incurred low costs KES 23.38 compared to AI-Cryopreserved with KES 24.47 but higher than natural mating with KES 20.96. On the other hand, AI-Cryopreserved strategy has generated additional returns KES 104.59 and profit KES 101.08 but lower by KES 0.61 in genetic gain compared to natural mating strategy. Implementation of genomic scheme has generated additional improvement across the three mating strategies in all the parameters measured compared to the conventional scheme. The gnomic scheme realised additional KES 11.54, 10.80 and 10.21 in genetic gain, KES 161.30, 183.48 and 175.90 returns, and 136.30, 158.48 and 150.90 profit in the natural mating, AI-Fresh semen and AI-Cryopreserved, respectively, compared to their counterparts

in conventional scheme. Genetic gain increased with increased nucleus population size up to 15% and thereafter, it declines in both conventional and genomic schemes with optimal nucleus size ranging between 14 % and 16 %. In conclusion, the current study demonstrated that adoption of reproductive technologies such as AI would optimize response to selection in dairy goat breeding programs in the tropics. The response to selection in such breeding programmes could be maximized in combination with genomic selection.

5.1 Introduction

Food security is a major challenge in sub-Saharan Africa. The food insecurity is attributed to low agricultural productivity, high population growth rate, inefficient systems and policies of food distribution, poverty and low income (Al-Baguri *et al.,* 2014). As one of the measures to address food insecurity, governments in collaboration with Non-Governmental Organisations are putting efforts to provide dairy goat to farmers, and this has stimulated the demand for dairy goats in sub-Saharan Africa (Bett *et al.,* 2009). Another driving force behind this increase in the demand to raise dairy goats is the decline in land sizes that can no longer support rearing of dairy cattle (Bett *et al.,* 2009). This has resulted to emergence of dairy goat farming as a high-return option for small-scale farmers (Mbindyo *et al*., 2018).

Despite the popularity of dairy goat farming among the small holder farmers, their production has been constrained by nutrition and feeding, breeding and reproduction, diseases, parasites, climate change, and underdeveloped dairy goat products markets (Kahi & Wasike, 2019). These constraints have been made worse by climate change, which has not only affected the feeds availability but has also resulted to high temperatures and emergence of resistant by disease causing pathogens leading to high mortality of breeding stock (Bett *et al.*, 2016; Nardone *et al.,* 2010; Rojas-Downing *et al.,* 2017). Availability of breeding stock in sub-Saharan Africa therefore, remains a limiting factor to genetic improvement (Kahi & Wasike, 2019). To address this challenge, buck rotation programmes have been practiced (Ahuye *et al.,* 2005; Bett *et al.,* 2009; Mbindyo *et al*., 2018). Although buck rotation increases access to breeding bucks, this approach could risk the spread of reproductive diseases across farms, and also lead to erosion of genetic diversity due to use of few bucks (Marete *et al.,* 2011).

Reproductive technologies such as artificial insemination and oestrous synchronisation could serve as a solution to the problems associated with buck rotation. Artificial insemination (AI) increases selection intensity, especially among sire and shortens genetic lag, while oestrous synchronisation concentrates the onset of oestrus and kidding, improve pregnancy and

prolificacy rates (Kor *et al*., 2011). The duration of semen storage before insemination or from semen collection to insemination is important in determining fertility (Roca *et al.*, 1997).

Fertility of 78-95 % following natural mating has been reported in previous studies (Agossou & Koluman, 2018; Amnate *et al.*, 2016) which is comparable to fertility arising from AI with liquid semen of between 70-90 % (Andreea *et al*, 2016; Gore & Khoboso, 2020; Luo *et al.*, 2019; Rajan, 2010) and in sheep (Fornazari *et al.*, 2018). Fertility rates associated with frozen semen range between 50-60% (Arrebola *et al.*, 2014; Kifaro *et al.*, 2007; Salvador *et al.*, 2005). These differences in fertility could be attributed to factors such as individual buck effect, semen collection method, semen processing, synchronisation protocol, semen deposition site, season of semen collection, age of buck and doe, and production system (Arrebola *et al.*, 2014; Hashemi & Safdarian, 2017).

In addition to reproductive technologies that help in quick genetic progress, there is genomic selection that allows selection of breeding animals from early age, and this reduces generation interval, increase accuracy of selection, genetic and economic returns (de Roos *et al.*, 2011; Egger-Danner *et al.*, 2014, 2012; Thomasen *et al.*, 2016;). Higher rates of genetic gain are realised by genomic selection (GS) over conventional selection (CS), because the former has high reliabilities of breeding values, and reduces generation interval as young animals without phenotypes can be evaluated (de Roos *et al.*, 2011; Schaeffer, 2006). In dairy cattle, it has demonstrated that combination of reproductive technologies and GS can improve response to selection (Pedersen *et al.*, 2012; Thomasen *et al.*, 2016). The adoption of reproductive technologies and GS to optimize response to selection of dairy goats in Sub-Sahara Africa has been limited. It is expected that incorporating these alternative strategies to buck rotation and conventional breeding could improve genetic and economic returns in dairy goat breeding programme. Based on these lines of reasoning, the current study investigated the premise that incorporation of reproductive technologies and GS would optimize response to selection of dairy goat breeding programmes in Sub-Sahara Africa. Using the Kenyan dairy goat breeding programme as an example, this hypothesis was tested by modelling the current and alternative breeding strategies using deterministic simulation approach.

5.2 Materials and Methods

5.2.1 Procedure

Deterministic simulation method was used to model and evaluate response to selection in conventional and genomic breeding schemes utilizing natural mating and artificial insemination strategies. The schemes were simulated in a closed two-tier system assuming a

uni-directional flow of genetic materials from the nucleus to the commercial tier. This is because the small holder high-potential (nucleus population) supplies smallholder low-and medium-potential (commercial population) with superior genetic breeding materials (Amayi *et al.,* 2016). The performance and pedigree recording, genetic evaluation, selection and mating decisions were done in the nucleus.

5.2.2 Breeding Goal and Production Systems

Development of breeding goal involves the identification of production systems, traits of economic importance and estimation of their economic values. The breeding goals for dairy goats in Kenya have been defined under different production systems. The traits considered in the breeding goal of Kenyan dairy goats regardless of production system are milk yield (MY), daily weight gain (WG), live weight (LW), doe mature weight (MW) and number of kids weaned per doe (NKW) (Bett *et al.,* 2007a). The economic values of these traits were estimated under different production systems. For the purpose of the current study MY, LW, MW and NKW were considered. Dairy goat production systems in Kenya are categorised into smallholder low, medium-and high-potential (Bett *et al.,* 2007a). Therefore, in this study, the smallholder-high potential production system was considered as the nucleus population, while the smallholder low- and medium-potential was grouped as the commercial population. The nucleus population was assumed to be 5 % of the commercial population (Amayi *et al.,* 2016).

5.2.3 Breeding System and Strategies

A two-tier closed nucleus breeding system with two schemes were considered. The two schemes included conventional and genomic. The conventional scheme represented the current breeding programme in Kenya where dairy goats are being selected based on pedigree and phenotypic information. The genomic selection, on the other hand was an alternative where the animals would not only be selected based on phenotype but also on genotype. It uses dense panels of single nucleotide polymorphism (SNP) markers (Ibtisham *et al.,* 2017). Genomic selection uses the quantitative trait locus (QTL) linked with a particular phenotypic trait and exploit them for selection purpose. In genomic selection both genotypic and phenotypic information in reference population is used to generate prediction equations of the genetic merit of individuals (de Koning, 2016). In each scheme, three mating strategies based on natural mating or reproductive technologies were considered. They included;

*Natural mating strategy (NS)***:** This is a breeding strategy where mating is done only using natural mating within the nucleus and transfer of superior genes to the commercial tier. This is the common strategy practiced in both nucleus and commercial tiers in dairy goat breeding in Kenya.

Artificial insemination (AI) with fresh semen strategy (FS): In this strategy, dissemination of superior genetic materials within the nucleus and commercial population solemnly relies on the use of fresh semen. This strategy is not common and rarely practiced in Kenya but could be an option for small holder dairy goat farmers with few does and therefore cannot keep bucks.

Artificial insemination (AI) with cryopreserved semen strategy (CS): This is similar to FS but frozen semen is used to inseminate does in both nucleus and commercial populations. This strategy, mainly mimic breeding farms that import frozen semen for breeding.

Each scheme was therefore, evaluated based on three mating strategies. The first scheme was conventional scheme using natural mating (CNS), AI-Fresh semen (CFS) and AI-Cryopreserved semen (CCS). The second scheme was genomic scheme using natural mating (GNS), AI-Fresh semen (GFS) and AI- Cryopreserved semen (GCS) strategies. The CNS breeding system represents the current dairy goat breeding programme in Kenya and therefore, formed the base scenario for comparison. The alternative breeding goal was a two-tier nucleus breeding system where reproductive technology was utilized.

5.2.4 Genetic and Phenotypic Parameters and Economic Values of Traits in the Breeding Goal

Genetic and phenotypic parameter estimates are some of the input parameters needed when modelling breeding programmes. They should be population specific to minimize biasness attributed to different sample sizes, data structures and evaluation models (de Oliveira *et al*., 2018; Jembere *et al*., 2017). The genetic and phenotypic parameters used in the current study were therefore sourced from previous studies conducted in Kenya (Bett *et al.,* 2007ab, 2011, 2012). Inclusion of traits of economic importance in the breeding goal requires estimation of their economic values (Amer *et al.,* 2001; Bytyqi *et al*., 2015). The economic value of a trait is the change in profit attributed to change in a unit genetic merit of a trait, holding other traits constant (Hazel, 1943). The economic values of traits in the breeding goal for dairy goats under different production systems in Kenya had been estimated by Bett *et al.* (2007a). These economic values were adopted in the current study but adjusted for inflation rates by multiplying each trait by its cumulated discounted expressions (Kearney *et al*., 2005).

The genetic and phenotypic parameter estimates and economic values for traits in the breeding goal for dairy goats are presented in Table 5.1.

Table 5. 1 Phenotypic standard deviations (σ_p), economic values (EVs) in Kenya Shillings (KES, 1US$ =KES 100), heritabilities (h^2), genetic (above diagonal) and phenotypic (below diagonal) of traits in the breeding goal

Parameters	σ_p	h^2	EVs	LW	MW	MY	NKW
LW	2.93	0.26	71.61	**1.00**	0.76	0.08	0.29
MW	4.08	0.58	2.12	0.76	**1.00**	0.16	0.33
DMY	3.01	0.38	20.90	0.43	0.09	**1.00**	0.38
NKW	0.94	0.15	13.68	0.10	0.09	0.08	**1.00**

MY, milk yield; LW, live weight; MW, doe mature weight; NKW, number of kids weaned

Source: Bett *et al.* (2007ab, 2011, 2012).

5.2.5 Genomic Information

Genomic information was simulated in selection index calculations with a correlated trait with heritability close to unity (0.8). The phenotypic and genetic correlations were computed using hr_{gg} and r_{gg}, respectively (Daetwyler *et al.*, 2007, 2008), where h is the square root of the heritability of the trait and r_{gg} is the accuracy of the genomic estimated breeding value.

$$r_{gg} = \sqrt{\frac{\lambda r^2}{\lambda r^2 + 1}} \quad (3)$$

where $\lambda = n_P/n_G$; n_G is the effective number of loci in the base population, depends on the effective size of the populations (N_E) considered in the study and the size of goat genome (L) (Siddiki *et al.*, 2019). The genome size was converted to Morgan by assuming 100Mb = 1 Morgan as reported by Mucha *et al.* (2015). The effective number of loci in the base population was calculated as $n_G = 2N_E L$, n_P is the size of the reference population, r is the correlation of the true breeding value of the genotyped individuals and their phenotypes. The - N_E was calculated based on the number of males and females considered in the study, and were 396 and 1538 for artificial insemination and natural mating strategies, respectively and the L was equal to 30. The same animals were genotyped and phenotyped to constitute the reference populations and therefore, $h^2 = r^2$.

5.2.6 Population Structure and Pathways

The study considered a population of 200,000 does, which represent the total population of dairy goats in Kenya (FAO, 2011). The proportion of the animals in the nucleus was assumed to be 5% while 95% were in the commercial populations (Amayi *et al.,* 2016). Breeding, selection and recording were assumed to be done in the nucleus. Out of the total population of 200, 000 does, five (5) different percentages of nucleus population considered were 1, 5, 10, 15, 20 and 25%. In the NS, the mating ratio used was one buck to twenty-five does (1:25) was considered while in the corresponding FS and CS strategies, the mating ratio used was one buck to one hundred does (1:100). The sex ratio considered was 0.5 male to female. The conception rates within the nucleus considered were 90, 80, and 60% for natural mating (CNM and GNM), AI-Fresh semen (CFS and GFS) and AI-Cryopreserved semen (CCS and GCS), respectively, while in commercial the corresponding conception rates were 80, 70 and 50%. The use of young bucks were considered in the current study to disseminate genetic materials from the nucleus to the commercial population (Amayi *et al*., 2016). The biological and technical parameters used in this study were obtained from previous studies on dairy goats in Kenya (Amayi *et al.,* 2016; Bett *et al.,* 2007ab, 2011, 2012) as presented in Table 5. 2a and b. The economic parameters used in the study are listed in Table 5. 3. Truncation selection was used to select the top performing males and females for breeding in the nucleus. In both the nucleus and commercial populations the main selection pathways were bucks to breed bucks (BB) and does (BD) and does to breed bucks (DB) and does (DD).

5.2.7 Sampling Procedures

Unrelated base populations of bucks and does were sampled to initiate each breeding system. For each animal i in the base population, a vector of true breeding values ($\mathbf{tbv_i}$) was calculated for all the simulated traits using the following equation:

$$\mathbf{tbv_i} = L' x r_1 \quad (4)$$

where L' is the Cholesky decomposition of the genetic (co) variance matrix G, and r_1 is a vector of random numbers from a standardised normal distribution. In a later generation $\mathbf{tbv_i}$ is simulated as:

$$\mathbf{tbv_i} = 0.5x\ (\mathbf{tbv_{i(sire)}} + \mathbf{tbv_{i(dam)}}) \quad (5)$$

The phenotypes of the traits for the i^{th} based animal were calculated as:

$$\mathbf{obs_i} = \mathbf{tbv_i} + C' x\ r \quad (6)$$

where **C'** is the Cholesky decomposition of the environmental (co)variance matrix **R**, and **r** is a vector of random numbers from a standardized normal distribution.

Table 5. 2 a Population, biological and technical information for the nucleus and commercial flocks.

Population	**Nucleus**	**Commercial**
Number of does in the nucleus and commercial	2000	200000
Percentage of does in the nucleus and commercial	1	99
Number of does in the nucleus and commercial	10000	190000
Percentage of does in the nucleus and commercial	5	95
Number of does in the nucleus and commercial	20000	180000
Percentage of does in the nucleus and commercial	10	90
Number of does in the nucleus and commercial	30000	170000
Percentage of does in the nucleus and commercial	15	85
Number of does in the nucleus and commercial	40000	160000
Percentage of does in the nucleus and commercial	20	80
Number of does in the nucleus and commercial	50000	150000
Percentage of does in the nucleus and commercial	25	75
Productive life time (years)		
Bucks in the nucleus to breed bucks in the nucleus	3	
Bucks in the nucleus to breed does in the nucleus	3	
Does in the nucleus to breed bucks	3	
Does in the nucleus to breed does	3	
Bucks in the nucleus to breed bucks and does in the commercial	3	
Does in the commercial to breed bucks in the commercial		4
Bucks in the commercial to breed does in the commercial		5

Table 5.2 b Population, biological and technical information for the nucleus and commercial flocks.

Age at first kidding (years)	**Nucleus**	**Commercial**
Bucks to breed bucks in the nucleus	1.5	
Bucks in the nucleus to breed does in the nucleus	1.5	
Does in the nucleus to breed bucks in the nucleus	1.6	
Does in the nucleus to breed does in the nucleus	1.6	
Bucks in the nucleus to breed bucks and does in the commercial	1.5	
Does in the commercial to breed bucks in the commercial		1.8
Bucks in the commercial to breed does in the commercial		1.7
Other parameters		
Pre-weaning survival rate	0.93	0.90
Post-weaning survival rate	0.95	0.92
Conception rate with Natural mating	0.90	0.80
Conception rate with AI-cryopreserved semen	0.60	0.50
Conception rate with AI-fresh semen	0.85	0.70
Proportion of bucks kept for replacement	0.25	0.25
Proportion of male kids suitable for breeding	0.89	0.80
Proportion of female kids suitable for breeding	0.90	0.81
Proportion of does kept for replacement	0.75	0.75

5.2.8 Estimation of Profitability

The annual profit per doe (π) was calculated as follows:

$$\pi = \sum_{t=0}^{T} \left(\frac{R_t - C_t}{(1+r)^t}\right) \quad (7)$$

where; T is the evaluation period (15 years), R_t is the annual benefits of genetic improvement calculated as realised genetic gain per doe per year, C_t is the costs of genetic improvement which include fixed and variable costs and r is the discounting rate.

The discounting rate of 5% was used as recommended by Bird & Mitchel (1980). Variable costs directly related to performance and pedigree recording used in the current study as presented in Table 5.3. Fixed costs were those incurred in one round of selection per year and

Table 5. 3 Economic parameters in Kenya shillings ((1US$ =KES 100) for nucleus and commercial populations

Cost elements per doe/year	Cost (KES)
Identification, pedigree recording and data processing	105
Milk recording	8.33
Live weight recording	50
Doe mature weight recording	8.33
Maintenance of buck	2081
Cost of oestrous synchronisation	422
Cost per dose of liquid semen	500
Cost per dose of frozen semen	700
Liquid nitrogen per straw/year	260
Cost of inseminator	500
Cost of genotyping using GoatSNP50 Bead Chip	10000

were the overhead costs of running the nucleus. The annual genetic gain, return, costs, accuracy of selection and profitability were calculated for an investment period of 15 years. Genetic gain was calculated per doe per year. The rate of genetic gain for each doe was predicted as linear regression of true breeding values for each trait in the breeding goal weighted by its corresponding economic values and expressed per year. Profitability was computed as the difference between the returns and the total costs. The costs related to management of buck per year were from Bett *et al.* (2012) and adjusted for price fluctuations based on the current inflation rates. The costs for fresh and cryopreserved semen were based on current market prices for local semen in Kenya. However, costs of imported cryopreserved goat semen can vary from KES 2000.00 to 5000.00 depending on genetic superiority of the buck and the exporting country. The cost of oestrous synchronisation in this study was estimated based on protocol that use progesterone (CIDR), Prostaglandin and equine chorionic gonadotropin (Karaca *et al.,* 2010; Pietroski *et al.,* 2013).

5.2.9 Evaluation Procedures

The breeding schemes and strategies were modelled and evaluated using a deterministic simulation approach. The ZPLAN computer programme (William *et al.,* 2008) was used to

model the schemes and strategies. The genetic, biological and economic parameters considered for the study were used to compute annual genetic gain, costs, returns and profits for the breeding schemes and strategies, and genetic gain for single traits without changing selection strategies over the investment period with one round of selection using the gene-flow method and selection index procedures.

5.3 Results

The annual genetic gain, returns, costs and profit per doe for the three mating strategies considered under conventional and genomic schemes after the investment period of 15 years are presented in Table 5.4. The study found that mating strategy and breeding scheme influenced annual genetic gain, returns, costs and profit per doe.

Table 5. 4 Annual genetic gain, returns, costs and profits per doe in Kenya Shillings (1US$ =KES 100) in different mating schemes and strategies

Parameters	Conventional strategies			Genomic strategies		
	CNM	CFS	CCS	GNM	GFS	GCS
Genetic gain	44.92	47.94	44.32	56.46	58.74	54.53
Return	620.32	771.63	724.91	781.62	955.11	900.81
Cost	20.96	23.38	24.47	45.96	48.38	49.47
Profit	599.36	748.25	700.44	735.66	906.73	851.34

*CNM, conventional natural mating; CFM, conventional fresh semen; CCS, conventional cryopreserved semen; GNM, genomic natural mating; GFS, genomic fresh semen; GCS, genomic cryopreserved semen.

Among the three mating strategies considered under conventional scheme, AI-Fresh semen (CFS) realised the highest response to selection compared to AI-Cryopreserved semen (CCS) and natural mating (CNM). A similar trend was observed under genomic selection (GS) scheme where AI-Fresh semen (CFS) realised the highest response to selection compared to AI-Cryopreserved semen (CCS) and natural mating (GNM). For instance, the CFS realised additional KES 3.00 and 3.61 in genetic gain compared to CNM and CCS, respectively. The CNM on the other hand out performed CCS by KES 0.61 in genetic gain. In terms of returns to selection per doe per year, CFS was superior to CNM and CCS by KES 151.31 and 46.72, respectively, while returns realised by CCS surpass those of CNM by KES 104.59. The highest costs per doe per year were realised in the AI-schemes with CCS and CFS realizing KES 24.47

and 23.38, respectively, compared to KES 20.96 obtained in CNM. Although, the AI schemes, realised, higher costs, they outperformed the CNM in profitability. The CFS was superior to CNM and CCS in profitability per doe per year by KES 148.89 and 47.81, respectively, while CCS realised additional profit of KES 101.08 compared to CNM. Although the trends remained similar across the three mating strategies under GS scheme as observed in conventional scheme, there were variations in the difference realised in all the parameters. For instance, the GFS realised additional KES 2.28 and 4.21 in genetic gain, KES 173.49 and 54.31 in returns, and KES 171.07 and 55.39 compared to CNM and CCS, respectively. The CNM on the other hand out performed CCS by KES 1.93, 119.19 and 115.68 in genetic gain, returns and profit, respectively. The highest costs per doe per year were realised in the AI-schemes with GCS and GFS realizing KES 49.47 and 48.38, respectively, compared to KES 45.96 obtained in GNM. As obtained in CCS, the GCS strategy incurred similar additional cost of KES 1.09) and 3.51 per doe per year compared to GFS and GNM, respectively. The GFS also incurred additional cost of 2.42 compared to GNM strategy.

In comparison to conventional, genomic scheme (GS) generally had high annual genetic gain, returns, costs and profit per doe. The trends, however, remained similar across the three mating strategies as observed under conventional scheme. The GS realised additional KES 11.54, 10.80 and 10.21 genetic gains in the GNM, GFS and GCS mating strategies, respectively, compared to those realised in CNM, CFS and CCS. The corresponding additional returns in the GS compared to CS schemes were KES 161.30, 183.48 and 175.90. All the mating strategies in the GS scheme had additional KES 25.00 per doe per year compared to CS mating strategies attributed to genotyping costs. The profitability in the GS scheme were higher than those in the CS scheme with GNM, GFS and GCS mating strategies realizing additional KES 136.30, 158.48 and 150.90, respectively, above the corresponding profits realised in CNM, CFS and CCS.

The response to selection for individual traits in the breeding goal followed the same trend to those observed in the overall breeding goal. The genetic gains for individual traits were affected by both mating schemes and strategies considered, as presented in Table 5.5. Generally, among the mating strategies, those that used fresh semen (CFS and GFS) realised high response for each individual trait followed by those that adopted natural mating (CNS and GFM). As observed under genetic gain in the overall breeding goal, the CCS and GCS strategies also reported the lowest response to individual traits. For instance, under CS scheme, the genetic gain for MY under CFS strategy surpassed those realised in CNM and CFS by 0.001 kg and 0.004 respectively. The CNM strategy realised additional genetic gain of 0.003 kg in

MY. The CFS also realised 0.02 and 0.02 kg more in LW compared to CNM and CCS, respectively. On the other hand, CNM outperformed CCS by 0.005 kg in LW. The CFS outperformed CNM and CCS by 0.04 and 0.05 kg, respectively, in MW, while the corresponding values were 0.001 and 0.001 kg in NKW. The CNM also realised additional 0.01 over CCS for MW but similar with CCS in NKW.

Under the GS scheme, the GLS realised additional genetic gain of 0.001 and 0.007 kg, 0.01 and 0.02 kg, and 0.03 and 0.05 kg in MY, LW and MW compared to GNM and GCS, respectively. On the other hand, the GNM realised additional genetic gain of 0.01, 0.01 and 0.02 kg in MY, LW and MW compared to GCS, respectively. The GFS realised additional 0.001 and 0.004 in NKW compared to GNM and GCS, respectively. The GNM realised additional 0.003 in NKW compared to GCS. For the individual traits under the GS scheme, all the performances surpassed those of CS scheme among all the three mating strategies. The MY under GS scheme realised additional 0.04, 0.04 and 0.04 kgs genetic gains for GNM, GFS and GCS, respectively, compared to those in CNM, CFS and CCS. The annual genetic gain for LW and MW in the GS scheme were higher than those in the CS scheme with GNM, GFS and GCS mating strategies realizing additional kgs 0.10, 0.08, 0.081, 0.13, 0.13 and 0.12 genetic gains, respectively, compared to those realised in CNM, CFS and CCS.

Table 5. 5 Annual genetic gain for individual traits in the three mating strategies in conventional and genomic breeding schemes.

Trait	Conventional strategies			Genomic strategies		
	CNM	CFS	CCS	GNM	GFS	GCS
MY (kg)	0.06	0.06	0.06	0.11	0.11	0.10
LW (kg)	0.19	0.21	0.20	0.29	0.30	0.28
MW (kg)	0.57	0.61	0.56	0.70	0.73	0.68
NKW(n)	0.02	0.02	0.02	0.07	0.07	0.06

*CNM, conventional natural mating; CFM, conventional fresh semen; CCS, conventional cryopreserved semen; GNM, genomic natural mating; GFS, genomic fresh semen; GCS, genomic cryopreserved semen; MY, milk yield; LW, live weight at 12 months; MW, doe mature weight; NKW, number of kids weaned; n, number of kids

For the NKW under GS, additional 0.04, 0.04 and 0.04 genetic gains were realised in GNM, GFS and GCS, respectively, compared to those in CNM, CFS and CCS mating strategies. The GS scheme generally, realised higher genetic gain for the individual traits than the CS scheme under all the three mating strategies considered.

Generally, irrespective of the mating strategies, the selection intensity was higher in males compared to females, and similar in both CS and GS schemes (Table 5.6). Mating strategies, however, influenced selection intensity of males but not females. The CFS realised high selection intensity (2.68) followed by CCS (2.56) and CNM (2.20). For the accuracy of selection, GS scheme had higher accuracy of selection irrespective of the mating strategies compared to CS scheme. Mating strategies also affected accuracy of selection in males but not females in both CS and GS. The CFS and GFS had the highest selection intensity in both males and females followed by CCS and GCS and CNM and GNS mating strategies.

Table 5. 6 Selection intensity and accuracy of selection for the three mating strategies

Parameters	Sex	Conventional Scheme			Genomic Scheme		
		CNM	CFS	CCS	GNM	GFS	GCS
Intensity	Buck	2.20	2.68	2.56	2.20	2.68	2.56
	Does	2.06	2.06	2.06	2.06	2.06	2.06
Accuracy (%)	Buck	78.00	88.00	85.00	88.00	93.00	92.00
	Does	70.00	71.00	70.00	84.00	85.00	85.00

*CNM, conventional natural mating; CFM, conventional fresh semen; CCS, conventional cryopreserved semen; GNM, genomic natural mating; GFS, genomic fresh semen; GCS, genomic cryopreserved semen.

Accuracy of selection was high for males in CFS and GFS, followed by CCS and GCS and CNM and GNM strategies. The females realised similar accuracies of selection in all the strategies in both conventional and genomic schemes. The GNM, GFS and GCS strategies under GS scheme realised additional accuracy of 0.10, 0.05 and 0.07 in males compared to CNM, CFS and CCS strategies under the CS scheme, respectively. The Females under the GS scheme realised additional accuracy of 0.14 compared to CS scheme.

The optimal nucleus size for the three mating strategies under CS and GS schemes were investigated by varying the nucleus population size to obtain trends on response to selection. The effects of changing the nucleus size on overall genetic gain and profitability of the breeding programme are presented in Figure 5.1. The findings demonstrate that, the three mating strategies followed the same trends in genetic gain as nucleus size population increased. The genetic gain in the three mating strategies increased with nucleus size at diminishing rate with CFS outperforming CNM and CCS in that order. Similar observation was made on the GS scheme, as GFS was ranked higher followed by GNM with GCS trailing. The GS scheme, however, ranked higher compared to CS scheme. In both schemes (CS and GS), although at 1% nucleus size the annual genetic gain between the three mating strategies was negligible, the differences became pronounced as from 10% with optimal gains being realised at 15% nucleus size followed by a decline thereafter. Although the overall genetic gain increased with increased in nucleus size up to 15%, the profitability per doe per year decreased. The highest profits were realised under low proportion of nucleus size with the profit decreasing at diminishing rate as population size increased. The highest profit was realised under low proportion of nucleus size with the profit decreasing at diminishing rate as population size increased. Although all the mating strategies in CS scheme realised profits irrespective of the decline with population size, losses were obtained in all the mating strategies in GS scheme when the nucleus population increased beyond 22%. The costs increased with increased nucleus population size in both conventional and genomic scheme (results not presented).

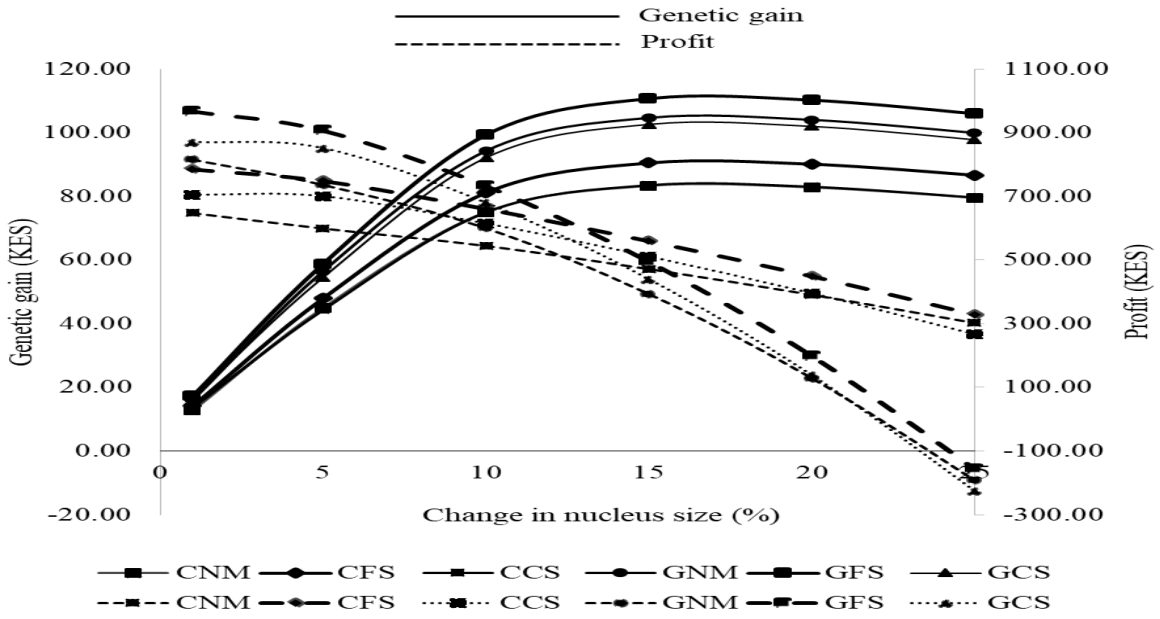

Figure 5. 1 Change in annual genetic gain and profit in (KES) with change in nucleus size in conventional and genomic schemes assuming the three mating strategies

5.4 Discussion

The present study has confirmed the hypothesis that mating strategies utilizing reproductive technologies and genomic selection could improve response to selection as compared to those utilizing natural mating and conventional selection. However, natural mating strategy slightly surpassed AI-Frozen semen strategy in terms of genetic gain. This study concurs with previous studies in cattle that reported high genetic and economic returns in artificial insemination strategy compared to natural mating (Gicheha *et al.,* 2018; Thomasen *et al.,* 2016).

The current study found that AI- Fresh semen strategies (CFS and GFS) were superior to natural mating (CNM and GNM) and AI-Cryopreserved semen (CCS and GCS) strategies in terms of annual genetic gain, returns and profit per doe. The superiority of AI-Fresh semen (CFS and GFS) over natural mating (CNM and GNM), AI-Cryopreserved semen (CCS and GCS) strategies could be attributed to high intensity and accuracy of selection as demonstrated in Table 5.6. The high intensity in CFS and GFS could be explained by two reasons. Firstly, in comparison to CNM and GNM, which used natural mating, CFS and GFS strategies used AI-Fresh semen. This increased the reproductive rate of males as each male was mated to 100 does compared to 25 does in CNM and GNM. Therefore, large number of offsprings per year per buck were obtained in CFS and GFS compared to CNM and GNM. Since fewer males are needed when using AI than natural mating, the selection pressure was higher in CFS and GFS where there were more bucks than in CNM and GNM strategies. This is evident in Table 6 of the current study. Secondly, although both AI-Fresh semen (CFS and GFS) and AI-Cryopreserved (CCS and GCS) strategies adopted reproductive technology (AI), that increased reproductive rate of the bucks, the fertility rate for the AI- Fresh semen based strategies (CFS and GFS) were higher 70-85% (Andreea *et al,* 2016; Luo *et al.,* 2019) than those of CCS and GCS (50-60%) (Arrebola *et al.,* 2014; Kifaro *et al.,* 2007; Salvador *et al.,* 2005). The high fertility in CFS and GFS contributed to higher number of potential males for selection hence high selection pressure than in CCS and GCS. These two lines of reasoning are in agreement with previous finding, which have demonstrated superiority of reproductive technologies such as AI to natural mating in response to selection (Gicheha *et al.,* 2018; Van Doormaal & Kistemaker, 2003) and superiority of fresh over preserved semen in terms of viability and fertility (Arrebola *et al.,* 2014; Juma, 2017). The superiority of AI-Fresh semen strategies (CFS and GFS) in accuracy of selection to natural mating (CNM and GNM) and AI-Cryopreserved semen (CCS and GCS) based strategies could be traced to the number of relatives providing information for the traits in the breeding goal. Since AI-Fresh semen strategies (CFS and GFS)

had high reproductive and fertility rates compared to natural mating (CNM and GNM) and AI-Cryopreserved semen (CCS and GCS), respectively, it had more sources of information for traits in the breeding goal. The more the number of information used to estimate the breeding value of an animal the higher the response to selection. This concurs with previous findings which have demonstrated the linear relationship between number information sources and response to selection (Rischkowsky & Pilling, 2007). These findings therefore demonstrate that, utilization of reproductive technologies such as AI using fresh semen would be more beneficial irrespective of the breeding scheme adopted.

The current study although has demonstrated the superiority of fresh semen over cryopreserved semen and natural mating, the use of cryopreserved semen and natural mating in dairy goats is common in the tropics. Cryopreserved semen is attributed to few dairy goat farmers and breeder groups who import semen from developed countries. Natural mating, however, is more common between both small holder and breeder groups who source their genetic materials locally. This study has demonstrated that, although natural mating is superior to cryopreserved semen in terms of genetic gain and low costs of production, it trails the use of cryopreserved semen in returns and profitability of the breeding program (Table 5.3). The superiority of natural mating strategies (CNM and GNM) in genetic gain could be attributed to high fertility rate when natural mating is used and no additional cost incurred in processing and storage of semen as in AI- cryopreserved semen strategies (CCS and GCS). Previous studies have demonstrated high fertility rate, which translates to high conception rates in natural mating as compared to use of cryopreserved semen (Agossou & Koluman, 2018). The superiority of AI-Cryopreserved semen (CCS and GCS) to natural mating (CNM and GNM) strategies in returns and profitability could be attributed to number of offsprings realised, which in turn increases accuracy of selection (Table 5.6) and therefore returns to selection per doe which could overcome the additional costs to realize profit (Okeno *et al.*, 2013). The use of AI-Cryopreserved semen is currently on the upward trajectory because of importation of dairy goat genetics from the developed countries. The utilization of reproductive technologies such as AI realised high selection intensity and therefore response to selection compared to breeding schemes that use natural mating (Gicheha *et al.*, 2018; Van Doormaal & Kistemaker, 2003).

The genetic gain under conventional scheme (CS) for milk yield (MY) and mature weight (MW) was high under AI-Fresh semen based strategy (CFS) compared to AI-Cryopreserved semen (CCS) and natural mating (CNM) based strategies. This outstanding performance of CFS semen was attributed to the fact that CFS was better than CCS in terms of fertility rate and CNM in terms of accuracy of selection. The same trend was observed as in the MY and

MW, however, unexpectedly genetic gain for live weight (LW) was high in CCS semen compared to CNM. The reason why genetic gain for LW in CCS was higher than in CNM was unclear. The number of kids weaned (NKW) was high in CFS compared to both CCS and CNM. This was attributed to the high fertility rate and high accuracy of selection in CFS strategy. The lack of difference in NKW between CCS and CNM strategies could be linked to low accuracy of selection in CS scheme and also given the fact that NKW is a trait of low heritability. Traits of low heritability are controlled by many genes with minor effect (Zhang *et al*., 2019). Generally, the annual genetic gain for all the individual traits followed similar trend as those reported for dairy goats in Kenya (Amayi *et al.,* 2016; Bett *et al.,* 2012). The productive traits in the current study also performed better than the reproductive trait (NKW). This could be attributed to the antagonistic relationship between productive and reproductive traits (Berry *et al.,* 2014; Carthy *et al.,* 2016).

Implementation of genomic scheme maintained similar trend across all the three mating strategies as in the conventional scheme, however, it had additional improvement in all the parameters measured. This additional improvement in the strategies under the genomic scheme was attributed to high accuracy of selection realised in the genomic compared to the conventional scheme. Genomic selection increases accuracy of selection (Meuwissen *et al.,* 2013). These findings concur with previous studies that reported high annual genetic gain following combination of reproductive technologies with genomic selection (de Roos *et al.,* 2011; Granleese *et al.*, 2015, 2017; Thomasen *et al.,* 2016). Under the genomic scheme (GS), MY and MW and LW followed similar trend as observed in CS scheme with exception to LW under GNM was high compared to GFS scheme. The clear difference observed in NKW between GFS and GNM could be attributed to high accuracy of selection in the GS scheme which works well with traits of low heritability such as NKW.

The current study also found that genetic gain increased with increased nucleus size up to 15% and thereafter, it declined in both conventional and genomic schemes. The increase in genetic gain with increase in nucleus population size could be attributed to the less variability in the small populations (Abdel-Salam *et al.,* 2007). On the other hand, the decline in genetic gain with increased nucleus population could be due to reduction in variance of the selection response (Meuwissen, 1990). The author mentioned that increase of the nucleus size hardly affected this variance. The persistence of similar variance in the selection response with time could lead to inbreeding depression that could influence response to selection negatively. Similar trends of increase and decline in genetic gain with increase nucleus population size have been observed in other studies (Abdel-Salam *et al.,* 2007; Kariuki *et al.,* 2014;

Meuwissen, 1990; Okeno *et al.,* 2013). Increasing nucleus population size is likely to reduce rate of inbreeding, as it increases the selection intensity in the males (Kariuki *et al.,* 2014). In the present study profit decreased with increased nucleus size. The decrease in the profit is attributed to increase in the cost of running the schemes with more animals. Taking into account genetic gain, costs and profit, the optimal nucleus population size profit was found to be between 14 and 16 % across all the mating strategies and breeding schemes. Therefore, it would not be economical increase nucleus size beyond 16 % as it would not yield increased genetic gain, and returns would not offset the costs leading to declining profitability of the breeding programme (Okeno *et al.,* 2013).

5.5 Conclusion

In conclusion, the current study demonstrated that adoption of reproductive technologies such as artificial insemination, especially those utilizing fresh semen would optimize response to selection in dairy goat breeding programmes in the tropics. The response to selection in such breeding programmes can be maximized in combination with genomic selection.

CHAPTER SIX

A COMBINATION OF REPRODUCTIVE TECHNOLOGY AND GENOMIC SELECTION OPTIMIZES RESPONSE TO SELECTION IN DAIRY GOAT BREEDING PROGRAMMES

Abstract

Artificial insemination (AI) can lead to faster genetic progress, however, intensive use of semen from few elite bucks could lead to increase in rate of inbreeding and reduction in genetic diversity as well as inbreeding depression in a flock. Genomic selection on the other hand, reduces the rate of inbreeding by accurately estimating the Mendelian sampling effects, which reduces the co-selection of relatives and lower rates of inbreeding. It was hypothesised that use of genomic selection combined with reproductive technology and appropriate mating designs would improve response to selection and reduce level of inbreeding. The premise was tested by modelling and evaluating two dairy goat breeding schemes utilising reproductive technology and different mating designs. The conventional scheme and genomic breeding scheme were modelled and evaluated using stochastic model. Five mating designs considered were: Random mating, positive assortative mating negative assortative mating, Minimising inbreeding and Maximising inbreeding. The findings demonstrated that genomic scheme was not significantly different from conventional scheme in terms of level of inbreeding. The genomic scheme, however, was significantly superior to conventional scheme in terms of genetic gain and accuracy of selection. Similar trend as in Rand mating design was also observed under negative assortative, Minimising and Maximising inbreeding mating designs with exception of positive assortative mating. The positive assortative mating design had significantly high level of inbreeding under genomic scheme compared to that in conventional scheme. The mating designs significantly influenced level of inbreeding, accuracy of selection across the two schemes with exception of genetic gain. The Minimising inbreeding mating scored the lowest level of inbreeding and Maximising inbreeding scored the highest from the rest of the mating designs in both conventional and genomic schemes. There was no significant difference between exotic and crossbred genotypes in terms of level of inbreeding in both conventional and genomic schemes. The genetic gain and accuracy of selection for crossbreds, however, was significantly different from the other goat genotypes. The levels of inbreeding and genetic gain increased with increased in number of generations in both conventional and

genomic schemes. The current study demonstrated that, breeding schemes that adopt a combination of reproductive technologies and genomic selection would optimize genetic gain compared to conventional schemes. It also demonstrated that the choice of mating design when using reproductive technologies and genomic selection is important for long-term genetic gain. Minimising inbreeding mating design constrained rate of inbreeding while maintaining rate of genetic gain compared to the other mating designs.

6.1 Introduction

The dairy goat industry is gaining popularity and more especially among the small holder resource households in the developing countries (Kahi & Wasike, 2019; Miller & Lu, 2019). This is because of decreasing land sizes for dairy cattle production (Bett *et al*., 2009; Mbindyo *et al.,* 2018), high goat milk quality and perception that goat milk is medicinal and could prevent or treat some diseases (Haenlein, 2004; Lad *et al.,* 2017; Zenebe *et al.,* 2014). Therefore, with such high demand in dairy goat, use of reproductive technologies such as artificial insemination in dairy goat industry could facilitate quick genetic progress, leading to faster genetic improvement. However, among local dairy goat farmers adoption of reproductive technologies is still low, and breeding is mainly by natural mating. A shortage of breeding bucks has led to the need to use reproductive technologies such as artificial insemination (AI) to avail breeding animals. These technologies, however, have not been used adequately in small ruminants (Amiridis & Cseh, 2012), particularly in dairy goats.

Artificial insemination (AI) can lead to faster genetic progress, however, intensive use of semen from few elite bucks could lead to adverse effect of inbreeding, reduce genetic diversity and inbreeding depression in a flock (Fernandez *et al.,* 2011; Mwangi *et al.,* 2020). The conventional Best Linear and Unbiased Prediction (BLUP) selection method cannot address the problems associated with use of reproductive technologies because of its inability to partition Mendelian sampling error leading to co-selection of relatives (Daetwyler *et al.,* 2007). Controlling rates of inbreeding to pre-determined levels leads to lower rate of gain (Mwangi *et al.,* 2020), thereby creating a challenge of meeting the high demand for animal products. There is therefore need for adoption of alternative breeding methods such as Genomic selection (GS).

Genomic selection (GS) reduces the rate of inbreeding by accurately estimating the Mendelian sampling effects, which reduces the co-selection of relatives and lower rates of inbreeding (Cao *et al.,* 2020; Buch *et al.,* 2012; Thomasen *et al.,* 2016). It uses DNA markers to estimates breeding value of an animal (Clark *et al.,* 2012; Yudin *et al.,* 2016), and as a result, accurately estimates the breeding value at an early age for breeding animals, giving high

accuracy of selection and reducing generation intervals (Van der Werf, 2013). The GS also assist breeding programmes that have objectives including traits which are difficult to measure such as meat quality, feed efficiency, reproduction, and disease resistance (Boichard *et al.,* 2016). The Use of GS for instance, has reduced the rate of inbreeding from 0.64 to 0.55 in dairy cattle (Thomasen *et al.,* 2016).

Although GS reduces rate of inbreeding, the mating design with which the selected animals are mated also has an impact on its effectiveness. Both phenotypic and genomic selection focus on improvement by truncation selection, mainly ignoring the role of mating and complementation as an evolutionary force (Akdemir & Sánchez, 2016). The GS focuses on best performance of parents before mating, while mating designs includes information on complementation of parents to be mated, making the later to be more sustainable in the longer term (Akdemir & Sánchez, 2016). Recent studies have reported substantial increase in the rate of inbreeding in dairy cattle after the introduction of GS (Doekes *et al.,* 2018; Makanjuola *et al.,* 2020; Maltecca *et al.,* 2020). These studies recommended the need for efficient management of genetic diversity in GS breeding schemes. One of the methods to manage GS breeding schemes could be through choosing appropriate mating designs that can increase long-term genetic gains and reduce rate of inbreeding, expression of inbreeding depression and loss genetic diversity (Henryon *et al.,* 2014; Liu *et al.,* 2017; Pryce *et al.,* 2012a). The current study, therefore, aimed at determining the rate of inbreeding, estimated breeding value and accuracy of selection in conventional and genomic schemes with different mating designs utilizing reproductive technology to optimize response to selection in dairy goats.

6.2 Materials and Methods

6.2.1 Population Structure

A historical population assumed comprised 20,000 animals with equal number of males and females with 15 generations. The reason being that effective population size in livestock populations generally shows a declining trend due to domestication (Henson, 1992). Therefore, the population considered should be larger than the recent population which was 10,000. Historical generations were simulated to create initial linkage disequilibrium (LD) depending on the populations considered and to establish mutation-drift equilibrium (Sargolzaei & Schenkel, 2009). Mutation introduces new variation and genetic drift shifts the variation to fixation. The mating system in historical generations was based on the union of gametes randomly sampled from the male and female gametic pools. Thereafter, recent populations of 10,000 females and 100 males with an effective population size (Ne) of 396 were simulated

with 15 generations. The number of offsprings per doe was considered to be 2 with a sex ratio of 0.5. The breeding strategy was artificial insemination (AI) with the mating ratio used of one buck to one hundred does (1:100). In the exotic populations, the total number of exotic dairy goats selected were the best 3100 females and 31 males from the common based population with a Ne of 123 (Paiva *et al*., 2020). The indigenous goat population were selected from the rest of the common based population with a total of 6800 females and 68 males with a Ne of 269 (Ogah, 2012). The parameters used in the study are summarized in Table 6.1.

Table 6. 1 Summary of the parameters used in the study

Parameters	**Values**
Number of chromosomes	29
Total chromosome length	2737cM
Number of markers	307
Number of QTL	109
Distribution of additive QTL effects	Gamma (Shape 0.4)
Milk yield heritability	0.38
Training population	20000
Validation population	10000
Number of replications	10
Number of generations	15

6.2.2 Breeding System, Schemes and Mating Designs

A two-tier closed nucleus breeding system was considered. The breeding system consisted of two-nucleus schemes, namely, conventional and Genomic schemes. The conventional scheme mimicked the current breeding system in Kenya, where animals are selected based of pedigree and phenotypic information. The genomic scheme, on the other hand represented an alternative scheme where selection is based on markers in addition to phenotypic information (Meuwissen *et al*., 2001; 2013). In each scheme, five mating designs using artificial insemination (AI) were considered. They included; Random mating (Rand), positive assortative mating (+ve), negative assortative mating (-ve), Minimising inbreeding (Min) and Maximising inbreeding (Max) (Sargolzaei & Schenkel, 2009). In random mating design (Rand), a sire and a dam were allocated at random for each new born progeny with a probability that was proportional to the genetic contribution that they received from the

selection algorithm, while in assortative matings, sires mate to dams based on similarity (+ve) or dissimilarity (-ve). On the other hand, in the optimised mating designs, pairs of mates were chosen such that inbreeding was minimized (Min) or maximized (Max) in the next generation using annealing method as described by Sonesson & Meuwissen (2000). Under conventional scheme the mating designs were described as conventional random (C^{Rand}), positive assortative mating (C^{+ve}), negative assortative mating (C^{-ve}), Minimising inbreeding (C^{Min}) and Maximising inbreeding (C^{Max}). In Genomic breeding scheme, they were described as genomic random (GRand), positive assortative mating (G+ve), negative assortative mating (G-ve), Minimising inbreeding (GMin) and Maximising inbreeding (GMax).

6.2.3 Genetic and Phenotypic Parameters of Traits in the Breeding Goal

Genetic and phenotypic parameter estimates are some of the input parameters needed when modelling breeding programmes. They should be population specific to minimize biasness attributed to different sample sizes, data structures and evaluation models (de Oliveira *et al*., 2018; Jembere *et al*., 2017; Ndung'u *et al*., 2020). Therefore, the genetic and phenotypic parameters used in the current study were sourced from previous studies conducted in Kenya (Bett *et al*. 2007ab, 2011, 2012). Single trait selection with milk yield (MY) being the trait in the breeding goal was considered. The heritability for MY was 0.38 and the phenotypic variance used was 9.06 (Bett *et al*., 2012).

6.2.4 Computation of Breeding Values in the Selection Schemes

Conventional Scheme

The model used to calculate estimated breeding value from the conventional BLUP model was according to Henderson (1984). The model is:

$$\boldsymbol{y = \mu 1_n + Z_a + e} \quad (8)$$

where $y =$ is the vector of trait phenotype, $\mu =$ is the overall mean, $1_n =$ vector of n ones, $a =$ vector of additive genetic effects of each individual, $Z =$ is a design matrix for additive genetic effect and $e =$ is the residual variance.

Genomic Scheme

The genomic scheme was an alternative to conventional scheme where animals were selected based on genetic markers. In this scheme, a total number of 307 markers with a chromosomes length of 2737 cM were considered (Schibler *et al.,* 1998). The number of quantitative trait loci for MY used was 109 (Martin *et al.,* 2017). The genomic heritability

closed to one (0.9) was considered in the current study (Dekkers, 2007). The allelic effects of the QTL were sampled from a gamma distribution with a shape parameter of 0.4 (Hayes & Goddard, 2001). The marker effects were estimated using the ridge regression model in the genomic scheme as described in Fernando *et al.* (2007) and Meuwissen *et al.* (2001). The statistical model used was:

$$\boldsymbol{y} = \boldsymbol{\mu}\mathbf{1}_{\boldsymbol{n}} + \boldsymbol{W}_{\boldsymbol{g}} + \boldsymbol{e} \quad (9)$$

where $y =$ is the vector of trait phenotype, $\mu =$ is the overall mean, $1_n =$ vector of n ones, $g =$ is a vector of allele substitution effects due to the i^{th} genotype, $W =$ is a design matrix that has 0, 1, 2 for the number of alleles of type g_i present in the j^{th} animal , $e =$ is the residual variance.

6.2.5 Evaluation Procedures

The breeding schemes and mating designs were modelled and evaluated using a stochastic simulation approach. The QMSim software (Sargolzaei & Schenkel, 2009) was used to model the schemes and different mating designs. The genetic and biological parameters considered for the study were used to compute estimated breeding values, inbreeding and accuracies for the breeding schemes and mating designs for single trait for each generation. The BLUP via an animal model approach and ridge regression method were used to compute estimated breeding values for conventional and genomic schemes, respectively. Statistical analyses were conducted using analysis of variance (ANOVA) with General Linear Model (GLM) of SAS (Version 9.0).

6.3 Results

The response to selection in the two breeding schemes evaluated in terms of inbreeding, genetic gain and accuracy of selection for each mating design are presented in Table 6.2. The random mating design (Rand) was used as a default mating design for comparing conventional (CS) and genomic (GS) schemes. The findings demonstrated that GS scheme was not significantly different compared to CS scheme in terms of level of inbreeding. The GS scheme, however, was significantly superior to CS scheme in terms of genetic gain and accuracy of selection (Table 6.2). For instance G^{rand} realised additional 11.3166 g and 0.391% genetic gain and accuracy of selection compared to Crand , respectively. Similar trend as in C^{Rand} and G^{Rand} mating designs was observed under C^{-ve} and G^{-ve}, C^{Min} and G^{Min} and C^{Max} and G^{Max} mating designs with exception of C^{+ve} and G^{+ve}. The G^{+ve} mating design had significantly high level of

inbreeding compared to that in C^{+ve} mating design. The mating designs significantly influenced level of inbreeding, accuracy of selection across the two schemes with exception of genetic gain. For instance, in the C^{Max} was significantly different (P> 0.05) from the rest of the mating designs in terms of level of inbreeding. On the other hand, C^{Rand}, C^{+ve} and C^{-ve} were not significantly different (P< 0.05) from each other as well as C^{Rand}, C^{-ve} and C^{Min} in terms of inbreeding. However, C^{Min} had the lowest level of inbreeding compared to the rest of the mating designs. In terms of accuracy of selection, C^{+ve}, C^{-ve} and C^{Max} each was significantly different (P< 0.05) from C^{Rand} and C^{Min}, while C^{Rand} and C^{Min} were not significantly different (P> 0.05) from each other.

The level of inbreeding for G^{Max} and G^{+ve} were significantly different from the rest of the mating strategies while G^{Rand}, G^{-ve} and G^{Min} were not significantly different (P> 0.05) from each other. The G^{Min} mating design had the lowest level of inbreeding compared to the other mating designs as observed in the C^{Min} mating design. In terms of accuracy of selection, G^{Max} significantly differed from G^{Min}, G^{+ve} and G^{Rand}. The G^{+ve} and G^{-ve} also differed significantly from each other. On the other hand, G^{Rand}, G^{+ve} and G^{Min} as well as G^{Rand}, G^{-ve} and G^{Min} were not significantly different from each other. The G^{-ve} and G^{Max} mating designs were also not significantly different from each other.

Table 6. 2 Average genetic gain, inbreeding and accuracy of EBV in conventional and genomic scheme with different mating designs utilising reproductive technology.

Mating design	Conventional Scheme			Genomic Scheme		
	Inbreeding	Genetic gain (g)	Accuracy (%)	Inbreeding	Genetic gain (g)	Accuracy (%)
Rand	0.01^{bc}	23.09^{a}	60^{b}	0.01^{c}	34.41^{a}	91^{ab}
+ve	0.02^{b}	23.61^{a}	61^{a}	0.09^{b}	37.31^{a}	92^{a}
-ve	0.02^{bc}	22.65^{a}	58^{c}	0.02^{c}	32.41^{a}	90^{bc}
Min	0.01^{c}	23.36^{a}	59^{b}	0.01^{c}	34.67^{a}	91^{ab}
Max	0.23^{a}	21.96^{a}	54^{d}	0.23^{a}	31.16^{a}	89^{c}

**Means with different superscripts within the same column differ significantly at P> 0.05*

*Rand: Random Mating, +ve: Positive assortative mating, -ve: Negative assortative mating, Min: Optimised mating by minimising inbreeding, Max: Optimised mating by maximising inbreeding, g:grams

The effect of goat genotypes on response to selection are presented in Table 6.3. Goat genotypes significantly affected level of inbreeding, genetic gain and accuracies of selection in both the CS and GS schemes. In Table 6.3, therefore only the results from C^{min} and G^{min} mating designs, which were found to be the most favourable in terms of response to selection in the two schemes are presented. In the CS scheme, there was no significant difference between exotic and crossbreds genotypes in terms of inbreeding. The level of inbreeding for indigenous goats differed significantly from the other goat genotypes. The genetic gain and accuracy of selection for crossbreds was significantly different from the other goat genotypes. In both exotic and indigenous goat genotypes, the genetic gain and accuracy were not significantly different. The level of inbreeding under GS scheme followed similar trend as observed in CS scheme. The genetic gain under GS, however, differed significantly among the three goat genotypes, with the crossbred realised the highest, followed by exotic and indigenous genotypes. There was no significant difference between indigenous and crossbred genotypes in terms of accuracy of selection. The exotic goat, however, differed from the rest of the goat genotypes in terms of accuracy of selection.

Table 6. 3 Average genetic gain, inbreeding and accuracy of estimated breeding values (EBV) in conventional and genomic scheme of different goat genotypes utilising Min mating and reproductive technology

Goat genotype	Conventional Scheme			Genomic Scheme		
	Inbreeding	Genetic gain (g)	Accuracy (%)	Inbreeding	Genetic gain (g)	Accuracy (%)
Exotic	0.03^{a}	22.16^{b}	60.00^{b}	0.03^{a}	33.05^{b}	91.00^{b}
Indigenous	0.02^{b}	15.49^{b}	60.00^{b}	0.02^{b}	24.29^{c}	92.00^{a}
Cross breds	0.03^{a}	30.88^{a}	73.00^{a}	0.03^{a}	44.73^{a}	93.00^{a}

**Means with different superscripts within the same column differ significantly at P> 0.05*

* g: grams

Figure 6.1 and 6.2 presents the trends in level of inbreeding and genetic gain under both CS and GS schemes utilising different mating designs over generations, respectively. The level of inbreeding increased with increased in number of generations in both CS and GS schemes. The level of inbreeding in G^{Max} was higher than C^{Max} during the first three generations, and thereafter it declined below C^{Max} as generation increased. It was observed that as generation increased, the difference in level of inbreeding widen between CS and GS across all the mating

designs with the difference more notable between C^{Max} and G^{Max}, and C^{+ve} and G^{+ve} mating designs. As the trend in the cumulated averages for different mating designs, C^{Max} and G^{Max} mating designs obtained high level of inbreeding with increased number of generations, followed by C^{+ve} and G^{+ve}, C^{-ve} and G^{-ve}, C^{Rand} and G^{Rand} and C^{Min} and G^{Min} mating designs (Figure 6.1).

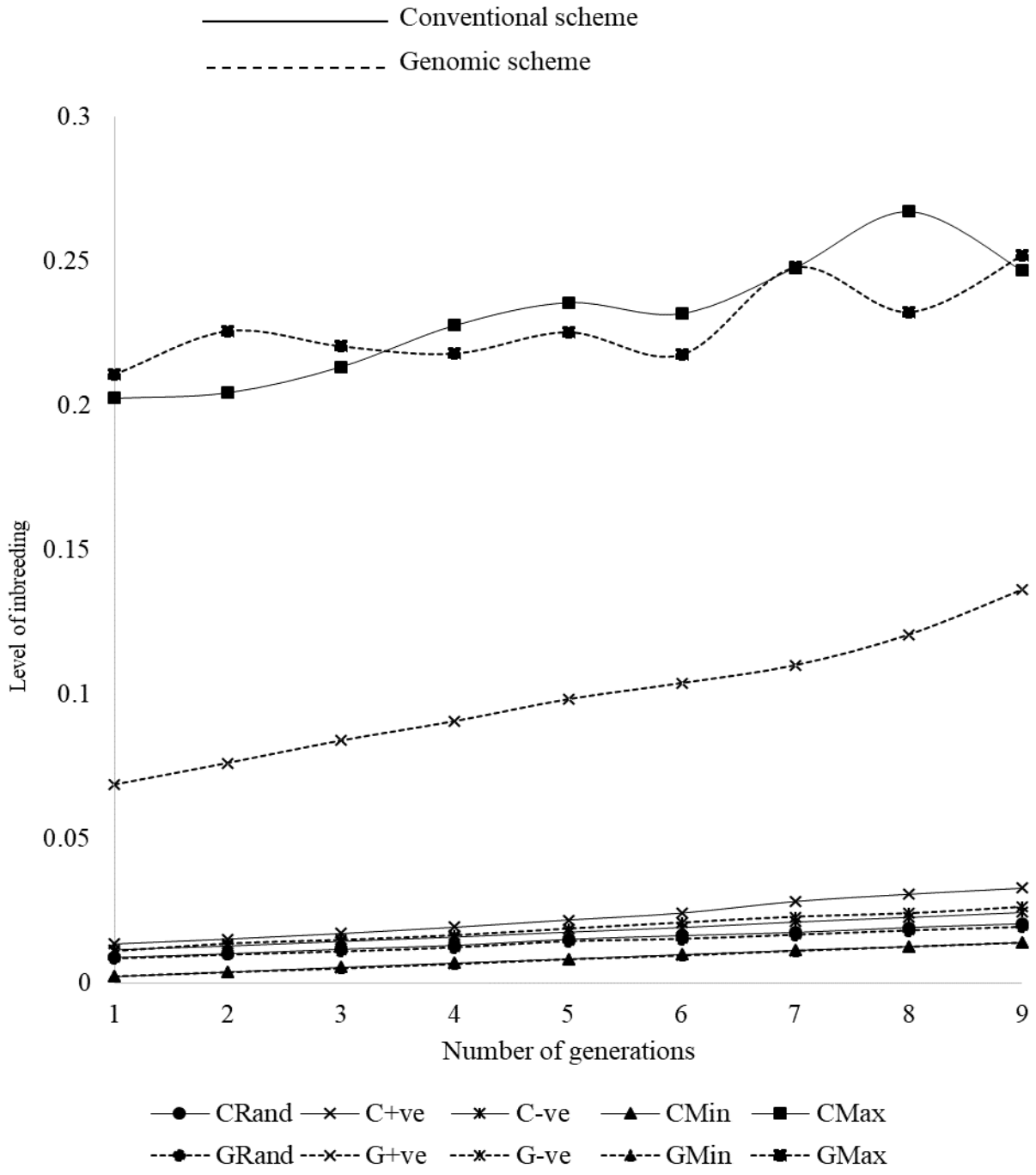

Figure 6. 1 Change in level of inbreeding in five mating designs over generations under conventional scheme

Genetic gain increased with increased generation in both CS and GS schemes. As observed for level of inbreeding, the difference in genetic gain widen between CS and GS across all the mating designs as generation increased. The trend for genetic gain under different mating designs over generations followed similar trend as in the cumulated averages. As the case in cumulated averages, the +ve realised high genetic gain, followed by Min, Rand and Max mating designs in CS and GS schemes (Figure 6. 2).

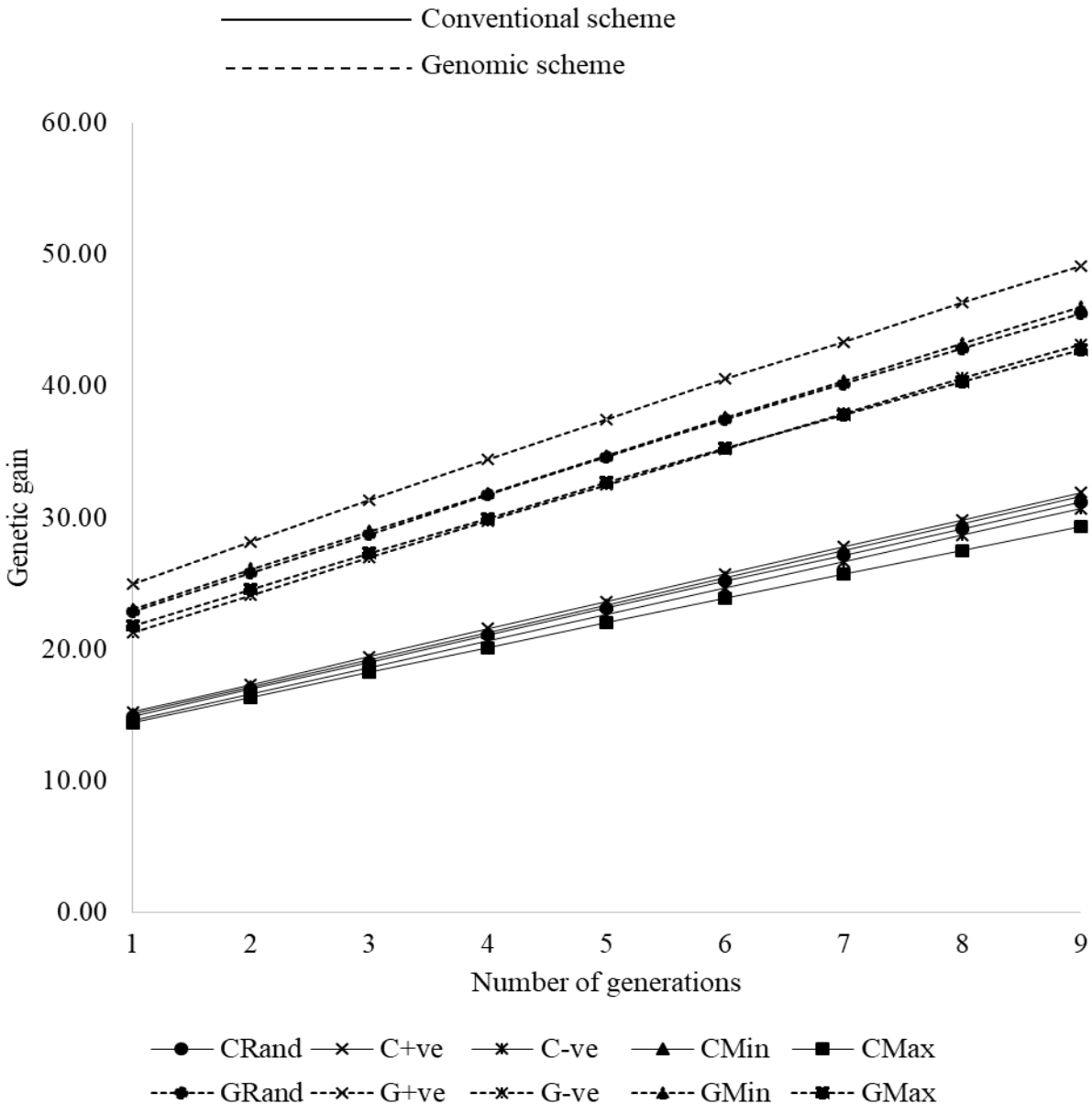

Figure 6. 2 Change in level of inbreeding in five mating designs over generations under genomic scheme

6.4 Discussion

The present study revealed that incorporation of genomic selection (GS) into dairy goat breeding programme utilising reproductive technology did not influenced level of inbreeding. The study however, found that incorporation of GS, improved genetic gain and accuracy of selection. Use of different mating designs influenced level of inbreeding, genetic gain and accuracy of selection. The study, further shown that different genotypes of goats influenced level of inbreeding, genetic gain and accuracy of selection.

The findings of the present study disagree with (Thomasen *et al.,* 2016) who reported that combination of reproductive technology with GS reduces the rate of inbreeding in dairy cattle. The difference could be due to differences in the modelling and evaluation softwares. However, the values observed in the current study, are close to those reported by Akano *et al.,* (2013). The high genetic gain obtained under the GS could be attributed to high accuracy of genomic genetic gain (Akanno *et al.,* 2014; Cao *et al.,* 2020; Shumbusho *et al.,* 2015). Genomic selection directly selects quantitative trait locus controlling the traits through its linkage disequilibrium with molecular markers and exploits Mendelian sampling errors (Daetwyler *et al.,* 2007; Meuwissen *et al.,* 2001). These findings agree with other studies that have reported high genetic gain under GS scheme (Granleese *et al.,* 2015, 2017; Thomasen *et al.,* 2016). The slight decrease in level of inbreeding under GS scheme in the present study could be due to the fact that GS improves prediction of the Mendelian sampling term, and thus reduces inbreeding (Lillehammer *et al.,* 2011; Nirea *et al.,* 2012; Wensch-Dorendorf *et al.,* 2011).

The differences attributed to mating designs in level of inbreeding, genetic gain and accuracy of selection could be associated to different mechanisms that each of the mating strategy uses to allocate mate selection (Sonesson & Meuwissen, 2000). The Min optimisation mating design realised the lowest level of inbreeding among all the other mating designs and could be because it minimises inbreeding using annealing method (Sonesson & Meuwissen, 2000). Previous studies have demonstrated that optimised mating design reduces inbreeding in cattle (Cervantes *et al.,* 2016; Colleau *et al.,* 2009; Mwangi *et al.,* 2020). The optimised Max mating designs, however, generated the highest level of inbreeding compared to the rest of all the other mating designs. The reasons being that Max design maximises inbreeding (Sargolzaei & Schenkel, 2009; Sonesson & Meuwissen, 2000). The high inbreeding realised in G+ve mating design could be due to the fact that assortative mating design select sires and dams based on similarity and GS further select closely related individuals accurately to mate among themselves. That is why although GS has been appreciated in terms of selecting the best

animals, there is need to further consider the mating design of the selected animals to control inbreeding in GS scheme (Doekes *et al.,* 2018; Makanjuola *et al*., 2020).

The high level of inbreeding observed in exotic and crossbred genotypes in the current study could be associated to low effective population size of these genotypes (Akano *et al.,* 2013). The better performance of the crossbreds could be attributed to hybrid-vigor. Similar trends have been observed in other studies where crossbreds were found to outperform pure lines in goats (Ahuya *et al.,* 2003; Kume *et al.,* 2012), cattle (Clasen *et al.,* 2017; Haile *et al.,* 2009) and in pigs (Akano *et al.,* 2013).

The increased trend in level of inbreeding over generations could be attributed to the fact that as the number of generation increased, there could be a likelihood that the relationship between selected parents for next generation becomes closer, and their genetic variance reduces (Akanno *et al.,* 2013). This could promote mating of closely related individuals, and possibly increases level of inbreeding. Similarly, the genetic gain increased over generations because of the selection of the best animals in each generation to breed offsprings for the next generation. The same trends were observed for both level inbreeding and genetic gain (Akanno *et al.,* 2013). The difference in level of inbreeding and genetic gain widen between CS and GS across all the mating designs as generation increased. The widen difference in level of inbreeding could be explained by two reasons: Firstly, uncontrollable increase in level of inbreeding under the CS scheme as animal population becomes related with increased generation. Secondly, although the animal population becomes related with increased population, GS scheme reduced selection of closely related individuals and possibly reduces rate of inbreeding (Daetwyler *et al.,* 2007; Lillehammer *et al.,* 2011; Nirea *et al.,* 2012). On the other hand, the widen difference in genetic gain could be attributed to the fact that with increased generation, animal population becomes more related, and this is an advantage for GS scheme to accurately select best performing individuals (Akanno *et al.,* 2014; Cao *et al.,* 2020; Shumbusho *et al.,* 2015). This allows GS scheme to continue outperforming CS scheme with increased generations.

6.5 Conclusion

The finding of the current study demonstrated that, breeding schemes that adopt a combination of reproductive technologies and genomic selection would optimize genetic gain compared to conventional schemes. It also demonstrated that the choice of mating design when using reproductive technologies and genomic selection is important for long-term genetic gain. Minimising inbreeding mating design constrained rate of inbreeding while maintaining rate of genetic gain compared to the other mating designs.

CHAPTER SEVEN

GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

7.1 Discussion

7.1.1 Goal of the Study

The study evaluated reproductive performance and response to selection of dairy goat breeding programme utilising reproductive technology and genomic selection. Both field experiments and simulations were conducted in the study. The thesis answered the following research questions.

i. What is the effect of breed and age on testicular and semen characteristics of dairy goats in Kenya?
ii. What is the effect of oestrous synchronisation protocol and type of service on reproductive performance of dairy goats?
iii. What is the response to selection in conventional and alternative following the incorporation of reproductive technology and genomic selection in dairy goat breeding programme?
iv. What are the rates of genetic gain and inbreeding in alternative dairy goat breeding programme utilizing reproductive technology, genomic selection and different mating designs?

7.1.2 Effect of Breed on Reproductive Performance of Dairy Goat Bucks in the Tropics

Generally, different breeds of livestock species have similarities and differences in terms of production performance, especially reproductive performance, and within breed effects due to age influenced reproductive performance of goats. The present study evaluated the effect of breed and age on testicular and semen characteristics of Saanen and Toggenburg bucks. The study found that testicular and most semen parameters for Toggenburg and Saanen bucks were not different (Chapter 3). Toggenburg bucks, however, had significantly higher semen concentration compared to Saanen. Saanen has been known to perform better than Toggenburg bucks in in terms of body weight, testicular and semen parameters under the temperate environment (Peacock, 1996). Ahuya *et al.* (2009) noted that Toggenburg goats can perform and thrive well under the low-input farming conditions, which is the case in most farming conditions in the tropics. These findings are an indication that tropical environment could be

favouring Toggenburg compared to Saanen when both are kept under the semi-intensive production system. The current study found body weight, large scrotal circumference, scrotal length, semen motility, semen density and sperm concentration were significantly (P<0.05) affected by age of bucks. Age of buck, however, did not influence semen volume, sperm live sperm cells and normal morphology. The current study has shown that Toggenburg bucks can produce high number of total spermatozoa and as a result higher semen doses for artificial insemination purposes.

7.1.3 Short-term Synchronisation Protocol as Alternative to Long-term Protocol Following Fixed Time Artificial Insemination and Natural Mating

The long-term protocol has been associated with low fertility rates (Diskin *et al.,* 2002; Pietroski *et al.,* 2013). This low fertility has been attributed to low serum progesterone concentrations which is associated with some abnormalities in follicular development, ovulation, oocyte health, luteal function (Evans *et al.,* 2001; Menchaca & Rubianes, 2001; Viñoles *et al.,* 2001). Due to these reasons and long period of treatment for protocol, efforts to replace long-term protocol with short-term protocol have been made. Application of artificial insemination at different time intervals also takes long time in performing breeding activities and may cause inconvenience in terms of management. The present study, therefore, evaluated effect of short and long-term synchronisation protocols following a single fixed-time artificial insemination and natural mating on reproductive performance of dairy goats.

The study reviled that long or short-term oestrous synchronisation protocol following natural mating and single fixed-time artificial insemination were not significantly (P>0.05) different (Chapter 4). The similarity between long and short-term protocols is due to the fact that, although CIDR was inserted for less number of days in short term protocol, it has been associated with high levels of progesterone concentration compared to the traditional lon term protocol. The high level of progesterone promotes follicular growth, increases ovulation and improve fertility (Karaca *et al.,* 2010; Menchaca & Rubianes, 2004, 2007; Viñoles *et al.,* 2001). This finding concurs with those of Karaca *et al.* (2010) and Pietroski *et al.* (2013). The comparable results between natural mating and artificial insemination could be attributed to good motility of the fresh cooled semen used for artificial insemination. Sperm motility has been reported to be associated with fertility in sheep (David *et al.,* 2015). In agreement with the finding of the current study, other studies have also reported comparable results between natural and artificial insemination with liquid semen (Andreea *et al.,* 2016; Fornazari *et al.,* 2018; Pietroski *et al.,* 2013). The short-term protocol following single fixed-time artificial

insemination and natural mating can therefore be alternative to long-term oestrous synchronisation protocol in dairy goats.

7.1.4 Incorporation of Genomic Selection in Dairy Goat Breeding Programme Utilizing Different Artificial Insemination and Mating Strategies

Adoption of reproductive technology such as artificial insemination (AI) in livestock breeding has been demonstrated to increases selection intensity, especially among sire and shortens genetic lag (Kor *et al*., 2011). Fertility rate, however, depends on the period of semen storage before insemination or from semen collection to insemination. In addition to reproductive technologies, genomic selection allows selection of breeding animals at an early age, reducing generation interval and rate of inbreeding, increase accuracy of selection, genetic and economic returns (Cao *et al.*, 2020; Egger-Danner *et al.*, 2012, 2014; Thomasen *et al.*, 2016). The study therefore, estimated response to selection and level of inbreeding following incorporation of genomic selection and different artificial insemination and mating strategies in dairy goat breeding programme.

The study found differences between different breeding strategies and schemes in the current study (Chapter 5). The favourable performance of AI-Fresh semen strategy compared to AI-Cryopreserved semen was attributed to high fertility rate in AI-Fresh semen strategy compared to AI- Cryopreserved semen (Andreea *et al*, 2016; Luo *et al.,* 2019). On the other hand, AI-Fresh semen outperformed natural mating strategy due to high selection intensity and accuracy of selection in AI-Fresh semen. The mating ratio in artificial insemination strategy was higher than that of in natural mating strategy. Implementation of genomic scheme maintained similar trend across all the three mating strategies as in the conventional scheme but had additional improvement in all the parameters measured. The high response to selection in the strategies under the genomic scheme is linked to high accuracy of genomic selection compared to the phenotypic selection (Akanno *et al.,* 2014; Cao *et al.,* 2020; Meuwissen *et al.,* 2013; Shumbusho *et al.,* 2016). These findings concur with previous studies that reported high annual genetic gain following combination of reproductive technologies with genomic selection (de Roos *et al.,* 2011; Granleese *et al.,* 2015, 2017; Thomasen *et al.,* 2016). The initial increase in genetic gain with increased population could be attributed to less variability in the small populations (Abdel-Salam *et al.,* 2007), while the decline in genetic gain is linked to reduction in genetic variance of response to selection (Meuwissen, 1990). The study shown that adoption of reproductive technologies and genomic selection would optimize response to selection in dairy goat breeding programmes in the tropics.

Incorporation of genomic selection into dairy goat breeding programme utilising reproductive technology increased rate of genetic gain but did not influence level of inbreeding (Chapter 6). The findings of the present study disagree with (Thomasen *et al.,* 2016) who reported that combination of reproductive technology with genomic selection reduces the rate of inbreeding in dairy cattle. The values observed in the current study, are close to those reported by Akano *et al.,* (2013). The high genetic gain obtained under the genomic selection could be attributed to high accuracy of selection (Akanno *et al.,* 2014; Cao *et al.,* 2020; Shumbusho *et al.,* 2016). The genomic selection uses molecular markers and partitions Mendelian sampling variance leading to reduced co-selection of sibs (Buch *et al.,* 2012; Daetwyler *et al.,* 2007; Meuwissen *et al.,* 2001). Consequently, this leads to reduction in rate of inbreeding (Cao *et al.,* 2020; Buch *et al.,* 2012; Thomasen *et al.,* 2016). These findings concur with other studies which reported high genetic gain under genomic selection scheme (Granleese *et al.,* 2015, 2017; Thomasen *et al.,* 2016). The slight decrease in level of inbreeding under genomic selection scheme in the present study, however, could be attributed to the fact that it improves prediction of the Mendelian sampling term, and possibly reduces inbreeding (Lillehammer *et al.,* 2011; Nirea *et al*., 2012; Wensch-Dorendorf *et al*., 2011).

The differences caused by different mating designs in level of inbreeding, genetic gain and accuracy of selection could be associated to different mechanisms that each of the mating design uses to allocate mate selection (Sonesson & Meuwissen, 2000). The Min optimisation mating design realised lowest level of inbreeding among all the other mating designs and this could be because it minimises inbreeding using annealing method (Sonesson & Meuwissen, 2000). Previous studies have demonstrated that optimised mating design reduces inbreeding in cattle (Cervantes *et al.,* 2016; Colleau *et al.,* 2009; Mwangi *et al.,* 2020). The optimised Max mating designs, however, generated the highest level of inbreeding compared to the rest of all the other mating strategies. The reasons being that Max mating design maximises rate of gain with total disregard of level inbreeding, often mating closely related individuals (Sargolzaei & Schenkel, 2009; Sonesson & Meuwissen, 2000). The higher inbreeding realised with positive assortative mating (+ve) mating design under the genomic scheme could be due to the fact that assortative mating design selected sires and dams based on similarity and dissimilarity and genomic selection further selected closely related individuals accurately to mate among themselves. Therefore, although genomic selection has been appreciated in terms of selecting the best animals, there is need to further consider the mating design of the selected animals to control inbreeding in genomic breeding schemes (Doekes *et al.,* 2018; Makanjuola *et al.,* 2020). The high level of inbreeding observed in exotic and crossbred genotypes in the current study

could be associated to low effective population size of these genotypes (Akano *et al.,* 2013). The high performance of the crossbreds could be attributed to hybrid vigor. Similar trends have been observed in other studies where crossbreds were found to outperform pure lines in goats (Ahuya *et al.,* 2003; Kume *et al.,* 2012), cattle (Clasen *et al.,* 2017; Haile *et al.,* 2009) and in pigs (Akano *et al.,* 2013).

The increased trend in level of inbreeding over generations could be attributed to the fact that as the number of generation increased, there could be a likelihood that the relationship between selected parents for next generation becomes closer, and their genetic variance reduces (Akanno *et al.,* 2013). This could promote mating of closely related individuals, and possibly increases level of inbreeding. Similarly, the genetic gain increased over generations because of the selection of the best animals in each generation to breed off-springs for the next generation. The same trends were observed for both level inbreeding and genetic gain (Akanno *et al.,* 2013). The difference in level of inbreeding and genetic gain widen between conventional and genomic breeding schemes across all the mating designs as generation increased. The widen difference in level of inbreeding could be explained by two reasons: First, uncontrollable increase in level of breeding under the conventional selection scheme as animal population becomes related with increased generation increase. Secondly, although the animal population becomes related with increased population, genomic selection scheme strive to reduce selection of closely related individuals and possibly reduces rate of inbreeding (Daetwyler *et al.,* 2007; Lillehammer *et al.,* 2011; Nirea *et al*., 2012). On the other hand, the widen difference in genetic gain could be attributed to the fact that with increased generation, animal population becomes more related, and this is an advantage for genomic selection scheme to accurately select best performing individuals (Akanno *et al.,* 2014; Cao *et al.,* 2020; Shumbusho *et al.,* 2015). This allows genomic selection scheme to continue outperforming conventional scheme with increased generation. Reproductive technology combined with genomic selection does not influence level of inbreeding, however, it increases genetic gain. The positive assortative mating design generated high level of inbreeding under genomic scheme than conventional scheme. The Min mating design realised acceptable genetic gain and the lowest level of inbreeding and therefore would optimize response to selection compared to other mating designs. Crossbreds realised genetic gain with intermediate level of inbreeding.

7.2 Practical Implication of the Study

The current dairy goat breeding programme in Kenya is utilising natural mating with artificial insemination only limited to a few farms using imported semen from superior genetic materials. The breeding is majorly done through use of buck rotational breeding due to lack of sufficient breeding bucks (Bett *et al.,* 2009; Mbindyo *et al.,* 2018). Additionally, in Kenya the current buck breeding soundness examination is limited to evaluation of scrotal and testicular parameters without evaluating the semen characteristics. In comparison to dairy goats artificial insemination programme, there is well established local dairy cattle artificial insemination programme in Kenya (Lawrence *et al.,* 2015), which supply majority of farms across the country. For instance, Kenya Animal Genetic Resources Centre (KAGRC) in Nairobi and Semen Production Centre under Agricultural Development Corporation based in Kitale, both process bull semen and distribute across the country. Through collaboration between these centres, ministry of agriculture and private sectors, enough artificial insemination technicians have been trained who conduct artificial insemination in cattle. Currently, there are no such semen processing centres operational for goats in the country, and no enough trained technical personnel to undertake artificial insemination in goats. In addition, both the dairy cattle and goat breeding programmes in Kenya, still rely on conventional selection even though genomic selection has been available for long time.

Adoption of artificial insemination in dairy goat breeding programme could not only contribute to faster genetic improvement but could also solve the problem of insufficient breeding bucks in Kenya and avoid transmission of diseases. Selecting breeding buck on the account of both scrotal and semen characteristics could lead to increased flock fertility whether in natural or artificial breeding. On the other hand, genomic selection could be considered in dairy goat breeding programme to improve genetic gain, increase accuracy of selection and reduce rate of inbreeding instead of traditional selection.

From the findings of the current study, fertility rate in artificial insemination programme has performed quite similar as in natural breeding whether with short or long-term synchronisation protocol. The response to selection in artificial insemination breeding outperformed natural breeding strategy, especially the artificial insemination with liquid semen. These proved that artificial insemination could be adopted for wider use in dairy goat breeding to replace buck rotational breeding programme in Kenya. The use of short-term protocol could reduce time spent by farmers to breed their animals. In addition, CIDR from short-term protocol can be re-used with effective oestrous synchronisation and pregnancy rate (Vilarino *et al.,* 2011, 2013). Use of single fixed-time artificial insemination with cooled

extended semen could offer an alternative option to buck rotational breeding for dairy goat farmers in Kenya. It was also found that genomic selection improves response to selection in dairy goat breeding programme, especially when combine with reproductive technology.

From the practical point of view, it is worth noting that farmers in Kenya could benefit from the use of reproductive technologies because adoption of reproductive technology such as artificial insemination can allow semen from the few available bucks to inseminate many number of does compared to natural mating, and this will alleviate the current shortage of breeding bucks in the country. This will lead to increase in accuracy of selection and reduction of genetic lag, consequently achieving faster genetic improvement. Artificial insemination can be used to produce enough number of closely related individuals to generate phenotypic and genotypic information that is required for the implementation of genomic selection in dairy goat breeding programme in Kenya. Introduction of genomic selection can help to accurately identify closely related individuals and this can lead to improve response to selection and allow for early selection of candidates.

The main challenge in adoption of these strategies by dairy goat farmers in Kenya is that most dairy goat farmers are smallholders as the case of most dairy farmers in the tropics. Consequently, it is difficult for them to afford establishment of semen processing centres and purchase of tools and materials for use in their individual farms. These could hinder spread of artificial insemination in dairy goat breeding programme. Most dairy goat farmers in Kenya cannot import superior genetic materials due to high cost. To implement genomic selection, it will require animals to have both phenotypic and genotypic information. In Kenya as the case in most countries in the tropics, however, dairy goat farmers do not do performance recording and thus lack phenotypic information. This poses serious challenge to implementation of genomic selection. Another challenge is that genomic selection is very expensive and as a result, dairy goat farmers cannot afford to implement it now because most farmers still operate under low-input farming conditions.

These challenges, however, can be addressed through collaboration between Dairy Goat Association of Kenya (DGAK) and the government agencies. Dairy Goat Association of Kenya (DGAK) should come up with plans to initiate and encourage use of artificial insemination especially fresh semen among dairy goat farms within the country instead of rotational breeding. Different regional or county farmers' groups in partnership with county governments can established small semen analysis laboratories prior to selection of breeding bucks. The Kenya government through the Ministry of Agriculture in collaboration with DGAK should come up with policies to promote dairy goat breeding programmes through integration of goat

semen processing in the existing bull semen processing centres in the country. This will allow smallholder dairy goat farmers to have option to purchase locally processed semen from the already imported superior goat genetic materials and cryopreserved goat semen for future use. Due to high price associated with pedigree animals, DGAK in collaboration with the Ministry of Agriculture should create awareness among farmers on the value of buying animals with pedigree information. They can team up with organizations such as Universities, Kenya Agriculture and Livestock Research Organization (KALRO) and International Livestock Research Institute (ILRI) to encourage farmers to do phenotyping and genotyping as well as register with Kenya Livestock Breeders Association (KLBA) for recognition. This can contribute to improved dairy goat recording system as a prior step to pave the way for genomic selection in dairy goat breeding programme in Kenya. Implementation of these strategies and advice would generally lead to improved response to selection in dairy goat breeding programme in Kenya and elsewhere in the tropics.

7.3 Conclusions

i. Breed of the bucks affect semen consistency and sperms concentration while age affect scrotal circumference and length, semen consistency, sperms concentration, mass activity and progressive motility
ii. Long and short-term synchronization protocols do not affect the reproductive performance parameters of does following a single fixed-time artificial insemination and natural mating in dairy goats
iii. Breeding schemes that adopted reproductive technologies such as artificial insemination, and genomic selection optimized response to selection
iv. Minimizing inbreeding mating design constrained rate of inbreeding while maintaining rate of genetic gain in conventional and genomic breeding schemes

7.4 Recommendations

i. Toggenburg bucks could be used for improvement breeding programmes in Kenya. Age should be considered when selecting a breeding buck.
ii. Use of short-term oestrous synchronisation following either natural mating or single fixed-time artificial insemination could be adopted in dairy goat breeding programmes
iii. Use of reproductive technology and genomic selection could be used to improve response to selection.

iv. Use of Minimising inbreeding mating design could be adopted to constrained rate of inbreeding in dairy goat breeding programmes.

7.5 Areas for further research

i. Further studies should consider other dairy goat breeds including crossbreds as well as production system and more number of experimental animals.

ii. Further studies should consider use of multiple ovulation and embryo transfer to estimate response to selection in dairy goat breeding programme utilising both conventional and genomic selection.

iii. Further studies should consider effect of genotype by environment interaction when evaluating response to selection.

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APPENDICES

Appendix 1: Results Summary

Appendix 1a: SAS Outputs for Objective One

Dependent Variable: SC

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	2	19.93750000	9.96875000	3.78	0.0771
Error	7	18.46250000	2.63750000		
Corrected Total	9	38.40000000			

R-Square	Coeff Var	Root MSE	SC Mean
0.519206	5.927147	1.624038	27.40000

Source	DF	Type I SS	Mean Square	F Value	Pr > F
BREED	1	6.40000000	6.40000000	2.43	0.1633
AGE	1	13.53750000	13.53750000	5.13	0.0579

Source	DF	Type III SS	Mean Square	F Value	Pr > F
BREED	1	3.03750000	3.03750000	1.15	0.3188
AGE	1	13.53750000	13.53750000	5.13	0.0579

Dependent Variable: SL

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	2	12.22916667	6.11458333	11.28	0.0065
Error	7	3.79583333	0.54226190		
Corrected Total	9	16.02500000			

R-Square	Coeff Var	Root MSE	SL Mean
0.763131	6.487968	0.736384	11.35000

Source	DF	Type I SS	Mean Square	F Value	Pr > F
BREED	1	3.02500000	3.02500000	5.58	0.0502
AGE	1	9.20416667	9.20416667	16.97	0.0045

Source	DF	Type III SS	Mean Square	F Value	Pr > F
BREED	1	1.20416667	1.20416667	2.22	0.1798
AGE	1	9.20416667	9.20416667	16.97	0.0045

Dependent Variable: WGT

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	2	1382.416667	691.208333	12.37	0.0050
Error	7	391.183333	55.883333		
Corrected Total	9	1773.600000			

R-Square	Coeff Var	Root MSE	WGT Mean
0.779441	15.97332	7.475516	46.80000

Source	DF	Type I SS	Mean Square	F Value	Pr > F
BREED	1	176.400000	176.400000	3.16	0.1189
AGE	1	1206.016667	1206.016667	21.58	0.0024

Source	DF	Type III SS	Mean Square	F Value	Pr > F
BREED	1	36.816667	36.816667	0.66	0.4437
AGE	1	1206.016667	1206.016667	21.58	0.0024

BREED	SC LSMEAN	Error	Pr > |t|	Pr > |t|
1	28.2000000	0.8944272	<.0001	0.2415
2	26.6000000	0.8944272	<.0001	

BREED	SL LSMEAN	Error	Pr > |t|	Pr > |t|
1	11.9000000	0.5700877	<.0001	0.2096
2	10.8000000	0.5700877	<.0001	

BREED	WGT LSMEAN	Error	Pr > |t|	Pr > |t|
1	51.0000000	6.3190189	<.0001	0.3747
2	42.6000000	6.3190189	0.0001	

AGE	SC LSMEAN	Error	Pr > |t|	Pr > |t|
1	26.1000000	0.7331439	<.0001	0.0365
2	28.7000000	0.7331439	<.0001	

AGE	SL LSMEAN	Error	Pr > |t|	Pr > |t|

1	10.3000000	0.3535534	<.0001	0.0030
2	12.4000000	0.3535534	<.0001	

AGE	WGT LSMEAN	Error	Pr > |t|	Pr > |t|
1	35.2000000	3.2710854	<.0001	0.0010
2	58.4000000	3.2710854	<.0001	

Dependent Variable: VOLUME

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	4.10480912	0.45608990	1.66	0.1226
Error	51	13.98371547	0.27419050		
Corrected Total	60	18.08852459			

R-Square	Coeff Var	Root MSE	VOLUME Mean
0.226929	52.10694	0.523632	1.004918

Source	DF	Type I SS	Mean Square	F Value	Pr > F
WEEK	6	3.34969919	0.55828320	2.04	0.0776
BREED	1	0.00112229	0.00112229	0.00	0.9492
AGE	1	0.62574635	0.62574635	2.28	0.1370
BREED*AGE	1	0.12824129	0.12824129	0.47	0.4971

Source	DF	Type III SS	Mean Square	F Value	Pr > F
WEEK	6	3.34086473	0.55681079	2.03	0.0784
BREED	1	0.00672589	0.00672589	0.02	0.8762
AGE	1	0.57575296	0.57575296	2.10	0.1534
BREED*AGE	1	0.12824129	0.12824129	0.47	0.4971

Dependent Variable: DENSITY

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	31.50287384	3.50031932	3.00	0.0061
Error	51	59.57909338	1.16821752		
Corrected Total	60	91.08196721			

R-Square	Coeff Var	Root MSE	DENSITY Mean
0.345874	46.75979	1.080841	2.311475

Source	DF	Type I SS	Mean Square	F Value	Pr > F
WEEK	6	5.41530055	0.90255009	0.77	0.5951
BREED	1	17.43334502	17.43334502	14.92	0.0003
AGE	1	8.47085726	8.47085726	7.25	0.0096
BREED*AGE	1	0.18337101	0.18337101	0.16	0.6936

Source	DF	Type III SS	Mean Square	F Value	Pr > F
WEEK	6	4.55561840	0.75926973	0.65	0.6899
BREED	1	20.82259262	20.82259262	17.82	<.0001
AGE	1	8.61943600	8.61943600	7.38	0.0090
BREED*AGE	1	0.18337101	0.18337101	0.16	0.6936

Dependent Variable: MM

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	10.45160191	1.16128910	1.75	0.1024
Error	51	33.90905383	0.66488341		
Corrected Total	60	44.36065574			

R-Square	Coeff Var	Root MSE	MM Mean
0.235605	21.25625	0.815404	3.836066

Source	DF	Type I SS	Mean Square	F Value	Pr > F
WEEK	6	5.70192558	0.95032093	1.43	0.2218
BREED	1	0.95739239	0.95739239	1.44	0.2357
AGE	1	3.78609561	3.78609561	5.69	0.0208
BREED*AGE	1	0.00618833	0.00618833	0.01	0.9235

Source	DF	Type III SS	Mean Square	F Value	Pr > F
WEEK	6	5.71688602	0.95281434	1.43	0.2204
BREED	1	1.57665639	1.57665639	2.37	0.1298
AGE	1	3.73516156	3.73516156	5.62	0.0216
BREED*AGE	1	0.00618833	0.00618833	0.01	0.9235

Dependent Variable: PM

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F

Model	9	2669.89870	296.65541	1.33	0.2430
Error	51	11336.65868	222.28743		
Corrected Total	60	14006.55738			

R-Square	Coeff Var	Root MSE	PM Mean
0.190618	19.51647	14.90931	76.39344

Source	DF	Type I SS	Mean Square	F Value	Pr > F
WEEK	6	965.287536	160.881256	0.72	0.6324
BREED	1	211.533390	211.533390	0.95	0.3339
AGE	1	1335.996117	1335.996117	6.01	0.0177
BREED*AGE	1	157.081652	157.081652	0.71	0.4045

Source	DF	Type III SS	Mean Square	F Value	Pr > F
WEEK	6	1059.472271	176.578712	0.79	0.5787
BREED	1	389.172418	389.172418	1.75	0.1917
AGE	1	1252.598426	1252.598426	5.64	0.0214
BREED*AGE	1	157.081652	157.081652	0.71	0.4045

Dependent Variable: LIVE

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	515.276924	57.252992	0.47	0.8859
Error	51	6171.185371	121.003635		
Corrected Total	60	6686.462295			

R-Square	Coeff Var	Root MSE	LIVE Mean
0.077063	12.61795	11.00017	87.17869

Source	DF	Type I SS	Mean Square	F Value	Pr > F
WEEK	6	417.9966602	69.6661100	0.58	0.7478
BREED	1	19.9196669	19.9196669	0.16	0.6866
AGE	1	5.4194372	5.4194372	0.04	0.8332
BREED*AGE	1	71.9411602	71.9411602	0.59	0.4442

Source	DF	Type III SS	Mean Square	F Value	Pr > F
WEEK	6	424.2759827	70.7126638	0.58	0.7411

BREED	1	23.1320827	23.1320827	0.19 0.6638
AGE	1	9.1210846	9.1210846	0.08 0.7848
BREED*AGE	1	71.9411602	71.9411602	0.59 0.4442

Dependent Variable: NORMAL

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	512.655040	56.961671	1.96	0.0644
Error	51	1484.779386	29.113321		
Corrected Total	60	1997.434426			

R-Square	Coeff Var	Root MSE	NORMAL Mean
0.256657	5.899028	5.395676	91.46721

Source	DF	Type I SS	Mean Square	F Value	Pr > F
WEEK	6	463.8173627	77.3028938	2.66	0.0256
BREED	1	0.1902018	0.1902018	0.01	0.9359
AGE	1	47.3633060	47.3633060	1.63	0.2079
BREED*AGE	1	1.2841698	1.2841698	0.04	0.8345

Source	DF	Type III SS	Mean Square	F Value	Pr > F
WEEK	6	453.6390430	75.6065072	2.60	0.0284
BREED	1	0.3550202	0.3550202	0.01	0.9125
AGE	1	48.3324213	48.3324213	1.66	0.2034
BREED*AGE	1	1.2841698	1.2841698	0.04	0.8345

Dependent Variable: CONC

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	46.1260229	5.1251137	2.68	0.0124
Error	51	97.4749968	1.9112744		
Corrected Total	60	143.6010197			

R-Square	Coeff Var	Root MSE	CONC Mean
0.321210	61.14101	1.382488	2.261148

Source	DF	Type I SS	Mean Square	F Value	Pr > F
WEEK	6	17.70842880	2.95140480	1.54	0.1829
BREED	1	17.58292258	17.58292258	9.20	0.0038
AGE	1	10.32913898	10.32913898	5.40	0.0241
BREED*AGE	1	0.50553255	0.50553255	0.26	0.6093

Source	DF	Type III SS	Mean Square	F Value	Pr > F
WEEK	6	15.17476913	2.52912819	1.32	0.2640
BREED	1	21.41403764	21.41403764	11.20	0.0015
AGE	1	10.63815042	10.63815042	5.57	0.0222
BREED*AGE	1	0.50553255	0.50553255	0.26	0.6093

	VOLUME		Standard	H0:LSMEAN=0	H0:LSMean1= LSMean2
BREED	LSMEAN		Error	Pr > |t|	Pr > |t|
1	0.99554816		0.10089693	<.0001	0.8762
2	0.97420351		0.09241393	<.0001	

	DENSITY		Standard	H0:LSMEAN=0	H0:LSMean1= LSMean2
BREED	LSMEAN		Error	Pr > |t|	Pr > |t|
1	2.94388997		0.20826371	<.0001	<.0001
2	1.75625805		0.19075375	<.0001	

		Standard	H0:LSMEAN=0	H0:LSMean1= LSMean2
BREED	MM LSMEAN	Error	Pr > |t|	Pr > |t|
1	4.01795591	0.15711748	<.0001	0.1298

2 3.69115520 0.14390768 <.0001

H0:LSMean1=

Standard H0:LSMEAN=0 LSMean2

BREED PM LSMEAN Error Pr > |t| Pr > |t|

1 79.2421286 2.8728251 <.0001 0.1917

2 74.1077784 2.6312897 <.0001

H0:LSMean1=

Standard H0:LSMEAN=0 LSMean2

BREED LIVE LSMEAN Error Pr > |t| Pr > |t|

1 86.2422257 2.1195856 <.0001 0.6638

2 87.4939879 1.9413795 <.0001

H0:LSMean1=

NORMAL Standard H0:LSMEAN=0 LSMean2

BREED LSMEAN Error Pr > |t| Pr > |t|

1 91.2369667 1.0396750 <.0001 0.9125

2 91.0818919 0.9522634 <.0001

H0:LSMean1=

Standard H0:LSMEAN=0 LSMean2

BREED CONC LSMEAN Error Pr > |t| Pr > |t|

1 2.87462290 0.26638715 <.0001 0.0015

2 1.67024232 0.24399041 <.0001

H0:LSMean1=

VOLUME Standard H0:LSMEAN=0 LSMean2

AGE LSMEAN Error Pr > |t| Pr > |t|

1 1.08395430 0.09778731 <.0001 0.1534

2 0.88579737 0.09602881 <.0001

H0:LSMean1=

DENSITY Standard H0:LSMEAN=0 LSMean2

AGE LSMEAN Error Pr > |t| Pr > |t|

1 2.73342853 0.20184508 <.0001 0.0090

2 1.96671949 0.19821532 <.0001

				H0:LSMean1=	
			Standard	H0:LSMEAN=0	LSMean2
AGE	MM LSMEAN		Error	Pr > |t|	Pr > |t|
1	4.10691285		0.15227516	<.0001	0.0216
2	3.60219827		0.14953681	<.0001	
				H0:LSMean1=	
			Standard	H0:LSMEAN=0	LSMean2
AGE	PM LSMEAN		Error	Pr > |t|	Pr > |t|
1	81.2962847		2.7842855	<.0001	0.0214
2	72.0536223		2.7342159	<.0001	
				H0:LSMean1=	
			Standard	H0:LSMEAN=0	LSMean2
AGE	LIVE LSMEAN		Error	Pr > |t|	Pr > |t|
1	86.4737545		2.0542605	<.0001	0.7848
2	87.2624591		2.0173189	<.0001	
				H0:LSMean1=	
	NORMAL	Standard	H0:LSMEAN=0	LSMean2	
AGE	LSMEAN	Error	Pr > |t|	Pr > |t|	
1	92.0672089	1.0076325	<.0001	0.2034	
2	90.2516497	0.9895124	<.0001		
				H0:LSMean1=	
			Standard	H0:LSMEAN=0	LSMean2
AGE	CONC LSMEAN		Error	Pr > |t|	Pr > |t|
1	2.69831946		0.25817717	<.0001	0.0222
2	1.84654577		0.25353439	<.0001	

Appendix 1b: SAS Outputs for Objective Two

Dependent Variable: Ons

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F

Model	1	19.4086022	19.4086022	1.74 0.1980
Error	29	324.3333333	11.1839080	
Corrected Total	30	343.7419355		

R-Square	Coeff Var	Root MSE	Ons Mean
0.056463	10.28485	3.344235	32.51613

Source	DF	Type I SS	Mean Square	F Value	Pr > F
Syn	1	19.40860215	19.40860215	1.74	0.1980

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Syn	1	19.40860215	19.40860215	1.74	0.1980

Dependent Variable: Dur

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	1	5.1634409	5.1634409	1.19	0.2845
Error	29	125.9333333	4.3425287		
Corrected Total	30	131.0967742			

R-Square	Coeff Var	Root MSE	Dur Mean
0.039386	6.646099	2.083873	31.35484

Source	DF	Type I SS	Mean Square	F Value	Pr > F
Syn	1	5.16344086	5.16344086	1.19	0.2845

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Syn	1	5.16344086	5.16344086	1.19	0.2845

Syn	Ons LSMEAN	Error	Pr > |t|	Pr > |t|
1	33.3333333	0.8634778	<.0001	0.1980
2	31.7500000	0.8360588	<.0001	

Syn	Dur LSMEAN	Error	Pr > |t|	Pr > |t|
1	30.9333333	0.5380538	<.0001	0.2845
2	31.7500000	0.5209684	<.0001	

Appendix 1c: ZPLAN Outputs for Objective Three

1. Conventional Natural Mating Strategy

BASIC RUN: RESULTS FOR THE SELECTION GROUPS

	I	1	2	3	4	5	6	7	8	9	10
	I	BNOB>BN	DN>BN	BNYB>DN	BNOB>DN	DN>DN	BNYB>BC	DC>BC	BNYB>DC	BC>DC	DC>DC
----------I----------											
SEL.ANIM.	I	10.000	166.667	133.333	10.000	3333.333	1773.333	47500.000	1773.333	456.000	47500.000
PROV.ANIM.	I	133.333	3333.333	3724.650	133.333	3766.500	3724.650	55404.000	3724.650	54720.000	55404.000
PROP.SEL.	I	0.075	0.050	0.036	0.075	0.885	0.476	0.857	0.476	0.008	0.857
SEL.INT(i)	I	1.862	2.061	2.196	1.862	0.219	0.836	0.263	0.836	2.726	0.263
GEN.INT	I	2.915	2.249	2.915	2.190	2.249	2.915	3.309	2.915	4.716	3.309
GENE-OFF	I	95.0	100.0	95.0	5.0	100.0	100.0	100.0	70.0	30.0	100.0
SD(AT)	I	90.425	100.897	90.425	3.732	74.272	19.686	0.000	128.172	0.000	0.000
RAI	I	0.883	0.834	0.883	0.883	0.834	0.834	0.834	0.834	0.834	0.834
LT-GENE	I	12.56	13.22	12.56	1.81	36.12	0.00	0.00	0.00	0.00	0.00
monGG(AT)	I	406.591	425.256	479.553	406.591	45.207	0.000	0.000	0.000	0.000	0.000
GG MY-1	I	0.575	0.568	0.678	0.575	0.060	0.230	0.000	0.230	0.000	0.000
GG LW-2	I	1.758	1.749	2.073	1.758	0.186	0.710	0.000	0.710	0.000	0.000
GG DWT-3	I	5.159	5.422	6.084	5.159	0.576	2.200	0.000	2.200	0.000	0.000

GG NKW-4 I 0.209 0.209 0.246 0.209 0.022 0.085 0.000 0.085 0.000 0.000

GG Dummy I 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

SDE MY-1 I 0.366 0.408 0.366 0.015 0.300 0.080 0.077 0.518 0.199 0.722

RETURN TOTI 148.650 173.478 175.325 6.135 13.575 13.734 0.000 89.423 0.000 0.000

RET LW-2 I 13.432 14.909 15.842 0.554 1.167 1.180 0.000 7.685 0.000 0.000

RET DWT-3 I 135.056 158.389 159.292 5.574 12.394 12.540 0.000 81.645 0.000 0.000

RET NKW-4I 0.162 0.181 0.191 0.007 0.014 0.014 0.000 0.093 0.000 0.000

RET DummyI 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

G E N E T I C G A I N per Year FOR THE SINGLE TRAITS

MY-1= 0.0621 LW-2 = 0.1906 DWT-3= 0.5710 NKW-= 0.0227 Dumm= 0.0000

Monetary G E N E T I C G A I N per Year 44.920

MEAN GENERATION INTERVAL 1.357

R E T U R N

RETURN TOTAL / UNIT 620.321

RETURN/TRAIT/UNIT:

LW-2 = 54.769 DWT-3= 564.890 NKW-= 0.662 Dumm= 0.000

C O S T S

COSTS TOTAL / UNIT 20.963

FIX = 9.709 PER DAM = 5.808 VARIABLE = 5.446

P R O F I T

PROFIT / UNIT 599.358

2. Conventional Liquid semen Strategy

BASIC RUN: RESULTS FOR THE SELECTION GROUPS

I	1	2	3	4	5	6	7	8	9	10
I	BNOB>BN	DN>BN	BNYB>DN	BNOB>DN	DN>DN	BNYB>BC	DC>BC	BNYB>DC	BC>DC	DC>DC
SEL.ANIM. I	2.500	166.667	33.333	2.500	3333.333	443.333	47500.000	443.333	114.000	47500.000
PROV.ANIM.I	33.333	3333.333	3517.725	33.333	3557.250	3517.725	48478.496	3517.725	47880.000	48478.496
PROP.SEL. I	0.075	0.050	0.009	0.075	0.937	0.126	0.980	0.126	0.002	0.980
SEL.INT(i)I	1.791	2.061	2.675	1.791	0.132	1.641	0.050	1.641	3.115	0.050
GEN.INT I	2.915	2.249	2.915	2.190	2.249	2.915	3.309	2.915	4.716	3.309
GENE-OFF I	95.0	100.0	95.0	5.0	100.0	100.0	100.0	70.0	30.0	100.0
SD(AT) I	90.425	100.897	90.425	3.732	74.272	19.686	0.000	128.172	0.000	0.000
RAI I	0.937	0.841	0.937	0.937	0.841	0.841	0.841	0.841	0.841	0.841
LT-GENE I	12.56	13.22	12.56	1.81	36.12	0.00	0.00	0.00	0.00	0.00
monGG(AT) I	415.062	428.498	619.867	415.062	27.405	0.000	0.000	0.000	0.000	0.000
GG MY-1 I	0.544	0.578	0.812	0.544	0.037	0.460	0.000	0.460	0.000	0.000
GG LW-2 I	1.907	1.801	2.848	1.907	0.115	1.434	0.000	1.434	0.000	0.000

GG DWT-3 I 5.233 5.452 7.815 5.233 0.349 4.341 0.000 4.341 0.000 0.000

GG NKW-4 I 0.213 0.212 0.318 0.213 0.014 0.169 0.000 0.169 0.000 0.000

GG Dummy I 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

SDE MY-1 I 0.366 0.408 0.366 0.015 0.300 0.080 0.077 0.518 0.199 0.722

RETURN TOTI 151.747 174.801 226.624 6.263 8.229 27.156 0.000 176.813 0.000 0.000

RET LW-2 I 14.573 15.353 21.764 0.601 0.723 2.385 0.000 15.530 0.000 0.000

RET DWT-3 I 137.009 159.264 204.614 5.655 7.498 24.743 0.000 161.098 0.000 0.000

RET NKW-4I 0.165 0.184 0.246 0.007 0.009 0.029 0.000 0.186 0.000 0.000

RET DummyI 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

G E N E T I C G A I N per Year FOR THE SINGLE TRAITS

MY-1= 0.0634 LW-2 = 0.2141 DWT-3= 0.6062 NKW-= 0.0243 Dumm= 0.0000

Monetary G E N E T I C G A I N per Year 47.936

MEAN GENERATION INTERVAL 1.357

R E T U R N

RETURN TOTAL / UNIT 771.634

RETURN/TRAIT/UNIT:

LW-2 = 70.929 DWT-3= 699.880 NKW-= 0.825 Dumm= 0.000

C O S T S

COSTS TOTAL / UNIT 23.384

FIX = 9.709 PER DAM = 5.808 VARIABLE = 7.867

P R O F I T

PROFIT / UNIT 748.250

3. Conventional Frozen Strategy

BASIC RUN: RESULTS FOR THE SELECTION GROUPS

I	1	2	3	4	5	6	7	8	9	10
I	BNOB>BN	DN>BN	BNYB>DN	BNOB>DN	DN>DN	BNYB>BC	DC>BC	BNYB>DC	BC>DC	DC>DC
SEL.ANIM. I	2.500	166.667	33.333	2.500	2511.000	443.333	34627.500	443.333	114.000	34627.500
PROV.ANIM.I	33.333	3333.333	2483.100	33.333	2511.000	2483.100	34627.500	2483.100	34200.000	34627.500
PROP.SEL. I	0.075	0.050	0.013	0.075	1.000	0.179	1.000	0.179	0.003	1.000
SEL.INT(i)I	1.791	2.061	2.556	1.791	0.000	1.461	0.000	1.461	3.009	0.000
GEN.INT I	2.915	2.249	2.915	2.190	2.249	2.915	3.309	2.915	4.716	3.309
GENE-OFF I	95.0	100.0	95.0	5.0	100.0	100.0	100.0	70.0	30.0	100.0
SD(AT) I	90.425	100.897	90.425	3.732	74.272	19.686	0.000	128.172	0.000	0.000
RAI I	0.923	0.839	0.923	0.923	0.839	0.839	0.839	0.839	0.839	0.839

LT-GENE I	12.56	13.22	12.56	1.81	36.12	0.00	0.00	0.00	0.00	0.00
monGG(AT) I	409.001	427.656	583.829	409.001	0.000	0.000	0.000	0.000	0.000	0.000
GG MY-1 I	0.547	0.575	0.781	0.547	0.000	0.408	0.000	0.408	0.000	0.000
GG LW-2 I	1.852	1.787	2.644	1.852	0.000	1.267	0.000	1.267	0.000	0.000
GG DWT-3 I	5.165	5.444	7.372	5.165	0.000	3.861	0.000	3.861	0.000	0.000
GG NKW-4 I	0.210	0.212	0.300	0.210	0.000	0.150	0.000	0.150	0.000	0.000
GG Dummy I	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SDE MY-1 I	0.366	0.408	0.366	0.015	0.300	0.080	0.077	0.518	0.199	0.722
RETURN TOTI	149.531	174.458	213.449	6.172	0.000	24.138	0.000	157.164	0.000	0.000
RET LW-2 I	14.154	15.236	20.204	0.584	0.000	2.108	0.000	13.726	0.000	0.000
RET DWT-3 I	135.214	159.038	193.012	5.581	0.000	22.005	0.000	143.273	0.000	0.000
RET NKW-4I	0.163	0.183	0.233	0.007	0.000	0.025	0.000	0.165	0.000	0.000
RET DummyI	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

G E N E T I C G A I N per Year FOR THE SINGLE TRAITS

MY-1= 0.0594 LW-2 = 0.1960 DWT-3= 0.5610 NKW-= 0.0225 Dumm= 0.0000

Monetary G E N E T I C G A I N per Year 44.315

MEAN GENERATION INTERVAL 1.357

R E T U R N

RETURN TOTAL / UNIT 724.911

RETURN/TRAIT/UNIT:

LW-2 = 66.012 DWT-3= 658.124 NKW-= 0.776 Dumm= 0.000

C O S T S

COSTS TOTAL / UNIT 24.469

FIX = 9.709 PER DAM = 5.808 VARIABLE = 8.952

P R O F I T

PROFIT / UNIT 700.442

4. Genomic Natural Mating Strategy

BASIC RUN: RESULTS FOR THE SELECTION GROUPS

I	1	2	3	4	5	6	7	8	9	10
I	BNOB>BN	DN>BN	BNYB>DN	BNOB>DN	DN>DN	BNYB>BC	DC>BC	BNYB>DC	BC>DC	DC>DC
SEL.ANIM. I	10.000	166.667	133.333	10.000	3333.333	1773.333	47500.000	1773.333	456.000	47500.000

PROV.ANIM.I 133.333 3333.333 3724.650 133.333 3766.500 3724.650 55404.000 3724.650 54720.000 55404.000

PROP.SEL. I 0.075 0.050 0.036 0.075 0.885 0.476 0.857 0.476 0.008 0.857

SEL.INT(i)I 1.862 2.061 2.196 1.862 0.219 0.836 0.263 0.836 2.726 0.263

GEN.INT I 2.915 2.249 2.915 2.190 2.249 2.915 3.309 2.915 4.716 3.309

GENE-OFF I 95.0 100.0 95.0 5.0 100.0 100.0 100.0 70.0 30.0 100.0

SD(AT) I 105.355 117.558 105.355 4.348 86.536 22.936 0.000 149.337 0.000 0.000

RAI I 0.940 0.918 0.940 0.940 0.918 0.918 0.918 0.918 0.918 0.918

LT-GENE I 12.56 13.22 12.56 1.81 36.12 0.00 0.00 0.00 0.00 0.00

monGG(AT) I 504.594 545.578 595.142 504.594 57.998 0.000 0.000 0.000 0.000 0.000

GG MY-1 I 1.191 1.191 1.405 1.191 0.127 0.483 0.000 0.483 0.000 0.000

GG LW-2 I 0.516 0.563 0.608 0.516 0.060 0.229 0.000 0.229 0.000 0.000

GG DW-3 I 2.161 2.403 2.548 2.161 0.255 0.975 0.000 0.975 0.000 0.000

GG NKW-4 I 0.177 0.190 0.208 0.177 0.020 0.077 0.000 0.077 0.000 0.000

GG MYGS-5 I 0.933 1.053 1.100 0.933 0.112 0.427 0.000 0.427 0.000 0.000

GG LWGS-6 I 2.567 2.787 3.028 2.567 0.296 1.131 0.000 1.131 0.000 0.000

GG DWGS- I 6.280 6.786 7.406 6.280 0.721 2.754 0.000 2.754 0.000 0.000

GG NKG I 0.598 0.643 0.705 0.598 0.068 0.261 0.000 0.261 0.000 0.000

GG D I 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

SDE MY-1 I 0.366 0.408 0.366 0.015 0.300 0.080 0.077 0.518 0.199 0.722

SDE NKW-4 I 0.290 0.328 0.290 0.011 0.229 0.064 0.061 0.447 0.167 0.621

RETURN TOTI 184.384 222.453 217.472 7.609 17.406 17.612 0.000 114.685 0.000 0.000

RET LWGS-6I 19.615 23.759 23.135 0.810 1.859 1.881 0.000 12.247 0.000 0.000

RET DWGS-I 164.402 198.247 193.903 6.785 15.514 15.695 0.000 102.190 0.000 0.000

RET NKGI 0.368 0.447 0.434 0.015 0.033 0.035 0.000 0.247 0.000 0.000

RET DI 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

G E N E T I C G A I N per Year FOR THE SINGLE TRAITS

MY-1= 0.1294 LW-2 = 0.0579 DW-3 = 0.2444 NKW-4= 0.0197 MYGS-= 0.1061 LWGS-= 0.2877 DWGS= 0.7025 NK= 0.0667
= 0.0000

Monetary G E N E T I C G A I N per Year 56.461

MEAN GENERATION INTERVAL 1.357

R E T U R N

RETURN TOTAL / UNIT 781.621

RETURN/TRAIT/UNIT:

LWGS-= 83.306 DWGS= 696.736 NK= 1.578 = 0.000

C O S T S

COSTS TOTAL / UNIT 45.962

FIX = 9.709 PER DAM = 5.808 VARIABLE = 30.445

P R O F I T

PROFIT / UNIT 735.659

5. Genomic Liquid Semen Strategy

BASIC RUN: RESULTS FOR THE SELECTION GROUPS

I	1	2	3	4	5	6	7	8	9	10
I	BNOB>BN	DN>BN	BNYB>DN	BNOB>DN	DN>DN	BNYB>BC	DC>BC	BNYB>DC	BC>DC	DC>DC
SEL.ANIM. I	2.500	166.667	33.333	2.500	3333.333	443.333	47500.000	443.333	114.000	47500.000
PROV.ANIM.I	33.333	3333.333	3517.725	33.333	3557.250	3517.725	48478.496	3517.725	47880.000	48478.496
PROP.SEL. I	0.075	0.050	0.009	0.075	0.937	0.126	0.980	0.126	0.002	0.980
SEL.INT(i)I	1.791	2.061	2.675	1.791	0.132	1.641	0.050	1.641	3.115	0.050
GEN.INT I	2.915	2.249	2.915	2.190	2.249	2.915	3.309	2.915	4.716	3.309
GENE-OFF I	95.0	100.0	95.0	5.0	100.0	100.0	100.0	70.0	30.0	100.0
SD(AT) I	105.355	117.558	105.355	4.348	86.536	22.936	0.000	149.337	0.000	0.000
RAI I	0.966	0.920	0.966	0.966	0.920	0.920	0.920	0.920	0.920	0.920
LT-GENE I	12.56	13.22	12.56	1.81	36.12	0.00	0.00	0.00	0.00	0.00
monGG(AT) I	498.592	546.435	744.614	498.592	34.948	0.000	0.000	0.000	0.000	0.000
GG MY-1 I	1.165	1.206	1.740	1.165	0.077	0.960	0.000	0.960	0.000	0.000
GG LW-2 I	0.532	0.574	0.795	0.532	0.037	0.457	0.000	0.457	0.000	0.000
GG DWT-3 I	2.090	2.403	3.121	2.090	0.154	1.913	0.000	1.913	0.000	0.000
GG NKW-4 I	0.172	0.190	0.257	0.172	0.012	0.151	0.000	0.151	0.000	0.000
GG MYGS- I	0.875	1.061	1.307	0.875	0.068	0.845	0.000	0.845	0.000	0.000

GG LWGS-6 I 2.524 2.793 3.769 2.524 0.179 2.224 0.000 2.224 0.000 0.000
GG DWGS- I 6.209 6.796 9.273 6.209 0.435 5.412 0.000 5.412 0.000 0.000
GG NKG I 0.573 0.647 0.856 0.573 0.041 0.515 0.000 0.515 0.000 0.000
GG D I 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
SDE MY-1 I 0.366 0.408 0.366 0.015 0.300 0.080 0.077 0.518 0.199 0.722
SDE NKW-4I 0.290 0.328 0.290 0.011 0.229 0.064 0.061 0.447 0.167 0.621
RETURN TOTI 182.194 222.802 272.095 7.519 10.488 34.614 0.000 225.400 0.000 0.000
RET LWGS-6I 19.285 23.817 28.800 0.796 1.121 3.700 0.000 24.091 0.000 0.000
RET DWGS-I 162.557 198.536 242.768 6.709 9.347 30.844 0.000 200.821 0.000 0.000
RET NKGI 0.353 0.449 0.527 0.014 0.020 0.070 0.000 0.488 0.000 0.000
RET DI 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

G E N E T I C G A I N per Year FOR THE SINGLE TRAITS
MY-1= 0.1347 LW-2 = 0.0624 DWT-3= 0.2503 NKW-= 0.0203 MYGS= 0.1068 LWGS-= 0.2983 DWGS= 0.7312 NK= 0.0682
= 0.0000

Monetary G E N E T I C G A I N per Year 58.740
MEAN GENERATION INTERVAL 1.357

R E T U R N
RETURN TOTAL / UNIT 955.112
RETURN/TRAIT/UNIT:
LWGS-= 101.610 DWGS= 851.581 NK= 1.920 = 0.000

C O S T S

COSTS TOTAL / UNIT 48.383
FIX = 9.709 PER DAM = 5.808 VARIABLE = 32.866

P R O F I T
PROFIT / UNIT 906.729

6. Genomic Frozen Semen Strategy

BASIC RUN: RESULTS FOR THE SELECTION GROUPS

I	1	2	3	4	5	6	7	8	9	10
I	BNOB>BN	DN>BN	BNYB>DN	BNOB>DN	DN>DN	BNYB>BC	DC>BC	BNYB>DC	BC>DC	DC>DC
SEL.ANIM. I	2.500	166.667	33.333	2.500	2511.000	443.333	34627.500	443.333	114.000	34627.500
PROV.ANIM.I	33.333	3333.333	2483.100	33.333	2511.000	2483.100	34627.500	2483.100	34200.000	34627.500
PROP.SEL. I	0.075	0.050	0.013	0.075	1.000	0.179	1.000	0.179	0.003	1.000
SEL.INT(i)I	1.791	2.061	2.556	1.791	0.000	1.461	0.000	1.461	3.009	0.000
GEN.INT I	2.915	2.249	2.915	2.190	2.249	2.915	3.309	2.915	4.716	3.309
GENE-OFF I	95.0	100.0	95.0	5.0	100.0	100.0	100.0	70.0	30.0	100.0
SD(AT) I	105.355	117.558	105.355	4.348	86.536	22.936	0.000	149.337	0.000	0.000
RAI I	0.959	0.919	0.959	0.959	0.919	0.919	0.919	0.919	0.919	0.919
LT-GENE I	12.56	13.22	12.56	1.81	36.12	0.00	0.00	0.00	0.00	0.00

monGG(AT) I 495.066 546.228 706.683 495.066 0.000 0.000 0.000 0.000 0.000 0.000

GG MY-1 I 1.165 1.203 1.663 1.165 0.000 0.853 0.000 0.853 0.000 0.000

GG LW-2 I 0.522 0.571 0.745 0.522 0.000 0.405 0.000 0.405 0.000 0.000

GG DWT-3 I 2.084 2.403 2.974 2.084 0.000 1.704 0.000 1.704 0.000 0.000

GG NKW-4 I 0.171 0.190 0.245 0.171 0.000 0.135 0.000 0.135 0.000 0.000

GG MYGS- I 0.880 1.060 1.257 0.880 0.000 0.751 0.000 0.751 0.000 0.000

GG LWGS-6 I 2.509 2.792 3.582 2.509 0.000 1.980 0.000 1.980 0.000 0.000

GG DWGS- I 6.164 6.794 8.799 6.164 0.000 4.818 0.000 4.818 0.000 0.000

GG NKG I 0.575 0.646 0.820 0.575 0.000 0.458 0.000 0.458 0.000 0.000

GG D I 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

SDE MY-1 I 0.366 0.408 0.366 0.015 0.300 0.080 0.077 0.518 0.199 0.722

SDE NKW-4I 0.290 0.328 0.290 0.011 0.229 0.064 0.061 0.447 0.167 0.621

RETURN TOTI 180.905 222.718 258.233 7.466 0.000 30.816 0.000 200.670 0.000 0.000

RET LWGS-6I 19.172 23.804 27.367 0.791 0.000 3.294 0.000 21.444 0.000 0.000

RET DWGS-I 161.379 198.465 230.361 6.661 0.000 27.460 0.000 178.792 0.000 0.000

RET NKGI 0.354 0.449 0.505 0.014 0.000 0.062 0.000 0.434 0.000 0.000

RET DI 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

G E N E T I C G A I N per Year FOR THE SINGLE TRAITS

MY-1= 0.1257 LW-2 = 0.0573 DWT-3= 0.2327 NKW-= 0.0189 MYGS= 0.0997 LWGS-= 0.2771 DWGS= 0.6787 NK= 0.0637

= 0.0000

Monetary G E N E T I C G A I N per Year 54.528

MEAN GENERATION INTERVAL 1.357

R E T U R N

RETURN TOTAL / UNIT 900.807

RETURN/TRAIT/UNIT:

LWGS-= 95.871 DWGS= 803.119 NK= 1.817 = 0.000

C O S T S

COSTS TOTAL / UNIT 49.468

FIX = 9.709 PER DAM = 5.808 VARIABLE = 33.951

P R O F I T

PROFIT / UNIT 851.339

Appendix 1d: QMSim Outputs for Objective Four

1. Conventional Random Mating

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0172	0.0139	0.0172	0.0139
1	0	0.0000	0.0000	0.0000	0.0000
2	208	0.1250	0.0000	0.0013	0.0127
3	1030	0.0520	0.0393	0.0027	0.0145
4	4074	0.0194	0.0265	0.0040	0.0143
5	12312	0.0102	0.0191	0.0063	0.0158
6	19422	0.0079	0.0158	0.0076	0.0156
7	20000	0.0090	0.0149	0.0090	0.0149
8	20000	0.0103	0.0147	0.0103	0.0147
9	20000	0.0119	0.0148	0.0119	0.0148
10	20000	0.0132	0.0140	0.0132	0.0140
11	20000	0.0153	0.0158	0.0153	0.0158
12	20000	0.0166	0.0150	0.0166	0.0150
13	20000	0.0177	0.0138	0.0177	0.0138
14	20000	0.0194	0.0148	0.0194	0.0148
15	20000	0.0207	0.0140	0.0207	0.0140
Overall	217046	0.0144	0.0167	0.0101	0.0154

---------- EBV ----------

Gen.	Mean	SD
0	0.14205872	1.15096690
1	2.52791959	1.01239510
2	4.69792614	0.98675654

3	6.78879302	0.97045081
4	8.85685005	0.94255401
5	10.90774098	0.92909287
6	12.86815555	0.92991996
7	14.90052253	0.95202871
8	16.99656456	0.95082405
9	19.02005625	0.93150419
10	21.08908835	0.93983142
11	23.15935306	0.92525581
12	25.19376453	0.93522114
13	27.13509584	0.92103806
14	29.15584315	0.93076960
15	31.19510753	0.93666265

2. Conventional Positive Assortative Mating

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0176	0.0151	0.0176	0.0151
1	0	0.0000	0.0000	0.0000	0.0000
2	196	0.1250	0.0000	0.0012	0.0123
3	1846	0.0438	0.0312	0.0040	0.0158
4	6834	0.0180	0.0213	0.0061	0.0151
5	15980	0.0107	0.0168	0.0086	0.0157
6	19964	0.0114	0.0152	0.0114	0.0152
7	20000	0.0137	0.0156	0.0137	0.0156
8	20000	0.0154	0.0151	0.0154	0.0151
9	20000	0.0173	0.0153	0.0173	0.0153
10	20000	0.0195	0.0158	0.0195	0.0158
11	20000	0.0220	0.0163	0.0220	0.0163
12	20000	0.0244	0.0154	0.0244	0.0154
13	20000	0.0284	0.0164	0.0284	0.0164
14	20000	0.0309	0.0163	0.0309	0.0163
15	20000	0.0330	0.0156	0.0330	0.0156
Overall	224820	0.0210	0.0181	0.0152	0.0180

---------- EBV ----------

Gen.	Mean	SD

0	0.16803801	1.15625423
1	2.68322306	1.06725710
2	4.88387153	1.00621342
3	7.03364860	1.00647737
4	9.07897449	0.97755122
5	11.09649687	0.97525923
6	13.19005825	0.95693648
7	15.26548585	0.96982375
8	17.30639583	0.98988053
9	19.47136944	0.96429329
10	21.57021743	0.96958480
11	23.64044815	0.98238332
12	25.73636164	0.97002634
13	27.79615780	0.97462842
14	29.82076311	0.94726296
15	31.90032821	0.97749662

3. Coventional Negative Assortative Mating

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0173	0.0138	0.0173	0.0138
1	0	0.0000	0.0000	0.0000	0.0000
2	184	0.1250	0.0000	0.0012	0.0119
3	2142	0.0395	0.0250	0.0042	0.0147
4	8478	0.0162	0.0200	0.0068	0.0153
5	17108	0.0098	0.0151	0.0084	0.0144
6	19972	0.0100	0.0144	0.0099	0.0144
7	20000	0.0117	0.0149	0.0117	0.0149
8	20000	0.0130	0.0145	0.0130	0.0145
9	20000	0.0146	0.0151	0.0146	0.0151
10	20000	0.0161	0.0152	0.0161	0.0152
11	20000	0.0178	0.0154	0.0178	0.0154
12	20000	0.0194	0.0149	0.0194	0.0149
13	20000	0.0213	0.0151	0.0213	0.0151
14	20000	0.0229	0.0149	0.0229	0.0149
15	20000	0.0246	0.0146	0.0246	0.0146
Overall	227884	0.0168	0.0164	0.0124	0.0159

---------- EBV ----------

Gen.	Mean	SD
0	-0.07553317	1.16155323
1	2.10738212	1.01988695
2	4.28053342	0.94941513
3	6.35648318	0.89435576

4	8.43371063	0.90868674
5	10.45548171	0.88169220
6	12.55736529	0.93100424
7	14.59466314	0.87942764
8	16.61422038	0.90491428
9	18.61486103	0.89227332
10	20.64872777	0.90220771
11	22.65689693	0.89732647
12	24.67115103	0.88218203
13	26.66213591	0.88593070
14	28.69511459	0.89144578
15	30.70108671	0.88743741

4. Conventional Minf mating

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0176	0.0137	0.0176	0.0137
1	0	0.0000	0.0000	0.0000	0.0000
2	0	0.0000	0.0000	0.0000	0.0000
3	0	0.0000	0.0000	0.0000	0.0000
4	0	0.0000	0.0000	0.0000	0.0000
5	0	0.0000	0.0000	0.0000	0.0000
6	18186	0.0009	0.0004	0.0008	0.0004
7	20000	0.0024	0.0004	0.0024	0.0004
8	20000	0.0040	0.0004	0.0040	0.0004
9	20000	0.0056	0.0004	0.0056	0.0004
10	20000	0.0071	0.0004	0.0071	0.0004
11	20000	0.0085	0.0004	0.0085	0.0004
12	20000	0.0100	0.0004	0.0100	0.0004
13	20000	0.0115	0.0004	0.0115	0.0004
14	20000	0.0128	0.0004	0.0128	0.0004
15	20000	0.0142	0.0004	0.0142	0.0004
Overall	198186	0.0078	0.0043	0.0050	0.0051

---------- EBV ----------

Gen.	Mean	SD
0	0.11430889	1.15590694
1	2.54738671	1.04315462
2	4.66100129	0.96815817
3	6.69205264	0.94745314
4	8.78493601	0.95308549
5	10.88999008	0.95432327
6	13.00243996	0.95834524
7	15.09788378	0.96692366
8	17.14412062	0.94771244
9	19.21886138	0.94472483
10	21.28007356	0.95437045
11	23.36501942	0.94240343
12	25.44272251	0.94518340
13	27.51161322	0.93726360
14	29.55242714	0.94575733
15	31.62903380	0.94349397

5. Conventional Maxf Mating

	---------- Inbreeding ----------			
	Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0178	0.0145	0.0178	0.0145
1	0	0.0000	0.0000	0.0000	0.0000
2	12878	0.1259	0.0106	0.0811	0.0609
3	13216	0.1549	0.0631	0.1024	0.0895
4	16674	0.1684	0.0890	0.1404	0.1026
5	18104	0.1913	0.1157	0.1731	0.1236
6	19440	0.1862	0.1233	0.1810	0.1254
7	19372	0.2026	0.1222	0.1962	0.1254
8	19384	0.2045	0.1325	0.1982	0.1351
9	19942	0.2135	0.1379	0.2129	0.1382
10	19880	0.2278	0.1379	0.2264	0.1386
11	20000	0.2357	0.1403	0.2357	0.1403
12	20000	0.2319	0.1445	0.2319	0.1445
13	20000	0.2478	0.1369	0.2478	0.1369
14	20000	0.2672	0.1304	0.2672	0.1304

15	20000	0.2468	0.1392	0.2468	0.1392
Overall	258890	0.2118	0.1297	0.1768	0.1422

---------- EBV ----------

Gen.	Mean	SD
0	-0.06007933	1.16806365
1	2.19470613	1.06167555
2	4.35446888	0.98865525
3	6.46366415	0.93105612
4	8.55455706	0.90584568
5	10.49997964	0.84430506
6	12.52049758	0.83379493
7	14.43357764	0.83211158
8	16.35194042	0.83220723
9	18.27405235	0.81485829
10	20.12973877	0.81182933
11	22.04262330	0.79856575
12	23.88807761	0.77204185
13	25.72155768	0.79674558
14	27.51846341	0.76105043
15	29.33106589	0.75176870

6. Conventional breeding using exotic goats

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	3030	0.0167	0.0142	0.0167	0.0142
1	0	0.0000	0.0000	0.0000	0.0000
2	0	0.0000	0.0000	0.0000	0.0000
3	0	0.0000	0.0000	0.0000	0.0000
4	1454	0.0144	0.0105	0.0035	0.0080
5	6000	0.0108	0.0026	0.0108	0.0026
6	6000	0.0142	0.0020	0.0142	0.0020
7	6000	0.0183	0.0016	0.0183	0.0016
8	6000	0.0221	0.0015	0.0221	0.0015
9	6000	0.0281	0.0023	0.0281	0.0023
10	6000	0.0330	0.0020	0.0330	0.0020
11	6000	0.0378	0.0014	0.0378	0.0014
12	6000	0.0415	0.0016	0.0415	0.0016
13	6000	0.0450	0.0014	0.0450	0.0014
14	6000	0.0494	0.0014	0.0494	0.0014
15	6000	0.0534	0.0015	0.0534	0.0015
Overall	67454	0.0318	0.0142	0.0230	0.0186

---------- EBV ----------

Gen.	Mean	SD
0	0.73369059	0.97437284

1	3.61375539	0.94188012
2	5.59323052	0.99154860
3	7.82688329	0.98260626
4	9.82956685	0.92324173
5	11.85045561	0.91645058
6	13.86574033	0.93498924
7	16.01335778	0.95257975
8	18.10281027	0.93369272
9	20.01318433	0.90741913
10	22.11108667	0.90188698
11	24.18619874	0.91357835
12	26.15115210	0.91420515
13	28.31397787	0.97232481
14	30.50310517	0.91482593
15	32.62302863	0.93155367

7. Conventional breeding using indigenous goats

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	5050	0.0167	0.0127	0.0167	0.0127
1	0	0.0000	0.0000	0.0000	0.0000
2	0	0.0000	0.0000	0.0000	0.0000
3	0	0.0000	0.0000	0.0000	0.0000
4	0	0.0000	0.0000	0.0000	0.0000
5	520	0.0020	0.0001	0.0001	0.0004
6	10000	0.0037	0.0010	0.0037	0.0010
7	10000	0.0071	0.0011	0.0071	0.0011
8	10000	0.0099	0.0007	0.0099	0.0007
9	10000	0.0124	0.0007	0.0124	0.0007
10	10000	0.0150	0.0009	0.0150	0.0009
11	10000	0.0177	0.0008	0.0177	0.0008
12	10000	0.0203	0.0008	0.0203	0.0008
13	10000	0.0229	0.0006	0.0229	0.0006
14	10000	0.0263	0.0011	0.0263	0.0011
15	10000	0.0286	0.0008	0.0286	0.0008
Overall	100520	0.0163	0.0079	0.0106	0.0101

---------- EBV ----------

Gen.	Mean	SD
0	-0.65997202	1.00362938
1	-3.58758773	0.93223321
2	-1.75954611	0.93626910
3	0.33438994	0.94578853
4	2.24759368	0.92944370
5	4.28546539	0.91735792

6	6.24314027	0.93582074
7	8.29487180	0.93550628
8	10.33971171	0.94491505
9	12.48610593	0.94569004
10	14.46452602	0.93917205
11	16.57266325	0.93466820
12	18.61363252	0.91108148
13	20.52686519	0.91745448
14	22.61783392	0.91302184
15	24.69969275	0.91811789

8. Conventional breeding using cross bred goats

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	3030	0.0289	0.0025	0.0289	0.0025
1	0	0.0000	0.0000	0.0000	0.0000
2	0	0.0000	0.0000	0.0000	0.0000
3	0	0.0000	0.0000	0.0000	0.0000
4	0	0.0000	0.0000	0.0000	0.0000
5	5672	0.0036	0.0014	0.0034	0.0016
6	6000	0.0074	0.0015	0.0074	0.0015
7	6000	0.0117	0.0012	0.0117	0.0012
8	6000	0.0153	0.0011	0.0153	0.0011
9	6000	0.0206	0.0026	0.0206	0.0026
10	6000	0.0257	0.0017	0.0257	0.0017
11	6000	0.0294	0.0013	0.0294	0.0013
12	6000	0.0329	0.0012	0.0329	0.0012
13	6000	0.0373	0.0017	0.0373	0.0017
14	6000	0.0418	0.0011	0.0418	0.0011
15	6000	0.0451	0.0010	0.0451	0.0010
Overall	65672	0.0247	0.0134	0.0174	0.0160

---------- EBV ----------

Gen.	Mean	SD
0	9.42567709	1.14046854
1	29.87541202	0.95205365
2	30.86336254	1.15938570
3	30.83891197	1.30501423
4	31.09055033	1.24618070
5	31.02539863	1.31819272
6	30.75792124	1.34570530
7	30.73670004	1.34870234
8	30.68895299	1.26345511
9	31.02861524	1.31207455
10	30.98770842	1.41889132
11	31.18249302	1.42776209
12	30.92164083	1.36946497
13	30.71492866	1.42910928
14	30.87570033	1.21100504
15	30.90207763	1.19912104

9. Genomic Random Mating

	---------- Inbreeding ----------			
	Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0173	0.0131	0.0173	0.0131
1	0	0.0000	0.0000	0.0000	0.0000
2	234	0.1261	0.0115	0.0015	0.0136
3	1148	0.0470	0.0349	0.0027	0.0138
4	4690	0.0179	0.0253	0.0042	0.0144
5	13170	0.0094	0.0185	0.0062	0.0157
6	19584	0.0074	0.0152	0.0073	0.0151
7	20000	0.0087	0.0147	0.0087	0.0147
8	20000	0.0100	0.0148	0.0100	0.0148
9	20000	0.0111	0.0138	0.0111	0.0138
10	20000	0.0125	0.0146	0.0125	0.0146
11	20000	0.0146	0.0160	0.0146	0.0160
12	20000	0.0154	0.0141	0.0154	0.0141
13	20000	0.0168	0.0140	0.0168	0.0140
14	20000	0.0183	0.0146	0.0183	0.0146

15	20000	0.0195	0.0148	0.0195	0.0148
Overall	218826	0.0136	0.0165	0.0096	0.0152

---------- EBV ----------

Gen.	Mean	SD
0	0.40598694	2.70032399
1	4.18679286	2.33707476
2	7.50043452	2.23999894
3	10.61424838	2.18756825
4	13.74299563	2.16862493
5	16.89504598	2.13415950
6	19.88657891	2.13494336
7	22.85129984	2.10880147
8	25.79896891	2.09392424
9	28.70713371	2.09720749
10	31.74478205	2.05461136
11	34.62222874	2.01015683
12	37.45269305	1.98757959
13	40.17186556	1.96230953
14	42.84939830	1.91784358
15	45.49610170	1.88409111

10. Genomic Positive Assortative Mating

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0176	0.0142	0.0176	0.0142
1	0	0.0000	0.0000	0.0000	0.0000
2	246	0.1250	0.0000	0.0015	0.0138
3	10462	0.0448	0.0215	0.0234	0.0272
4	19682	0.0414	0.0255	0.0407	0.0258
5	20000	0.0507	0.0248	0.0507	0.0248
6	20000	0.0585	0.0255	0.0585	0.0255
7	20000	0.0688	0.0255	0.0688	0.0255
8	20000	0.0763	0.0233	0.0763	0.0233
9	20000	0.0841	0.0218	0.0841	0.0218
10	20000	0.0908	0.0208	0.0908	0.0208
11	20000	0.0984	0.0209	0.0984	0.0209
12	20000	0.1040	0.0189	0.1040	0.0189
13	20000	0.1102	0.0203	0.1102	0.0203
14	20000	0.1208	0.0224	0.1208	0.0224
15	20000	0.1364	0.0250	0.1364	0.0250
Overall	250390	0.0850	0.0365	0.0687	0.0469

---------- EBV ----------

Gen.	Mean	SD

0	-0.63855258	2.73614121
1	3.02549890	2.53935807
2	6.92362611	2.56372880
3	10.77688131	2.46802678
4	14.57356269	2.41627422
5	18.12287776	2.39315541
6	21.61110231	2.30303571
7	24.95008431	2.25506406
8	28.18107417	2.21933378
9	31.35402981	2.15200827
10	34.43414381	2.12309360
11	37.47054030	2.11881332
12	40.55140780	2.08584520
13	43.36497741	2.01722938
14	46.34846416	2.01907477
15	49.12676966	1.98226498

11. Genomic Negative Assortative Mating

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0172	0.0137	0.0172	0.0137
1	0	0.0000	0.0000	0.0000	0.0000
2	192	0.1250	0.0000	0.0012	0.0122
3	1586	0.0441	0.0319	0.0035	0.0149
4	5886	0.0167	0.0214	0.0049	0.0139
5	14304	0.0097	0.0168	0.0069	0.0148
6	19818	0.0089	0.0155	0.0088	0.0154
7	20000	0.0112	0.0156	0.0112	0.0156
8	20000	0.0138	0.0163	0.0138	0.0163
9	20000	0.0151	0.0152	0.0151	0.0152
10	20000	0.0167	0.0146	0.0167	0.0146
11	20000	0.0190	0.0153	0.0190	0.0153
12	20000	0.0211	0.0157	0.0211	0.0157
13	20000	0.0231	0.0160	0.0231	0.0160
14	20000	0.0243	0.0142	0.0243	0.0142
15	20000	0.0265	0.0148	0.0265	0.0148
Overall	221786	0.0177	0.0172	0.0127	0.0166

---------- EBV ----------

Gen.	Mean	SD
0	-0.21604478	2.80695364
1	3.49079217	2.19167167
2	6.63704192	2.04059161
3	9.56184147	2.04588758

4	12.52558322	2.04159208
5	15.52309099	2.02876961
6	18.40760176	1.99376136
7	21.25719936	1.96424975
8	24.10022493	1.98017499
9	26.99192078	1.96313658
10	29.79121654	1.95064708
11	32.50053532	1.93955856
12	35.24253219	1.90542108
13	37.95087366	1.85929634
14	40.64232625	1.83810379
15	43.20819398	1.83485472

12. Genomic Minf mating

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0174	0.0136	0.0174	0.0136
1	0	0.0000	0.0000	0.0000	0.0000
2	0	0.0000	0.0000	0.0000	0.0000
3	0	0.0000	0.0000	0.0000	0.0000
4	0	0.0000	0.0000	0.0000	0.0000
5	0	0.0000	0.0000	0.0000	0.0000
6	19164	0.0011	0.0004	0.0010	0.0005
7	20000	0.0026	0.0004	0.0026	0.0004
8	20000	0.0040	0.0004	0.0040	0.0004
9	20000	0.0053	0.0004	0.0053	0.0004
10	20000	0.0068	0.0005	0.0068	0.0005
11	20000	0.0084	0.0004	0.0084	0.0004
12	20000	0.0097	0.0004	0.0097	0.0004
13	20000	0.0113	0.0004	0.0113	0.0004
14	20000	0.0127	0.0004	0.0127	0.0004
15	20000	0.0141	0.0004	0.0141	0.0004
Overall	199164	0.0076	0.0042	0.0049	0.0049

---------- EBV ----------

Gen.	Mean	SD
0	0.71479276	2.66898116
1	4.45858287	2.29177709
2	7.73847268	2.18924253
3	10.84627470	2.16111367
4	13.85751680	2.16322584
5	16.88932767	2.16458466
6	19.95382751	2.15524699
7	23.07514837	2.13017423

8	26.11417576	2.10019198
9	28.98983126	2.08327775
10	31.84866681	2.06487876
11	34.74271210	2.02235777
12	37.61729440	2.02166342
13	40.39477450	1.98199503
14	43.24928299	1.95345286
15	46.02311868	1.91867931

13. Genomic Maxf Mating

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	10100	0.0182	0.0156	0.0182	0.0156
1	0	0.0000	0.0000	0.0000	0.0000
2	11930	0.1260	0.0111	0.0751	0.0624
3	13792	0.1635	0.0592	0.1127	0.0902
4	17162	0.1612	0.0935	0.1383	0.1033
5	17832	0.1919	0.1121	0.1711	0.1215
6	18962	0.2108	0.1255	0.1998	0.1308
7	19752	0.2108	0.1300	0.2082	0.1313
8	19702	0.2259	0.1455	0.2226	0.1470
9	19616	0.2206	0.1412	0.2164	0.1431
10	20000	0.2181	0.1473	0.2181	0.1473
11	20000	0.2255	0.1431	0.2255	0.1431
12	20000	0.2177	0.1359	0.2177	0.1359
13	20000	0.2480	0.1256	0.2480	0.1256
14	20000	0.2325	0.1375	0.2325	0.1375
15	20000	0.2522	0.1394	0.2522	0.1394
Overall	258748	0.2117	0.1305	0.1766	0.1429

---------- EBV ----------

Gen.	Mean	SD
0	-0.47348785	2.86533556
1	3.43967579	2.38102265

2	6.89312858	2.25808323
3	10.22114706	2.17003244
4	13.26168925	2.09823733
5	16.15375958	2.01309589
6	19.01283877	1.94096882
7	21.77527401	1.92281212
8	24.55539187	1.89000240
9	27.31602425	1.86001836
10	29.95710563	1.81238203
11	32.70100633	1.83518924
12	35.29895608	1.81080056
13	37.83428503	1.77201764
14	40.36248454	1.71871500
15	42.77230900	1.70701559

14. Genomic breeding using exotic goats

	---------- Inbreeding ----------			
	Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	3030	0.0173	0.0144	0.0173	0.0144
1	0	0.0000	0.0000	0.0000	0.0000
2	0	0.0000	0.0000	0.0000	0.0000
3	0	0.0000	0.0000	0.0000	0.0000
4	1210	0.0078	0.0000	0.0016	0.0031
5	6000	0.0059	0.0029	0.0059	0.0029
6	6000	0.0114	0.0018	0.0114	0.0018
7	6000	0.0170	0.0013	0.0170	0.0013
8	6000	0.0219	0.0012	0.0219	0.0012
9	6000	0.0266	0.0013	0.0266	0.0013
10	6000	0.0307	0.0014	0.0307	0.0014
11	6000	0.0350	0.0014	0.0350	0.0014
12	6000	0.0402	0.0013	0.0402	0.0013
13	6000	0.0465	0.0027	0.0465	0.0027
14	6000	0.0500	0.0014	0.0500	0.0014
15	6000	0.0542	0.0014	0.0542	0.0014
Overall	67210	0.0304	0.0155	0.0220	0.0190

---------- EBV ----------

Gen.	Mean	SD
0	3.41207833	1.64117844
1	6.52711365	2.01150590
2	9.37595472	2.14977693
3	12.45317110	2.18170248
4	15.65585783	2.17785213
5	18.75272728	2.17554308
6	21.73444148	2.11848844
7	24.67590306	2.10812645
8	27.65348459	2.07411237
9	30.56685970	2.01904268
10	33.29866751	1.97505098
11	36.01237567	1.95324738
12	38.81404295	1.89732533
13	41.48898248	1.86728084
14	44.05969181	1.81451066
15	46.54215698	1.77105113

15. Genomic breeding using indigenous goats

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	5050	0.0173	0.0149	0.0173	0.0149
1	0	0.0000	0.0000	0.0000	0.0000
2	0	0.0000	0.0000	0.0000	0.0000
3	0	0.0000	0.0000	0.0000	0.0000
4	0	0.0000	0.0000	0.0000	0.0000
5	4964	0.0020	0.0001	0.0010	0.0010
6	10000	0.0034	0.0010	0.0034	0.0010
7	10000	0.0063	0.0008	0.0063	0.0008
8	10000	0.0091	0.0009	0.0091	0.0009
9	10000	0.0117	0.0007	0.0117	0.0007
10	10000	0.0145	0.0007	0.0145	0.0007
11	10000	0.0169	0.0006	0.0169	0.0006
12	10000	0.0198	0.0009	0.0198	0.0009
13	10000	0.0231	0.0010	0.0231	0.0010
14	10000	0.0257	0.0008	0.0257	0.0008
15	10000	0.0290	0.0010	0.0290	0.0010
Overall	104964	0.0153	0.0085	0.0103	0.0100

---------- EBV ----------

Gen.	Mean	SD
0	-1.77844071	1.81539302
1	-4.71813882	2.04239279

2	-1.82714603	2.14188251
3	1.15612205	2.23134355
4	4.35651249	2.26870738
5	7.55708106	2.24785841
6	10.60441375	2.24162350
7	13.66688752	2.22819308
8	16.79306913	2.21455437
9	19.94235297	2.19904387
10	22.91298957	2.15640968
11	26.08657459	2.10182368
12	28.96322428	2.06487010
13	31.83606956	2.02152397
14	34.63681024	1.96704371
15	37.46445395	1.90891229

16. Genomic breeding using cross bred goats

---------- Inbreeding ----------

		Inbred		All	
Gen.	No.	Mean	SD	Mean	SD
0	3030	0.0292	0.0027	0.0292	0.0027
1	0	0.0000	0.0000	0.0000	0.0000
2	0	0.0000	0.0000	0.0000	0.0000
3	0	0.0000	0.0000	0.0000	0.0000
4	0	0.0000	0.0000	0.0000	0.0000
5	4912	0.0033	0.0014	0.0027	0.0018
6	6000	0.0078	0.0017	0.0078	0.0017
7	6000	0.0126	0.0014	0.0126	0.0014
8	6000	0.0170	0.0013	0.0170	0.0013
9	6000	0.0204	0.0012	0.0204	0.0012
10	6000	0.0242	0.0012	0.0242	0.0012
11	6000	0.0274	0.0009	0.0274	0.0009
12	6000	0.0314	0.0012	0.0314	0.0012
13	6000	0.0355	0.0013	0.0355	0.0013
14	6000	0.0407	0.0021	0.0407	0.0021
15	6000	0.0448	0.0012	0.0448	0.0012
Overall	64912	0.0244	0.0127	0.0171	0.0154

---------- EBV ----------

Gen.	Mean	SD
0	33.82393527	2.30639046
1	44.32819284	1.83039270
2	44.71142639	2.05146695

3	44.67610944	2.13650726
4	44.37050539	2.25495218
5	44.53073775	2.19496454
6	44.79277071	2.19837437
7	44.76472593	2.18058527
8	45.28119336	2.24934431
9	45.27315986	2.25384773
10	45.11840320	2.10300405
11	44.72998694	2.13296149
12	44.69015987	2.16820935
13	44.22004392	2.26289934
14	44.15654985	2.18593153
15	44.27857316	2.15489822

Appendix 2: Abstract of Published Paper on Objective One of this Thesis

Tropical Animal Health and Production
https://doi.org/10.1007/s11250-020-02297-4

REGULAR ARTICLES

Comparative reproductive performance of Saanen and Toggenburg bucks raised under tropical environment

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Abstract

The objective of this study was to evaluate the effect of breed and age on scrotal measurements and semen characteristics of Saanen and Toggenburg bucks raised under extensive system in the tropic. The study was conducted using Toggenburg and Saanen bucks; the bucks were allocated into two different groups based on breed and age in 2 × 2 factorial completely randomized design. The body weight was determined using a hanging weighing scale expressed in kilogrammes (kg). Scrotal circumference and scrotal length were measured using metal measuring tape. Semen characteristics evaluated were volume, consistency, mass activity and progressive motility, live sperm cells, normal morphology and spermatozoa concentration. The current study found that breed of bucks had no influence on body weight, scrotal circumference, scrotal length, volume, mass activity, progressive motility, live sperm cells and sperm morphology. The study also found that Toggenburg bucks had higher semen consistency and spermatozoa concentration as compared with Saanen bucks. Therefore, it can be concluded that Toggenburg bucks can produce high number of total spermatozoa and as a result higher semen doses for artificial insemination purposes. Further studies with more number of animals are recommended.

Keywords Breed · Goat · Scrotal measurements · Semen characteristics

Appendix 3: Abstract of Published Paper on Objective Two of this Thesis

Contents lists available at ScienceDirect

Small Ruminant Research

journal homepage: www.elsevier.com/locate/smallrumres

Short communication

Short-term oestrous synchronisation protocol following single fixed-time artificial insemination and natural mating as alternative to long-term protocol in dairy goats

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Keywords:
Conception rate
oestrous response
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ABSTRACT

This study investigated the hypothesis that the use of short-term synchronisation protocol following single fixed-time artificial insemination (AI) with extended cooled semen and natural mating in fertility management of dairy goats could be as good as or better than traditional long-term protocol. This was tested by designing an experiment using Toggenburg dairy goats raised under semi-intensive production system in the tropics. Twenty-eight (28) females Toggenburg dairy goats were randomly allocated to two synchronisation protocols in completely randomised design and within each synchronisation protocol the animals were further subdivided into two mating methods. Oestrus was synchronised using short (7 days) and long-term (12 days) protocols and animals mated using natural mating and AI. The onset and the duration of oestrus were monitored using two intact-aproned bucks following controlled internal drug release (CIDR) devices withdrawal. The non-return to oestrus method was used to determine conception rate. The onset and duration of oestrus, response to oestrus and conception rate were evaluated. The onset and duration of oestrus was analysed using one-way ANOVA, while response to oestrus, conception rate and kidding rate were analysed by using Chi-Square test. Generally, the two protocols realised 100 % response to oestrus. Onset and duration of oestrus in short-term protocol were 31.75 hrs and 31.70 hrs, respectively, while the corresponding values for long-term protocol were 33.33 hrs and 30.93 hrs. The two protocols did not significantly differ in onset and duration of oestrus, conception, kidding and twining rate. Similarly, the two mating methods did not differ significantly on conception, kidding and twining rates. The current study has an overall of conception rate, kidding and twinning rate of 71.42, 64.29 and 44.50 %, respectively. The short-term protocol following single fixed-time AI and natural mating therefore, can be alternative to long-term oestrous synchronisation protocol in dairy goats.

Appendix 4: Paper Accepted for Publication on Objective Three of this Thesis

Gore, D. L. M., Okeno, T. O., Muasya, T. K., & Mburu, J. N. Improved response to selection in dairy goat breeding programme through reproductive technology and genomic selection in the tropics. *Accepted for publication in Small Ruminant Research*

Appendix 5: Poster Presentation on Objective One of this Thesis at 13th Egerton University International Conference

Combination of scrotal and semen characteristics is more informative when selecting dairy goat bucks for breeding

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Aim

To evaluate the effect of breed and age on scrotal measurements, semen characteristics and the correlations among these traits in dairy bucks raised under extensive system.

Introduction

Breeding of goats requires proper selection of breeding bucks through consideration of their breeding soundness. Selection of breeding bucks is the most critical decision for improvement of a flock, and it largely depends on factors like scrotal circumference and semen quality.

Materials and Methods

- This study was conducted at the Tatton Agriculture Park (TAP), Egerton University, Njoro.
- The study was conducted using total of twelve (12) healthy bucks, six (6) were Toggenburg and the other were six (6) Saanen bucks.
- The body weight (BW), Scrotal circumference (SC) and scrotal length (SL) were measured.
- Semen samples were evaluated for volume, mass motility and sperm concentration.
- The data were analysed using ANOVA in General Linear Model (GLM) and correlation was analysed using Pearson's product-moment procedures of SAS (Version 9.0).

Findings

- The results of the present study found that there was no significant (P >0.05) difference between the two breeds in terms of body weight and scrotal measurements, ejaculate volume and motility (Table I).
- The breed effect, was however, significant (P <0.05) for semen concentration. Age of the bucks had significant (P <0.05) effects on body weight, scrotal and in semen quality characteristics (Table I).
- The results shown that scrotal circumference, scrotal length and body weight had positive correlation among each other (Table II).
- Sperm concentration had a positive correlation with mass motility. Semen volume was also positively correlated with scrotal circumference, testicular length and body weight, but negatively correlated with sperm concentration.

ELIB ...nurturing life

Conclusion

- Toggenburg bucks could produce higher semen doses for artificial insemination purposes compared to Saanen bucks under extensive system.
- Selection of breeding bucks should not be based on scrotal traits only, but semen characteristics should also be considered.

Table I: Effect of breed and age on body weight, scrotal measurements and semen characteristics of Saanen and Toggenburg dairy goats

Parameters	Breed		Age in years	
	Toggenburg (lsmean ± SE)	Saanen (lsmean ± SE)	1-2 (lsmean ± SE)	3-6 (lsmean ± SE)
Scrotal characteristics				
Body weight (kg)	51.00±6.31[a]	42.60±6.31[a]	35.20±3.27[b]	58.40±3.27[a]
Scrotal circumference (cm)	28.20±0.89[a]	26.60±0.89[a]	26.10±0.73[b]	28.70±0.73[a]
Scrotal length (cm)	11.90±0.57[a]	10.80±0.57[a]	10.30±0.35[b]	12.40±0.35[a]
Semen characteristics				
Volume (ml)	1.00±0.10[a]	0.97±0.09[a]	0.89±0.10[a]	1.08±0.10[a]
Mass motility (0-5)	4.02±0.16[a]	3.69±2.87[a]	3.60±0.15[b]	4.12±0.16[a]
Concentration (x10[9]/ml)	2.87±0.27[a]	1.67±0.24[b]	1.85±0.25[b]	2.70±0.26[a]

Means with different superscripts within the same row differ significantly at P< 0.05

Table II: Pearson's product moment correlation coefficients among body weight, scrotal measurements and semen characteristics of Saanen and Toggenburg goats

Parameters	Correlation (r)
Scrotal circumference and body weight	0.74*
Testicular length and body weight	0.83**
Scrotal circumference and testicular length	0.96**
Volume and scrotal circumference	0.07
Volume and testicular length	0.08
Volume and body weight	0.05
Volume and sperm concentration	›0.44
Scrotal circumference and sperm concentration	›0.01
Testicular length and sperm concentration	›0.14
Scrotal circumference and mass motility	›0.31
Testicular length and mass motility	›0.43
Mass motility and sperm concentration	0.85**

Significant
**Highly significant*

Figure 1: Top left: Toggengurg and Saanen bucks, bottom left: Scrotal circumference measurement, top middle: Electro ejaculator Semen collection from a buck, bottom middle: Semen collection from a buck, Right: Microscope mounted with a camera display buck spermatozoa on the screen

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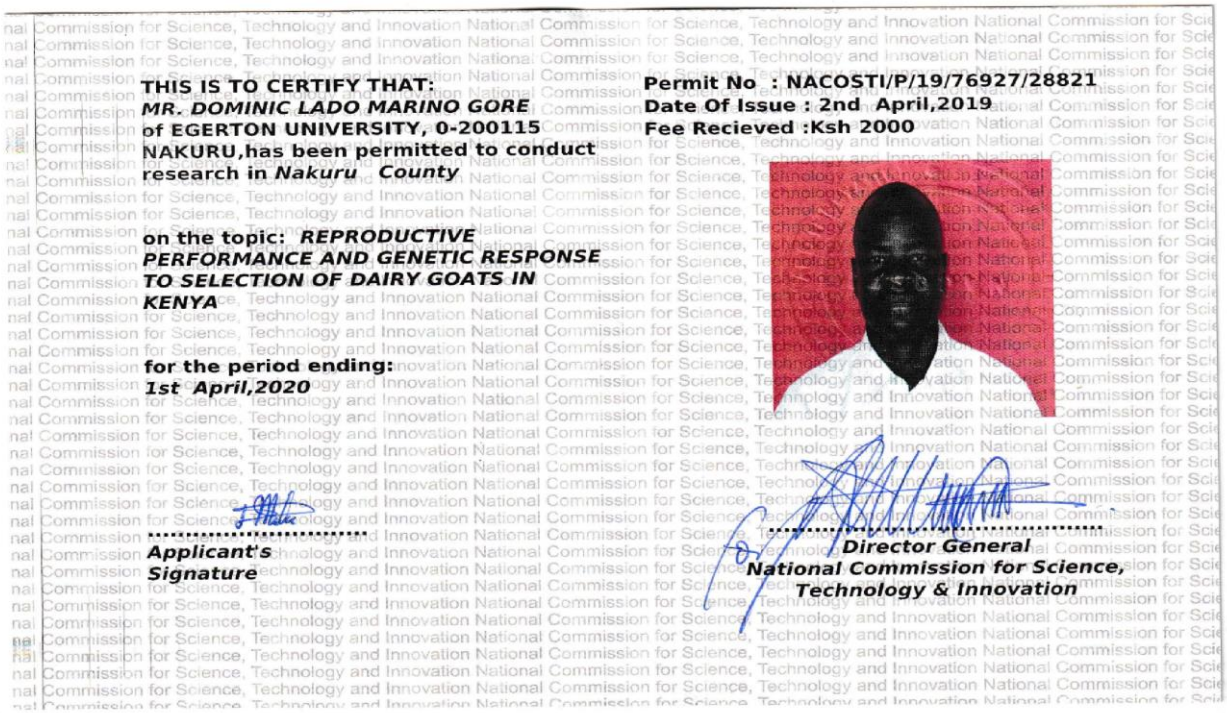
Appendix 6: Manuscript under Review on Objective Four of this Thesis

Gore, D. L. M., Okeno, T. O., Muasya, T. K., & Mburu, J. N. A combination of reproductive technology and genomic selection optimises response to selection in dairy goat breeding programmes. *Submitted for publication in South African Journal of Animal Science*.

Appendix 7: NACOSTI and Ethical Approvals

Appendix 7a: NACOSTI Approval



THIS IS TO CERTIFY THAT:
MR. DOMINIC LADO MARINO GORE
of EGERTON UNIVERSITY, 0-200115
NAKURU,has been permitted to conduct
research in *Nakuru County*

on the topic: *REPRODUCTIVE PERFORMANCE AND GENETIC RESPONSE TO SELECTION OF DAIRY GOATS IN KENYA*

for the period ending:
1st April,2020

Permit No : NACOSTI/P/19/76927/28821
Date Of Issue : 2nd April,2019
Fee Recieved :Ksh 2000

.....
Applicant's Signature

.....
Director General
National Commission for Science, Technology & Innovation

Appendix 7b: Ethical Approval

INSTITUTE OF PRIMATE RESEARCH
P. O. Box 24481 - 00502 Karen, Nairobi Kenya | Tel: +254-20 2606235 | Fax: +254-20 2606231
URL: www.primateresearch.org | Email: directoripr@primateresearch.org
"Translating Life Science"
NATIONAL MUSEUMS OF KENYA
WHERE HERITAGE LIVES ON

INSTITUTIONAL REVIEW COMMITTEE (IRC)

FINAL PROPOSAL APPROVAL FORM

Our ref: **ISERC/10/19**

Dear **Mr. Dominic Gore**

It is my pleasure to inform you that your proposal entitled **"REPRODUCTIVE PERFORMANCE AND GENETIC RESPONSE TO SELECTION OF DAIRY GOATS IN KENYA"** has been reviewed by the Institutional Review Committee (IRC) following a meeting held on 19th September 2019. The proposal was reviewed on the scientific merit and ethical considerations on the use of animals for research purposes.
The committee is guided by the Institutional guidelines as well as International regulations, including those of WHO, NIH, PVEN and Helsinki Convention on the humane treatment of animals for scientific purposes and GLP.

This proposal has been approved and you are bound by the IPR Intellectual Property Policy.

Signed……Chairman IRC: DR. NGALA JILLANI

Signed ……. Secretary IRC: DR. FAITH ONDITI

Date

INSTITUTE OF PRIMATE RESEARCH
INSTITUTIONAL REVIEW COMMITTEE
P. O. Box 24481-00502 KAREN
NAIROBI - KENYA
APPROVED 22/11/2019