GENETIC AND PHENOTYPIC CORRELATION OF MILK COMPONENT TRAITS IN SAANEN GOATS OF SOUTH AFRICA

by

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(MINI-) DISSERTATION

Submitted in (partial) fulfilment of the requirements for the degree of

MASTER OF SCIENCE IN ANIMAL PRODUCTION

in the

FACULTY OF SCIENCE AND AGRICULTURE

(School of Agricultural and Environmental Sciences)

at the

UNIVERSITY OF LIMPOPO

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2021

DEDICATION

This work is dedicated to my parents (Masilo and Lydia), my grandmothers (Kgaogelo and Melobe) and my daughter (Tintswalo) who are my motivation for the willingness in me to succeed.

DECLARATION

I declare that the mini-dissertation hereby submitted to the University of Limpopo, for the degree of Master of Science in Agriculture (Animal Production) has not previously been submitted by me for a degree at this or any other University; that it is my work in design and in execution, and that all material contained herein has been duly acknowledged.

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ACKNOWLEGEMENTS

Firstly, I would like to express my gratitude towards God, who guided me from start to finish and provided me with strength to carry on.

I would like to take this opportunity to thank both my supervisors Dr. Obert Tada and Mr. Khetho Nemutandani. I appreciate the opportunity given to work with you. Thank you for your patience, teachings, support, encouragements and guide on ASReml software operation.

Thanks a lot, to Dr. Japie van der Westhuizen, the people at South African stud book and MILCH Goat Breeders’ Society for making it possible to obtain both performance and pedigree data files that enabled this study to take place.

Thanks to the National Research Foundation (NRF) for providing the funds that enabled the study to take place.

Lastly, my sincere appreciation to my family and friends for being there until the end.

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Production traits and components

MY	Milk yield
FY	Fat yield
PY	Protein yield
LY	Lactose yield
Urea	Urea concentration yield
NR	Net returns
P	Persistency
SCCI	Somatic cell count index
SCC	Somatic cell count
SCS	Somatic cell score

(Co) variance components and genetic parameters

σ^2_a	Direct additive variance
σ^2_p	Phenotypic variance
σ^2_c	Environmental variance
σ^2_e	Error/uncontrollable variance
h^2	Direct heritability
σ^2_m	Maternal additive variance
σ^2_{mpe}	Maternal permanent environmental variance
σ^2_{am}	Genetic covariance between animal and doe effects
r_G	Genetic correlation
r_P	Phenotypic correlation
r_E	Environmental correlation

Other

ANOVA	Analysis of variance
DKA	Dam kidding age
DKS	Dam kidding season
LogL	Log likelihood
REML	Restricted maximum likelihood

ABSTRACT

Initial analysis was conducted to test significance of dam parity, litter size, birth season, birth year, kidding season and kidding age on lactation milking performance of various milk production traits and components, as well as to calculate phenotypic correlation between dam kidding age and these traits. Analysis of variance (ANOVA) was carried out using 16 407 non-pedigreed lactation records to test for non-genetic significant effects, while Pearson's correlation coefficients were calculated using Minitab software. The second analysis included 2 960 fully pedigreed lactation records that were analysed to estimate (co) variance components and direct heritability values for milk production and component traits applying uni-variate linear analysis, as well as genetic and phenotypic correlations between them using bi-variate linear analysis. Both analyses used secondary data of all grade and registered Saanen goats participating in the official Milk Recording and Performance Testing Scheme of the Animal Improvement Institute of the Agricultural Research Council of South Africa. From ANOVA, dam parity and year of birth significantly influenced ($p < 0.05$) all traits investigated, with better lactation milking performances estimated in 3rd parity groups and animals born during recent years respectively. Birth season only affected ($p < 0.05$) MY, urea and NR with animals born during spring season yielding a better lactation milking performance. Kidding season influenced ($p < 0.05$) all traits except PY and urea, with highest lactation milking performance estimated in animals kidding during spring season. All traits except FY and PY were significantly influenced ($p < 0.05$) by litter size, with multiple litter kidding groups yielding highest, while kidding age effects were not significant ($p > 0.05$) on NR, SCCI and urea. Pearson's correlation estimations showed negative associations between kidding age (r_p = -0.30, -0.004, -0.057, -0.051, -0.015, -0.265 and -0.271 for urea, MY, FY, PY, LY, NR and P respectively) except for SCCI (r_p= 0.189). From uni-variate and bi-variate linear analyses, direct heritability estimates ranged from moderate to high (h^2 = 0.42 ± 0.03, 0.38 ± 0.03, 0.39 ± 0.03, 0.22 ± 0.03, 0.40 ± 0.03, 0.38 ± 0.03, 0.28 ± 0.05 and 0.20 ± 0.03 for MY, FY, PY, LY, Urea, NR, P and SCCI respectively), with MY having highest value. Genetic correlation estimates between MY and traits such as FY, PY, urea, NR and P were all high and positive indicating favorable correlated responses (r_g =0.97, 0.94, 0.95, 0.99 and 0.74 respectively). Furthermore, phenotypic correlation estimates between MY and these traits except P (r_p = 0.33) were close to their respective genetic correlation values (r_p =0.95, 0.91, 0.92 and 0.92 for FY, PY, urea and NR respectively). Genetic correlation between MY and LY, and between MY and SCCI were not significant ($p > 0.05$), while phenotypic correlations between MY and these traits were significant ($p < 0.05$), positive and low (r_p =0.03 and 0.02 for LY and SCCI respectively). It was concluded that non-genetic factors determine to what extent the genetic potential of an animal is expressed thus, their inclusion in genetic evaluation models is crucial. Selecting for increased MY would increase herd lactation NR and improve lactation milking performance of other traits such as FY, PY and P. Selection against SCCI needs to be applied more in the population to avoid losses attributed to intra-mammary infections.

Keywords: *non-genetic effects; lactation milking performance; genetic parameters; fully pedigreed records; non-pedigreed records*

CHAPTER ONE

1.0 INTRODUCTION

1.1 Problem statement

Dairy goat production is among the fastest growing livestock industries in South Africa (DAFF, 2016). However, the production of fresh milk and by-products serves a niche market in South Africa, while most of the products are marketed through informal ways either by selling at various informal markets and directly to consumers through on-farm sales (Visser and Van Marle-Köster, 2017). The South African dairy goat industry has been described as being “small” compared to the dairy cow industry and other goat milk producing countries by several authors (Bosman *et al*., 2014; Visser and Van Marle-Köster, 2017; Grobler *et al*., 2017). Meat breeds such as the South African Boer and other indigenous goat breeds are milked for household consumption in South Africa (Casey and Van Niekerk, 1988). The reason behind this may be attributed to the fact that in the country, goats are not a significant source of milk. Therefore, as a result goat milk is categorized as a niche product in the country because it focuses on a specific section within a large industry and market (DAFF, 2016).

According to Muller (2005) goats in developing countries generally have low individual genetic potential for milk production. The low milking performance may be pertained with various factors and among those are poor nutrition, the use of genetically inferior animals for milk production in breeding programs as a result of poor selection methods that are not based on genetic predictions due to the lack of sufficient performance and pedigree data to allow estimation of genetic parameters to be conducted with ease. Because South African dairy goats were imported from countries that experience large seasonal fluctuations during daylight, dairy goat production in the country is seasonal (Muller, 2005). Although freezing of goat milk can ensure a sufficient annual supply to the markets, the overall production of goat milk in the country is not sufficient to attract large scale investments in both preserving and processing facilities as compared to the dairy cattle industry (NAMC, 2005).

It is vital for livestock breeders and keepers to have the ability to differentiate between improved herd performance attributed to the genetic make-up of animals and those that are due to non-genetic effects. Knowledge on heritability estimates of various traits of economic importance, as well as correlated responses that exist between these traits is essential in making effective herd selection decisions that will result in improved herd genetic progress where selective breeding is applied.

1.2 Background

Generally, the livestock industry plays a vital role in the agriculture sector by providing socio-economic welfare, cultural well-being and food security (Bettencourt *et al*., 2013). Although dairy goat breeds come from developed countries, goats are widely distributed globally, with about 95% found in less developed countries (Serradilla, 2001). According to DAFF (2016) Africa, Asia, Europe and America are the four main producers of goat milk with production estimates of 25.2%, 57.8%, 13.7% and 3.2% respectively towards the global goat milk production. Globally, about 80% of the goats are kept in Asia and Africa (Hirst, 2017). In the year 2013, the top three goat milk producing countries globally were India, Bangladesh, and Sudan with annual production estimates of 3.7 million tons, 1.7 million tons and 1.3 million tons respectively (DAFF, 2016).

In South Africa, there are about 4 000 registered dairy goats (SA Studbook, 2015). Saanen, Toggenburg and British Alpine breeds are the recognized dairy goat breeds in the country (NAMC, 2005). Goats are distributed throughout the country with Limpopo, Eastern Cape and KwaZulu-Natal leading as the top producers with possession estimates of 1 million, 2 million and 700 thousand respectively. According to SA Studbook (2015) there are 45 registered dairy goat herds in South Africa, constituting approximately 15 561 animals.

1.3 Justification

Goats can be managed with ease compared to cattle because they are browsers and also small in size (Berry *et al*., 2002; Richardson, 2009). Non-genetic factors affecting milk production traits and components, as well as both genetic and phenotypic relationships that exist between them have been widely investigated in dairy goat populations across the globe (Muller, 2005; Brito *et al*., 2011; Rupp *et al*., 2011; Bagnicka *et al*., 2015; Idowu *et al*., 2017; Rout *et al*., 2017). Indeed, there is sufficient evidence that milk production is not solely dependent on the genetic merit of animals. Because these factors determine whether an animal’s full genetic merit gets expressed or not. This implies that, it is in the best interests of animal breeders to know to what extent these factors influence performances of economic traits of importance for efficiency in management of herds and accuracy in genetic predictions.

Muller (2005) stated that selecting genetically superior animals as parents of the next generation can increase genetic progress in dairy herds. In many developed parts of the world, phenotypic selection programs have been set up as a support to programs that aid in the improvement of the performance of small ruminant animals (Gizaw *et al*., 2014; Mirkela *et al*., 2012). However, Mucha *et al*. (2014) found that scarcity of high-quality data is one of major paradigms in estimation of genetic parameters for dairy goats in developing countries. Accuracy in determining the genetic worth of animals is dependent on a host of factors. According to Josiane *et al*. (2020) effectiveness of phenotypic selection is dependent on how good estimation of genetic parameters for the traits in question was carried out. Furthermore, indirect selection that is based on correlation between traits can aid in improvement of phenotypic selection by using easily measurable traits with a favourable correlation as indicators to traits of economic importance that are difficult to measure.

Genetic parameter estimates for milk production traits such as lactation milk yield, fat yield and protein yields have been previously estimated for the South African dairy goat population (Muller, 2005). However, past estimates were based on a relatively small data set with incomplete pedigree profile and lactation length, while estimates were not done for other traits such as average lactation persistency and somatic cell count index. Furthermore, due to the sample size used in past estimates, there is a possibility that the genetic variability in the population was very high thus, influencing variance components. Due to changes in the environment over time (climate, management practices), there is a need to estimate genetic parameters and determine non-genetic significant effects in the South African Saanen goat population based on current records.

1.4 Objectives

The objectives of the study were to:

I. Determine non-genetic factors affecting milk production and components traits in the South African Saanen goat population using non-pedigreed lactation records.

II. Estimate phenotypic correlation between dam kidding age and milk production traits together with components in the South African Saanen goat population using non-pedigreed lactation records.
III. Estimate (co) variance components and direct heritability for milk production traits together with components in the South African Saanen goat population using fully pedigreed lactation records.
IV. Estimate both genetic and phenotypic correlations between milk production and components traits in the South African Saanen goat population using fully pedigreed lactation records.

1.5 Hypotheses

I. There are no non-genetic factors affecting milk production and components traits of the South African Saanen goat population.
II. Phenotypic correlation between dam kidding age and milk production traits together with components in the South African Saanen goat population do not exist ($r_p = 0$).
III. The degree of variation between lactation milking performance of milk production traits and components in the South African Saanen goat population, is not due to genetic variation between individuals in the population.
IV. There are no genetic ($r_g = 0$) and phenotypic ($r_p = 0$) relationships that exist between milk production and components in the South African Saanen goat population.

CHAPTER TWO

2.0. LITERATURE REVIEW

2.1. Introduction

Dairy goat milk brokers collect milk and send it to processors with the aim of manufacturing by-products such as cheese and butter (Statistics Canada, 2016). Because in South Africa dairy goat milk production is seasonal, the country has been importing goat milk in powder form as an attempt to meet the demand for goat milk when out of season (NAMC, 2005). According to DAFF (2016) between the period 2006 and 2015 South Africa imported more goat cheese compared to exportations, with an exception being between the period 2009 and 2011. Based on previous and current statistics, there may be a high demand for goat milk together with its by-products in the country. Therefore, dairy goat production can yield positive results in the country by improving both socio-economic and welfare statuses in the country, if supported.

Serradilla (2001) stated that although Europe constitutes about 2.5% of the global goat population, it contributes significantly towards the global goat milk production with a contribution estimate of approximately 20.7%. Muller (2005) further noted that dairy goat populations in developing countries generally have low milk production potential. Both these observations may have been influenced by a variety of factors, among them being that majority of dairy type breeds were developed in Europe thus, they thrive under the European environment, application of more intense selection methods that are based on genetic predictions, development of effective selection schemes that enable availability of sufficient performance data linked to pedigree while permitting genetic predictions to be conducted with ease, as well as the prominent use of biotechnology methods such as artificial insemination that also allow a widespread of superior germplasm in developed countries.

For the year 2009, FAO Statistical Databases (2016) reported a contribution of about 1.3% (696.6 tons) from goats towards the overall global milk production. Rashmi *et al*. (2013) found that about 2% of the overall annual global milk supply comes from goats. Although previous statistics demonstrate that from a global perspective, goats are not a prominent source of milk compared to cattle and other livestock species (FAO

Statistical Database, 2016; Rashmi et al., 2013) Some demonstrate that there has been an increase in the production of goat milk in recent years (DAFF, 2016).

About 63% of goats in South Africa constituted of unimproved indigenous types kept under small-holder systems (Visser and Van Marle-Köster, 2017). There are about 4 000 registered dairy type goats in South Africa (SA Studbook, 2015) that constitute of the following commercial breeds: Saanen, Toggenburg and British Alpine (NAMC, 2005). Although the 45 registered herds in the country constitute a total of 16 561 animals, only 16 herds comprising of approximately 1 217 animals participate in the official recording (SA Studbook, 2015). This indicates that there is a serious lack of participation by dairy goat farmers in official milk recording in the country. According to Hallowell *et al*. (2000) the statistics of dairy goats in the country are not a true reflection of the dairy goat industry because in the rural areas of South Africa, there are large numbers of dairy goats with no performance and pedigree information.

2.2. History and distribution of South African Saanen breed

The first South African Saanen group was imported from Switzerland, with three Saanen bucks and twelve does imported to the Graag-Reinet district by the South African Cape Agricultural Department in the year 1898 (Snyman, 2014). However, Hofmeyr *et al.* (1965) stated that nothing much resulted from the initial group that was imported from Switzerland as they all died with no progeny. The modern-day Saanen strains in South Africa are a product of one buck and a doe that were both imported from Germany in 1923 and other importations from England and Switzerland between the period 1923 and 1976 (Snyman, 2014).

Between the period 1958 and 1985, the South African Studbook and livestock improvement association registered about 530 Saanen bucks and 2 388 Saanen does, while a total of 139 does and 42 bucks were registered between the period 1985 and 1991. Sufficient records to allow genetic parameter estimates in the country only became available in the year 1985 (Muller, 2005).

2.3. Traits of economic importance in dairy goat breeding

In dairy goat breeding, the main traits of economic importance are productive, reproductive, growth and survival. Park (2007) stated that the main constituents of goat milk are fat, protein, lactose, ash and SNF with estimates of 3.8%, 3.4%, 4.1%, 0.8% and 8.9% respectively. Moreover, Iqbal *et* al. (2008) further stated that among the constituents of goat milk, water occupies almost 87%. The current study focuses on traits associated with the production of milk and components in the South African Saanen goat population. Among those studied are lactation milking performances of milk (MY), fat (FY), protein (PY), lactose (LY), urea concentration (urea), net returns (NR), persistency (P) and somatic cell count index per lactation (SCCI).

According to Jeretina *et al*. (2017) somatic cell count index (SCCI) can be defined as sum of the differences between calculated log(SCC) values that are interpolated and the standard SCC curve shape values for a given period divided by the area above the standard SCC curve shape. Furthermore, SCCI can be reliably used as a tool for detecting intra-mammary infections. Therefore, the inclusion of this trait in selection indices for this population can aid in accurately predicting lactation and daily milk yield losses that are due to increases in concentrations of body cells found in milk.

2.4. Non-genetic factors with significant effects on milk production traits in global dairy goat breeds

According to Assan (2015) various non-genetic factors affect milk production and components traits in goats. Knowledge on significance of various non-genetic factors influencing these traits can improve herd management efficiency. Moreover, these factors should be incorporated in statistical models of genetic predictions to account for non-genetic sources of variation as well as increase the accuracy of predictions. Non-genetic factors affect both the survival and productivity of animals (Idowu and Adewumi, 2017). Subsequently, they also influence enterprise net returns. Various significant non-genetic effects on milk production and components traits have been widely reported in literature by several authors in the past. Parity, litter size, dam kidding age and year-season effects are among those that have been reported previously (Rabasco *et al*., 1993; Torres-Vázquez *et al*., 2009; Brito *et al*., 2011; Assan, 2015). From past investigations, it is evident that these factors indeed influence the production of various traits of economic importance to certain extents. Results and observations previously reported on the significance of various non-genetic factors affecting milk production and components traits in global dairy goat populations and other livestock species are discussed further below.

2.4.1. Parity

According to Ishag *et al*. (2012) milk production tends to increase with advancement in lactation order because parity and age are closely related. This is probably due to the fact that older animals are large in size and tend to have a more prominent udder compared to the young ones. The effects of parity on SCC depends on the udder health status (Jimenez-Granado *et al*., 2014). Older animals have higher number of lactations compared to young dams and therefore, they have more experience and larger teat canals. Assan (2015) found that older animals are more vulnerable to pathogens accumulated from lying on surfaces because the production and storage of milk in the mammary gland increases with advances in lactation order rather than being reduced. Thus, the size of functional tissues responsible for the secretion of milk also increase.

Using South African Saanen goat lactation records from 1st to 8th parity, Muller (2005) observed a maintenance of high lactation yields of milk, fat and protein from 1st to 5th lactation; thereafter, followed by a decline in yields from 6th parity onwards. These observations may be attributed to only few dams having reached beyond 5th parity in the data used for analysis, probably as a result of culling of dams beyond this parity in most herds. Moreover, highest lactation milking performances for milk, fat and lactose yields were estimated to occur in 3rd parity animals (945kg, 29kg and 41.5 for milk, fat and lactose respectively), while 5th lactation groups gave the highest protein yield (25.8kg). According to Park and Haenlein (2010) milk from young does has more fat compared to that of older dams. For fat percentage, Šlyžius *et al.* (2017) found highest estimates in 4th lactation animals for the Croatian Czech White Shorthaired population (5.07%), the highest percentage in Croatian Saanen population was estimated in 6th parity groups (4.1%). For the South African Toggenburg population, Muller (2005) estimated highest lactation milk yield in 4th lactation dams (970kg), while the least lactation milk yield was reported in 1st parity animals (586kg).

For a Bangladesh Black Bengal population, Mia *et al.* (2014) found the least daily milk yield in 1st parity groups (305.2 ± 30.91g). Zahraddeen *et al*. (2007) detected the least milk fat content in 1st lactation groups of indigenous goats (4.39 ± 0.02%), with 3rd parity animals yielding the highest content (5.54 ± 0.03%). Glauber (2007) found significant effects of parity on lactation persistency, with first calving cows having highest persistency. In a study on an Egyptian Damascus goat population, Ayasrah *et* *al*. (2013) reported significant effects of parity on persistency, with a higher persistency determined in animals with fewer lactations compare compared to those with more lactation experience. These observations were probably influenced by the lactation curve of first parity animals being flat and thus, resulting in a greater persistency (Glauber, 2007; Ayasrah *et al*., 2013). Contrary to the previously mentioned findings, Ruvuna *et al*. (1995) estimated high persistency values in older animals; in a study on crosses between Galla and Toggenburg, and East African and Anglo Nubian goat populations. Using evening milk tests in Saanen population, Pala and Savaş (2005) found increases in milk yield up to the 4th parity, while highest persistency was reported in 2nd parity groups.

In a Girgentana goat population, Giaccone *et al*. (2007) found significant effects of parity on urea concentration, with highest level of urea concentration detected in 2nd parity groups (45.03 ± 0.33mg/dl), followed by groups beyond 3rd lactation (44.43 ± 0.33mg/dl), while the least urea concentration yield was reported in 1st parity animals (41.09 ± 0.52mg/dl). Simčič *et al*. (2018) estimated the least SCC in 1st lactation groups (8.59 ± 0.07ml^{-1}), while highest yield was detected in 6th parity dams (9.64 ± 0.07ml^{-1}*)* for Saanen and Alpine goat populations*.* Poonia *et al*. (2018) found increases in levels of SCC as parity advanced (5.774 ± 0.193cells/ml, 5.895 ± 0.119cells/ml and 5.972 ± 0.109cells/ml for 1st, 2nd and 3rd lactation groups respectively). In Slovakian dairy sheep breeds, Oravcová *et al*. (2018) reported increases in SCC levels with advancement in the level of parity (5.04 ± 0.04ml^{-1}, 5.11 ± 0.04ml^{-1} and 5.38 ± 0.04ml^{-1} for 1st, 2nd and 3rd lactation dams respectively). The past reports suggest that goat milk may have higher levels of SCC compared to sheep milk.

2.4.2. Litter size

According to Rabasco *et al*. (1993) about 11% of the differences in milk yield is attributed to variations in litter size, with multiple kidding dams producing more milk compared to single litter kidding groups. The reason behind this may be due to the fact that during gestation, the mammary gland development gets affected by litter size and therefore, the udder size and hormonal activities also increase leading to increased milk production (Gall, 1981; Mourad, 1992). Studies have been conducted in the past to determine effects of litter size on milk production in various dairy goat populations. Although the majority have reported significant effects of litter size, with milk production reported to increase as litter size advances (Browning *et al*., 1995; Akpa *et al*., 2002; Mia *et al*., 2014; Ibnelbachyr *et al*., 2015). However, some studies have reported non-significant effects of kidding prolificacy on milk yield (Williams, 1993; Giaccone *et al*., 2007; Fatal, 2008; Bagnicka *et al*., 2016).

For a Polish dairy goat population, Bagnicka *et al*., (2016) found non-significant effects of litter size on lactose content, with highest value detected in single litter kidding groups (4.57%), while least content was estimated in multiple litter kidding dams (4.49%). In a study on Italian Girgentana goat population, Giaccone *et al*., (2007) reported non-significant effects of litter size on urea concentration. The highest levels were estimated in single litter kidding animals, while groups kidding twins yielded the least concentrations (43.57mg/dl and 43.47mg/dl for does that kidded singles and twins respectively). Mia *et* al. (2014) reported significant effects of litter size on daily milk yield for a Bangladesh Black Bengal goat population. Furthermore, increases in daily milk yield as prolificacy advanced were reported (457.4g/day vs 303.4g/day for groups that kidded twins and singles respectively). In Draa goat population, Ibnelbachyr *et al*. (2015) reported significant effects of parity with highest total milk yield observed in multiple litter kidding groups (80.0kg), while least yields were reported in single litter kidding animals (71.9kg).

Browning *et al*. (1995) reported significant effects of litter size on lactation milk yield, with highest yields reported in dams with multiple prolificacy (775kg, 834kg and 903kg for animals that kidded singles, twins and triplets respectively). In a Polish dairy goat population, Bagnicka *et al*. (2015) found significant effects of kidding prolificacy on lactation milk yield, with highest yields (623.3kg vs 569.6kg), fat yield (21.74kg vs 20.39kg) and protein yield (18.33kg vs 16.95 kg) estimated in multiple litter kidding groups compared to single litter kidding groups. Akpa *et al*. (2002) estimated increases in total milk yield of indigenous goats as litter size increased (106.9kg and 74.4kg for dams that kidded triplets and singles respectively).

Rojo-Rubio *et al*. (2016) detected a higher persistency value in single litter kidding Mexican dairy goats while, a lower value was reported in groups that kidded twins. In a Sihori goat population, Poonia *et al*. (2018) reported significant effects of litter size on SCC, with milk from single prolificacy groups having least levels (5.885 ± 0.135cells/ml), while highest levels were reported in multiple litter kidding groups (5.915 ± 0.155cells/ml). Increases in milk production and SCC levels that are due to increased litter size are probably due to the fact that during gestation the udder volume of animals carrying multiples increases and thus the capacity for milk production and number of body cells found in milk also increase.

2.3.3. Year-season

Studies have been previously carried out to investigate the significance of both year and season on milk production parameters in dairy goat populations (Muller, 2005; Mioč *et al.,* 2008; Ishag *et a*l., 2012). Indeed, year-season effects influence the production of milk together with components. Furthermore, the interaction between the animal's genotype with the environment performance was measured influence these effects. According to Gall (1981) the production of milk and milk components can be influenced by kidding season of the dam. Lu (1989) found that dairy goats are susceptible to heat stress, while Mourad (1992) noted that weather conditions that are extremely cold may result in reduced milk production. Muller (2005) stated that almost 82% of animals in the South African dairy goat kid during Spring season (between August and September). This suggest that dairy goat production in the country is seasonal. Therefore, knowledge on the ideal breeding season to achieve optimal lactation milking performance of various economic traits of importance is essential.

In a Saanen goat population raised under Sudan semi-arid conditions, Ishag *et al*. (2012) found significant effects of year-season of kidding, with highest milking performances for total and daily milk yields both observed in groups kidding during the winter season (377.47kg and 1.68kg for total and daily milk yields respectively). Ibnelbachyr *et al*. (2015) estimated highest and least total milk yield in Draa goats kidding during spring and autumn seasons to be 80.4kg and 68.5kg respectively. Furthermore, dams kidding during summer season gave highest vlaues for both fat and lactose (5.46% and 6.17%), while highest protein content was estimated in groups kidding during autumn (4.81%). In Croatian Alpine and Saanen goat populations, Mioč *et al*. (2008) found a better milking performance in groups kidding during winter season (December to February) compared to animals kidding during spring season (March to May).

For an Ethiopian Begait goat population Abraham *et al*. (2018) reported significant effects of kidding season on lactation milk yield, with dams kidding during wet and dry seasons reported to yield highest and least respectively (77.1kg and 59kg respectively). The reason behind this observation was probably a result availability of quality fodder during wet season. Therefore, as a result also enhancing milk production. Ciappesoni *et al*. (2004) estimated better daily milking performance in groups kidding during the autumn season (2.733kg/day), while animals kidding between winter and early summer (May to November) gave highest fat and protein percentages (3.89% and 2.93% respectively). Furthermore, groups kidding during spring season had the least daily milking performance (2.668kg/day, 3.70% and 2.87% for daily milk yield, fat and protein percentages respectively).

In Cuban Anglo Nubia and Criolla crosses, Pesántez *et al*. (2014) estimated highest lactation persistency value in groups kidding during the rainy season (79%), while dry kidding season gave the least persistency value (72.1%). For a Kenyan Alpine goat population, Marete *et al*. (2014) also observed highest lactation persistency values in dams kidding during the rainy season. Availability of quality fodder as a result of increased rainfall during the rainy season may have influenced past observations. Sandrucci *et al*. (2018) found highest levels of SCC (5.93SCC/ml) in Italian dairy goats kidding between late autumn and winter seasons (November-February), while lower levels of SCC (5.665.93SCC/ml) were reported in groups kidding during late summer season (August).

According to Brown (1955) for optimal milking performance, the ideal season for breeding goats more especially in southern hemisphere countries is between March and April to allow them to kid during spring and early summer because the average gestation period in goat production is 150 days. Variations in estimates and observations between past studies are probably due to various genotype responses to different environments.

2.4.4. Dam age

According to Capuco *et al*. (2001) and Carnicella *et al*. (2008) the production of milk increases as dam age advances. As dam age increases factors associated with the production of milk also increase. Among the factors are hormonal levels, intake of nutrients, udder size, secretory cells and metabolic activity. The most ideal age at first breeding for young does is usually between 7 and 8 months. However, age at first breeding is dependent on a variety of animal factors such as breed, health and weight. Muller (2005) found that in South African dairy goat population, both age at first kidding and age at last kidding are largely influenced by management and environmental factors such as breeding season.

Mburu *et al*. (2014) found significant effects of dam age on milk yield in a Kenyan Alpine goat population. Recording commenced at 2 years, while a better milking performance was observed at the age of 6 years (4.2 litres/day). In crosses between Norwegian and Small East African goats, Ketto *et al*. (2014) found monthly milk yield performance to be highly affected by dam age, with a better performance observed for groups between 26 and 28 months of age (41.7 litres/month).

2.5. Estimation of genetic parameters for production traits and components in dairy goats

For desired herd genetic improvements, genetic characterization in selection programs for traits of economic importance is essential (Rout *et al*., 2017). This means that setting up a proper and effective breeding program is essential for genetic progress in any herd. However, this task requires animal breeders to have sound knowledge on variance components estimates for various economic traits of importance in selection indices. Furthermore, having knowledge of both direct and correlated responses amongst traits included in selection indices is just equally important. According to Visser and van Marle-Köster (2017) genetic improvement of goats has been much slower compared to sheep and other livestock species in South Africa. This may be attributed to the lack of sufficient high-quality performance data linked to the pedigree to warrant accurate genetic predictions.

The lack of data may be due to limited participation by dairy goat farmers in livestock improvement schemes. Unlike in dairy cattle, past genetic parameter estimates for production traits in dairy goat production have been focused heavily on particularly yields for milk (Rout *et al*., 2017; Pizarro-Inostroza *et al*., 2020), fat (Muller, 2005*;* Brito *et al*.,2011), protein (Torres-Vázquez., *et al*., 2009; Solis-Ramirez, 2014), lactose (Morris *et al*., 2011; Bagnicka *et al*., 2016) and somatic cell count/score (Morris *et al*., 2011; Scholtens *et al*., 2018). Currently, no information exists on genetic parameter estimates for lactation persistency, urea, milk net returns and somatic cell count index for the South African Saanen population. Thus, the present study is the first of its kind to estimate genetic parameters for the mentioned traits. Summary of literature values on genetic parameter estimates for various milk production traits in global dairy goat populations is presented in Tables 2.1 and 2.2.

2.5.1. Accuracy of genetic parameter estimations

Muller (2005) stated that it is important to note that genetic parameters are fixed for a certain population. In any breeding program, background on both genetic and environmental sources of variation for traits under selection is vital (Maxa *et al*., 2007). According to Van Vleck (1968) and Hofer (2011), it is necessary to apply the correct model of analysis in genetic parameter estimates. Using correct models of analyses in estimation of genetic parameters for traits of economic importance is essential in obtaining more accurate genetic values through unbiased genetic prediction, predicting both correlated and direct selection responses, as well as developing economic multi-trait selection indices.

According to Thompson (2008) for unbiased genetic predictions, multi-trait animal models are preferred over single-trait animal models. Gilmour *et al*. (2009) found that various possible models could be developed by including direct additive together with maternal additive genetic effects, either with or without a co-variance among them, and maternal permanent environmental effects in various combinations. Genetic progress can be achieved through efficient selection. However, selection efficiency is dependent on a variety of factors. Among those are the number of animals being evaluated, number of traits included in selection indices, as well as the accuracy of evaluation. Mucha *et al*. (2014) stated that one of the major paradigms in genetic evaluations of dairy goat flocks in less developed and developing parts of the world is the lack of sufficient high-quality performance and pedigree data.

2.5.2. Genetic parameters for milk component traits

Genetic correlation, heritability and repeatability are the most significant genetic parameters in animal breeding (Hussain *et al*., 2013). For the purpose of this study, variance components and direct heritability values were computed for various milk production and components traits, while genetic and phenotypic correlations between these traits were also estimated. There is limited information on genetic parameter estimates for SCC and lactose content in goat populations (Bagnicka *et al*., 2016). Subsequently, the present study is the first of its kind to do so for the South African Saanen goat population. A summaryummary of published literature values on genetic parameter estimates for various economic traits of importance in dairy goat populations, obtained using various procedures is presented in Tables 2.1 and 2.2.

2.5.2.1. Heritability

According to Visscher *et* al. (2008) heritability can be defined as the ratio of variances due to the difference in the additive genetic effects, particularly the portion of the total variance in a population for a particular trait, measured at a particular age or time. To reduce biasness and increase selection efficiency, when estimating variance components and heritability values, maternal additive genetic effects should be incorporated in statistical models of predictions where they have significant effects (Nasholm and Danell, 1996). To achieve optimal genetic progress through selection, there is a need for accuracy and reliability in results from genetic predictions which selection is based upon. A summary of values recorded in literature on variance components and heritability estimates obtained using various methods is presented in Table 2.1.

2.5.2.2. Correlation

Correlation coefficients measure the strength (consistency, reliability) of the linear relationship between two variables and are described based on the strength, direction, shape and statistical significance (Moore *et al.,* 2013). Phenotypic correlation measures the relationship among records of two traits measured on the same animal, while genetic correlation estimates measure the association between an animal's genetic values for two traits also measured on the same animal, environmental correlation occurs when two traits are influenced by the same random effects (Searle, 1961). Lynch and Walsh (1998) stated that when the genetic correlation between two traits is high, the gene effects of both genes are usually co-inherited. According to Visscher *et al*. (2014) the sampling variance of estimated genetic correlation is highly dependent on sampling variance of estimated heritability. This implies that for accurate estimation of genetic correlations a large sample size is required. Table 2.2 shows a summary of values reported in literature on genetic, phenotypic and environmental correlations in various dairy goat breeds.

2.5.2.3. Repeatability

According to Biro and Stamps (2015) repeatability measures the extent to which variations in individual animal performances for a particular trait are maintained over time. A repeatability model is arguably the simplest method for analysing repeated measured data (Nemutandani, 2017). Olivier (2014) stated that repeatability model analysis renders variances of repeated records equal. In concurrence with the previous statement, Jennrick and Schluchter (1986) also found that repeatability models assume that the performances of the same animal measured for a single trait at different ages have a uniform variance and correlation among them. However, according to Meyer and Hill (1997) such assumptions are not applicable in cases where the variance changes depending on the amount of time elapsed between measurements.

Table 2.1. Summary of values recorded in literature on (co) variance components and heritability estimates of milk production traits and components in dairy goat populations across the globe

Breed (Country)	**h^2**	**σ^2_a**	**σ^2_c**	**σ^2_e**	**σ^2_p**	**Reference**
			Milk yield			
Saanen (South Africa)	0.21	7580.22	7353.36	21491.30	36424.88	Muller, 2005
Jamunapari (India)	0.25	35325.8	61547.6	24724.5	140000	Rout *et al*., 2017
Saanen & Alpine (Brasil)	0.19	6.458	-	-	6.23	Brito *et al*., 2011
Saanen (Mexico)	0.17	6895	10.55	23.38	40.83	Torres-Vázquez *et al*., 2009
Polish dairy goats	0.21	-	-	-	-	Bagnicka *et al*., 2015
New Zealand dairy goats	0.21	9413.27	-	-	45247.92	Solis-ramirez, 2014
Murciano-Granadina (Spain)	0.46	0.75450	0.140011	0.74180	1.63632	Pizarro-Inostroza *et al*., 2020
			Fat yield			
Saanen (South Africa)	0.19	8.0429	6.9782	26.8517	41.8728	Muller, 2005
Saanen & Alpine (Brasil)	0.10	4.638	-	-	4.558	Brito *et al*., 2011
Saanen (Mexico)	0.19	8.51	10.14	25.74	44.39	Torres-Vázquez *et al*., 2009
Polish dairy goats	0.18	-	-	-	-	Bagnicka *et al*., 2015
New Zealand dairy goats	0.21	11.93	-	-	56.73	Solis-ramirez, 2014
			Protein yield			
Saanen (South Africa)	0.20	5.4912	5.3670	16.2562	27.2562	Muller, 2005
Saanen & Alpine (Brasil)	0.12	4.228	-	-	4.085	Brito *et al*., 2011
Saanen (Mexico)	0.17	4.66	6.79	15.72	27.17	Torres-Vázquez *et al*., 2009

Polish dairy goats	0.19	-	-	-	-	Bagnicka *et al*., 2015
New Zealand dairy goats	0.21	7.69	-	-	37.46	Solis-ramirez, 2014
			Lactose yield			
Saanen & Alpine (Brasil)	0.15	9.815	-	-	7.959	Brito *et al*., 2011
Polish dairy goats	0.27	-	-	-	-	Bagnicka *et al*., 2016
Saanen (New Zealand)	0.35		-	-	-	Morris *et al*., 2011
Murciano-Granadina (Spain)	0.30	0.03361	0.0213750	0.05699	0.11198	Pizarro-Inostroza *et al*., 2020
			Persistency			
Murciano-Granadina (Spain)	0.08	0.005	0.001	0.056	0.062	Miranda *et al*., 2019
Saanen & Alpine (Brasil)	0.04	-	-	-	-	Siqueira *et al*., 2017
			Somatic cell count /score			
Saanen (New Zealand	0.20	-	-	-	-	Morris *et al*., 2011
Polish dairy goats	0.21	-	-	-		Bagnicka *et al*., 2016
New Zealand dairy goats	0.22	0.31	-	-	1.44	Solis-Ramirez, 2014
New Zealand mixed breed dairy goats	0.21	0.32	0.42	0.79	-	Scholtens *et al*., 2018

h^2 = direct heritability; σ^2_a = additive variance; σ^2_c = permanent environment variance; σ^2_e = uncontrollable/error variance; σ^2_p = phenotypic variance; - = component not estimated

Table 2.2. Summary of values on genetic correlation (r_g), phenotypic correlation (r_p) and environmental correlation (r_e) between milk production traits and components recorded in literature on various dairy goat breeds

Trait	**Breed**	r_g	r_p	r_e	**Reference**
MY ×					
FY	Saanen	0.75	0.80	0.78	Muller, 2005
	Saanen	0.72	0.85	0.90	Torres-Vázquez *et al*., 2009
	Saanen & Alpine	0.86	-	-	Brito *et al*., 2011
PY	Saanen	0.92	0.95	0.93	Muller, 2005
	Polish dairy goats	0.86	0.96	-	Bagnicka *et al*., 2015
	Saanen	0.87	0.95	0.97	Torres-Vázquez *et al*., 2009
LY	Saanen & Alpine	0.98	-	-	Brito *et al*., 2011
	Murciano-Granadina	-0.07	0.12	-	Pizarro-Inostroza *et al*., 2020
	Polish dairy goats	-0.46	-	-	Bagnicka *et al*., 2016
Urea	Saanen	-0.18	-	-	Čobanovič *et al*., 2019
P	Murciano-Granadina	-0.05	0.007	-	Miranda *et al*., 2019
	Saanen & Alpine	0.39	-	-	Siqueira *et al*., 2017
SCC/SCS	Polish dairy goats	0.31	-	-	Bagnicka *et al*., 2016
	New Zealand mixed breed dairy goats	-0.02	-0.10	-	Scholtens *et al*., 2018
	Saudi dairy goats	-0.32	-0.37	-	Amin *et al*., 2017
FY ×					
PY	Saanen	0.86	0.80	0.81	Muller, 2005
	Saanen & Alpine	0.93	-	-	Brito *et al*., 2011
	New Zealand mixed breed dairy goats	0.93	0.93	-	Scholtens *et al*., 2018
LY	Saanen & Alpine	0.88	-	-	Brito *et al*., 2011
	Polish dairy goats	0.62	-	-	Bagnicka *et al*., 2016
Urea	Saanen & Alpine	0.34	-	-	Čobanovič *et al*., 2019
SCC/SCS	Saanen	-0.12	0.25	-	Morris *et al*., 2011

PY×					
LY	Murciano-Granadina	-0.20	-0.29	-	Pizarro-Inostroza *et al*., 2020
SCC/SCS	New Zealand mixed breed dairy goats	-0.04	-0.08	-	Scholtens *et al*., 2018
LY ×					
SCC/SCS	Murciano-Granadina	-0.22	-0.38	-	Pizarro-Inostroza *et al*., 2020
	Polish dairy goats	-0.14	-	-	Bagnicka *et al*., 2016

r_g = genetic correlation; r_p = phenotypic correlation; r_e = environmental correlation; - = correlation not estimated; MY = milk yield; FY = fat yield; PY = protein yield; LY = lactose yield; Urea = urea concentration yield; SCC = somatic cell count; SCS = somatic cell score

CHAPTER 3

3.0. RESEARCH METHODOLOGY AND ANALYTICAL PROCEDURES

3.1. Introduction

The aim of the study was to test significance of non-genetic factors on lactation milking performance of various milk production traits and components, as well as to estimate genetic parameters of these traits. These were performed using non-pedigreed and fully pedigreed lactation records of all grades and registered Saanen goats participating in the official Milk Recording and Performance Testing Scheme of the Animal Improvement Institute of the Agricultural Research Council of South Africa. Analysis of variance (ANOVA) was carried out using non-pedigreed lactation records to test for non-genetic significant effects, while fully pedigreed lactation records were analysed to estimate (co) variance components and direct heritability values of milk various production and component traits through uni-variate linear analysis, as well as genetic and phenotypic correlations between them using bi-variate linear analysis.

3.2. Study site

The study used secondary data on lactation milking performance of registered Saanen goats across South Africa, which is the southernmost country in Africa. The seasons in the country are as follows: Summer (November - January), Autumn (February - April), Winter (May - July) and Spring (September - October). In Summer, most parts of the country are characterized by hot weather during the day and experience thunderstorms in the afternoon. The average annual rainfall for South Africa is about 464 mm but large and unpredictable variations are common. The land of South Africa covers an area of 1 221 040 square kilometers.

3.3. Experimental units

All grade and registered Saanen goats participating in the official Milk Recording and Performance Testing Scheme of the Animal Improvement Institute of the Agricultural Research Council of South Africa kidding between 1955 and 2018 were used in this study.

3.4. Animal management

Records on animals, that were raised under conventional dairy goats' management principles for farming system, housing, feeding and vaccination as suggested by SA MILCH breeders' society and Studbook were used.

3.5. Data collection

SA studbook together with MILCH breeders' society availed a total of 31 295 lactation performance records and 29 807 pedigree records from the LOGIX national database. Both data sets were of Saanen goats participating in the official Milk Recording and Performance Testing Scheme of the Animal Improvement Institute of the Agricultural Research Council of South Africa kidding from 1955 to 2018. Repeated lactation performance data on milk yield (MY), fat yield (FY), protein yield (PY), lactose yield (LY), urea concentration (urea), net returns (NR), persistency (P) and somatic cell count index (SCCI) were of interest for the purpose of this study. Data on fixed factors in the study included dam parity, litter size, kidding season, two factor interaction between dam year and season of birth. Dam kidding age was the only random factor included in analysis. Pedigree data used included identities of animal, sire and dam. Average lactation milking performances of all traits were determined using international standard procedures as suggested by the International Committee for Animal Recording (ICAR).

3.6. Statistical analyses

3.6.1. Analysis of variance for non-genetic significant effects

3.6.1.1. Data editing

Data edits included checks for lactation length and milk yield using data of animals kidding between 1955 and 2018 (63 years). Almost 15 518 (49.6%) of animals in the original performance file had incomplete lactation length and no information on lactation milk yield. These animals were subsequently discarded from the data file subjected to analysis of variance (ANOVA) for significant effects.

3.6.1.2. Data analysis

A total of 16 407 non-pedigreed lactation performance records were analysed to test if there are any significant effects of dam parity, litter size, season of kidding, season of birth and year of birth on lactation milking performances of milk yield (MY), fat yield

(FY), protein yield (PY) lactose yield (LY), urea concentration (urea), net returns (NR), persistency (P) and somatic cell count index (SCCI). Fixed factors and their respective levels are shown on Table 3.1. Analysis of variance (ANOVA) was carried out using Minitab software (Version 18 of 2017) while multiple comparisons between groups were done using Fisher's least significant difference (LSD) method at 95% confidence. Pearson's correlation coefficients were calculated for milk production traits and components, where dam kidding age was used as a co-variate. The employed mixed model was (in matrix notation):

$Y_{ijk} = \mu + xb_{i+} za_{j} + e_{ijk.}$

Where:

Y = the response measured: MY, FY, PY, LY, SCCI, urea, NR and P.

μ = Overall mean.

xb_{I} = Vector for random factors: Dam kidding age (9 - 150 months).

za_{j} = Vector for fixed factors: Parity, litter size, dam birth season, dam kidding season and dam birth year.

e_{ijk} = Random residual error associated with individual animal.

Table 3.1 Fixed factors and their respective levels

Factor	Levels
Parity	1, 2, 3, 4, 5, 6 and ≥7
Litter size	1 (single), 2 (twins) and 3 (triplets)
Kidding season	Summer (Nov - Jan), Autumn (Feb - Apr), Winter (May - Jul) and Spring (Aug - Oct)
Doe birth season	Summer (Nov - Jan), Autumn (Feb - Apr), Winter (May - Jul) and Spring (Aug - Oct)
Birth year	1955 - 2016

3.6.2. Estimation of genetic parameters and variance components

3.6.2.1. Data editing

SAS (2013) software version 9.4 was used to trim and merge both data files by animal identity. The resulting data file from editing contained 2 960 fully pedigreed lactation records that were subjected to analysis.

For animal records to be included in analyses they had to comply with the following criteria:

a) 305d milk yield > 0
b) have litter size range between 1 and 3
c) have parity range between 1 and ≥7
d) kidding age range between 9 and 132 months
e) record on birth date
f) and ancestry data on both sire and dam.

3.6.2.2. Data analysis

3.6.2.2.1. Fixed effects

Fixed factors subjected to analysis for significance included the two-way interaction between dam year-season of birth, kidding season, litter size and parity. While dam kidding age was included as a covariate. ASReml software package version 4.1 developed by Gilmour *et al*. (2018) was used to determine the significance of fixed factors on various milk production traits and components.

The model below was applied for all traits investigated (in matrix):

$Y_{i\,j\,k} = \mu + Xb_{i} + Za_{j} + A_{g} + e_{i\,j\,k}.$

Where:

Y = the response measured: MY, FY, PY, LY, SCCI, urea, NR and P.

μ = Overall mean.

xb_l = Vector for random factors: Dam kidding age (9 - 132 months).

za_j = Vector for fixed factors: Parity, litter size, kidding season and birth year-season.

A_g = Direct additive genetic effects (Sire and dam).

e_{ijk} = Random residual error associated with individual animal.

3.6.6.2.2. Univariate and bi-variate linear models

Both uni-variate and bi-variate linear models were fitted under reduced maximum likelihood (REML) using ASReml software package version 4.1 developed by Gilmour *et al*. (2018). Direct and maternal additive genetic effects, either without or with a co-variance among them together with maternal permanent environmental effects were tested for all traits investigated in six various combinations. The resulting models were (in matrix):

$Y = Xb + Z_1a + e$ (1)

$Y = Xb + Z_1a + Z_2mpe + e$ (2)

$Y = Xb + Z_1a + Z_2mpe + e$; with $cov(a,m) = 0$ (3)

$Y = Xb + Z_1a + Z_2mpe + e$; with $cov(a,m) = A\sigma_{am}$ (4)

$Y = Xb + Z_1a + Z_2mpe + Z_3mpe + e$; with $cov(a,m) = 0$ (5)

$Y = Xb + Z_1a + Z_2mpe + Z_3mpe + e$; with $cov(a,m) = A\sigma_{am}$ (6)

Where:

Y was performance of the animal for the trait measured; X, Z_1, Z_2 and Z_3 respectively represented incidence matrices of relating fixed effects, direct animal additive genetic effects, maternal additive genetic effects and maternal permanent environmental effects on the phenotype of the animal; e was the random residual error associated with individual animal; b was vector for fixed effects; a represented the direct animal additive genetic effects; while doe additive genetic effects were represented by m; maternal permanent environmental effects were represented by mpe; A represented numerator relationship matrices, while σ_{am} was the covariance between direct animal additive genetic and maternal additive genetic effects. All components were derived at convergence.

It was assumed that: $V(a) = A\sigma^2_a$; $V(m) = A\sigma^2_m$; $V(mpe) = I\sigma^2_{mpe}$; $V(e) = I\sigma^2_e$, where I represented the identity matrix; while direct animal additive genetic variance, maternal additive genetic variance, doe permanent environmental effects and environmental variance were respectively represented by σ^2_a, σ^2_m, σ^2_{mpe}, σ^2_e . The sum of all variances was the phenotypic variance (σ^2_p). Log likelihood ratios were tested for determination of the most suitable model for each trait investigated in uni-variate analysis. The model with highest likelihood was considered the most suitable, with assumptions that the number of random effects is the same and fixed effects models are identical. Non- genetic factors were considered to significantly influence various milk production and component traits, given that their inclusion in the models significantly increased Log likelihood ratios. Moreover, a significance level of $p \leq 0.05$ was applied for all factors in the present study. Subsequently, the most suitable model as determined from uni-variate analyses was fitted for in bi-variate analyses. Bi-variate analyses allowed relevant estimations of (co) variance components and both direct and maternal permanent environmental correlations.

CHAPTER 4

4.0. NON-GENETIC FACTORS AFFECTING MILK PRODUCTION AND COMPONENTS TRAITS IN THE SOUTH AFRICAN SAANEN GOAT POPULATION

4.1. Introduction

The primary role of animal breeding in dairy goat production is to improve traits that are associated with milk production. According to Muller (2005) both yield and composition of milk production parameters in dairy animals depends on a variety of factors. These factors are dependent on differences in the environment animals are subjected to, as well as the genotype between animals. This implies that phenotypic expression of an animal for traits of economic importance is influenced by the interaction between the animal's genotype and the in which environment performance was measured. Subsequently, the previous statement highlights that non-genetic effects dictate whether the genetic potential of an animal gets attained or not. Idowu and Adewumi (2017) reported that various non-genetic factors influence both the productivity and survival of animals. Furthermore, these factors can be partitioned into management (kidding age and nutrition), animal (parity and age) and environmental factors (photoperiod and temperature). The mentioned factors may also be either fixed (parity and breed) or random (milking frequency and kidding age) in nature.

In South Africa, commercial production of dairy goats is seasonal because South African dairy goats were developed in countries with large seasonal fluctuations in daylight (NAMC, 2005). This further entail that for optimal lactation milking performance, planned breeding should be used. The modern day South African dairy goat population originated primarily from Switzerland and the United Kingdom (Visser and van Marle-Köster, 2017). Although dairy goats are not native to South Africa, they should thrive under local conditions given that some parts of the country experience similar climatic conditions like countries they were imported from (Muller, 2005). However, with constant changing environmental conditions due to global warming, animals are forced to adapt for survivability and productivity. This study was aimed at estimating phenotypic correlations between dam kidding age and milk production traits, as well as investigating the significance of dam parity, litter size, season of kidding, age, year and season of birth on lactation milking performances of these traits in the South African Saanen goat population using non-pedigreed lactation records.

4.2. Rationale

It is important for livestock breeders to be able to differentiate between improved herd performances that are attributed to the genetic make-up of animals and non-genetic effects. Non-genetic significant sources of variation on milk production traits together with components should be investigated because when estimating genetic parameters for milk performance of both sires and dams, their effects should be accounted for in statistical models of genetic evaluations. Non-genetic effects on milk production traits including components have been widely reported in various South African livestock populations including South African dairy goat population (Muller, 2005), cattle (Glauber, 2007) and Polish dairy goats (Bagnicka *et al*., 2015). There is indeed sufficient evidence that they do influence phenotype of animals.

Because non-genetic factors can influence phenotypic performance of various traits of economic importance in animals. Amongst these factors are improved use of biotechnology applications and techniques that allow easy access to superior germplasm, improved recording and inclusion of other traits in selection schemes, changes in climate, increase in population size and improved management practices attributed to advances in research practices. It is important to investigate the significance of these factors on the phenotype of animals in this population. The current study is the first of this kind to determine the significance of dam birth season and year, as well as kidding age on lactation milking performances of these traits in this population.

4.3. Objectives

The objectives were to:

I. Determine significance of dam parity, litter size, kidding season, birth season, birth year and kidding age on lactation milking performances of milk yield, fat yield, protein yield, lactose yield, urea concentration, persistency, net returns and somatic cell count index in the South African Saanen goat population using non-pedigreed lactation records.
II. Estimate phenotypic correlation between dam kidding age and milk production traits together with components in the South African Saanen goat population using non-pedigreed lactation records.

4.4. Hypotheses

I. Dam parity, litter size, kidding season, birth season, birth year and kidding age do not influence lactation milking performances for milk yield, fat yield, protein yield, lactose yield, urea concentration, persistency, net returns and somatic cell count index in the South African Saanen goat population.

II. Phenotypic correlation between dam kidding age and milk production traits as well as components do not exist ($r_p = 0$) in the South African Saanen goat population.

4.5. Results and Discussion

4.5.1. Parity effects

Table 4.1 depict average lactation milking performances (305d) of MY, FY, PY and LY, their respective standard errors and mean separations across various parity levels. The results from ANOVA for significance revealed highly significant ($p < 0.01$) effects on average lactation performances of all mentioned traits as shown in Appendices 7.1 to 7.4. Average lactation milking performance of FY was statistically the same ($p > 0.05$) between groups in their 1st, 4th and 5th lactations. While average lactation yields from dams in 2nd and 3rd parities were also not significantly different. Average lactation PY was not significantly different ($p > 0.05$) between dams in their 1st and 4th lactations, as well as between those in 2nd and 3rd parities. Average LY lactation yield between 2nd and 3rd lactations was statistically the same ($p < 0.05$), while yields between dams ins 1st, 4th and 5th parities were also not significantly different.

Average lactation milking performances of MY, FY, PY and LY all follow a similar trend, with dams maintaining high yields from 1st to 5th lactation. Third parity animals gave highest lactation yields of MY, FY, PY and LY (1073.40 ± 40Kg, 40.57 ± 1.61kg, 31.30 ± 1.35kg and 46.73 ± 1.86kg respectively), while least lactation yields for these traits were all estimated in ≥7th lactation animals (775.40 ± 56.60Kg, 29.47 ± 2.28kg, 20.64 ± 1.96kg and 32.99 ± 2.89kg for MY, FY, PY and LY respectively). The current results compared well with findings of other studies previously reported in literature. Similar production patterns were reported by Muller (2005) who observed a maintenance of high lactation yields of MY, FY, PY and LY from 1st to 5th parity in the South African dairy goat population. Furthermore, highest lactation milking performances of MY, FY and LY for the Saanen population were also estimated in 3rd parity animals (945kg, 29kg and 41.5kg respectively).

In a study on Bangladesh Black Bengal goat population, Mia *et al.* (2014) detected highest milking performance of daily milk yield in 3rd lactation dams (480.0 ± 52.02g). Zahraddeen *et al*. (2007) observed a higher milking performance for fat content in 3rd parity does (5.54 ± 0.03%) In Nigerian indigenous goat populations. In other animal species such as Camels, Zeleke (2007) estimated highest milking performances of daily milk yield and percentages of both fat and protein in 3rd parity groups (5.43 ± 0.19l, 5.32 ± 0.44% and 3.16 ± 0.26% for daily milk yield, fat and protein percentages

Table 4.1 Average lactation milking performances of milk yield (kg), fat yield (kg), protein yield (kg) and lactose yield (kg); their respective standard errors and mean separations across various levels of parity

Parity	Milk yield	Fat yield	Protein yield	Lactose yield
1	947.30 ± 40.20^{cd}	37.34 ± 1.62^{b}	29.37 ± 1.31^{b}	42.63 ± 1.82^{bc}
2	1043.20 ± 39.70^{b}	39.77 ± 1.60^{a}	31.06 ± 1.32^{a}	45.90 ± 1.82^{a}
3	1073.40 ± 40.00^{a}	40.57 ± 1.61^{a}	31.30 ± 1.35^{a}	46.73 ± 1.88^{a}
4	1020.30 ± 41.40^{b}	38.33 ± 1.67^{b}	28.82 ± 1.43^{b}	44.05 ± 2.01^{b}
5	972.80 ± 44.20^{c}	37.14 ± 1.78^{b}	27.48 ± 1.55^{c}	42.12 ± 2.20^{c}
6	901.60 ± 48.60^{d}	34.08 ± 1.96^{c}	24.58 ± 1.71^{d}	38.44 ± 2.48^{d}
≥7	775.40 ± 56.60^{e}	29.47 ± 2.28^{d}	20.64 ± 1.96^{e}	32.99 ± 2.89^{e}

Within a column, means that share a superscript are not significantly different ($p > 0.05$).

respectively). While least milking performances were reported in 6th lactation dams (3.01 ± 0.11l, 2.62 ± 0.12% and 2.64 ± 0.07% respectively). Both present and past observations may have been associated with few animals in the populations reaching beyond 6th parity as a result of culling older animals due to their low-quality milk. Both past and present findings suggest that average lactation milking performances of these traits increase from 1st to 3rd parity (where peak yields are reached), followed by slight decline in yields (usually from 4th to 5th parity) while maintaining high yields. Thereafter, followed by rapid decline in yields beyond 5th parity.

Present results did not concur the findings of Ishag *et al.* (2012) who obtained least and highest milking performance of total milk yield in 5th and 1st parity groups respectively (368.58 ± 23.63kg and 278.97 ± 11.28kg for 5th respectively) for Saanen population raised under Sudan conditions. Difference in observations and estimations between past and current study are probably attributed to the variations in number of records (16 407 vs 404), the environment in which performance of animals was measured (South African climate vs Sudan semi-arid conditions), as well as lactation length (only 69 animals from the previous study had surpassed 300 days in lactation). In a Polish dairy goat population, Bagnicka *et al*. (2015) found the highest average lactation milking performances of MY, FY and PY in 4th parity groups (625.4 ± 6.5kg, 22.08 ± 0.26kg and 18.44 ± 0.19kg for MY, FY and PY respectively). While least lactation yields were determined in 1st lactation does (525.1 ± 4.4kg, 18.91 ± 0.17kg and 15.69 ± 0.13kg respectively). Muller (2005) estimated highest average lactation milking performance of MY in 4th parity dams (970kg), with least yield calculated in 1st lactation does (586kg) for South African Toggenburg goat population. Differences between breeds (Saanen vs Polish dairy goat population and Toggenburg) probably influenced variation in results between current and past studies.

For the South African Saanen population, Muller (2005) obtained highest average lactation PY in 5th parity Saanen groups (25.8kg). Variation in number of records probably influenced the difference between present and past estimations (1st and 2nd parity animals accounted for 67% of the total records used in the previous study). In Czech White Shorthaired and Saanen goat populations, Šlyžius *et al.* (2017) detected highest fat percentage in 4th and 6th parity groups respectively (5.07% and 4.1% for Czech White Shorthaired and Saanen populations respectively). Zahraddeen *et al*. (2007) observed least milking performance of fat content in 1st lactation indigenous goat populations (4.39 ± 0.02%).

Generally, variation in findings between the past and present investigations may be due to a host of factors. Amongst those are differences between breeds/strains, number of records used in each level of parity, days in milk/lactation length, management practices such as feeding and also gene-environment interaction whereby various genotypes respond to the different environments they are subjected to.

Average lactation milking performances for urea, SCCI, P and NR; their respective standard errors, together with mean separations across various parity levels are shown on Table 4.2. Parity effects were highly significant ($p < 0.01$) on lactation milking performance for all mentioned traits as shown in Appendices 7.5 to 7.8. Average lactation urea yield was statistically the same ($p > 0.05$) across groups in their 6th and ≥7th lactations. While there was also no significant difference ($p > 0.05$) in concentrations of SCCI between groups in 3rd, 4th and 5th parities, as well as between those in 6th and ≥7th parities. Average lactation NR were statistically not significantly different ($p > 0.05$) across all parity levels, while P levels were also statistically the same ($p > 0.05$) between groups in their 3rd, 4th and 6th lactations.

Average SCCI increased from 1st to 5th lactation, with 1st and 5th parity dams yielding least and highest respectively (2.24 ± 0.26cells/ml and 3.46 ± 0.32cells/ml respectively), followed by a decrease in yields from 6th to ≥7th lactation. The decline in SCCI levels beyond 5th lactation could be attributed to fewer number of observations in 6th and ≥7th parities. According to Jimenez-Granado *et al*. (2014) parity effects on SCC depend on udder health status. Furthermore, older animals are more exposed to pathogens accumulated from lying on surfaces compared to young ones due to their prominent teat canals as they have been milked more and have higher parity orders. Selection effects may have also played a role in influencing current estimations whereby, majority of animals diagnosed with abnormal levels of body cells in their milk get culled from herds.

The present study is the first of its kind to investigate significance of parity on SCCI in South African dairy goat populations. However, the results obtained did not differ substantially with past values reported on both SCC and SCCI. Simčič *et al*. (2018) detected least and highest concentrations of SCC in 1st and 6th parity dams respectively (8.59 ± 0.07ml^{-1} and 9.64 ± 0.07ml^{-1} for 1st and 6th lactation dams respectively). For Croatian Alpine goat population, Poonia *et al*. (2018) obse+rved

Table 4.2 Average lactation milking performance of urea concentration (mg/dl), somatic cell county index (cells/ml), persistency (%) and net returns (rands); their standard errors and mean separations across various levels of parity

Parity	**Urea concentration**	**Somatic cell count index**	**Net returns**	**Persistency**
1	25.91 ± 0.65^{bc}	2.24 ± 0.26^{c}	1084.60 ± 46.5^{a}	103.87 ± 5.83^{a}
2	25.28 ± 0.63^{d}	2.93 ± 0.25^{b}	912.60 ± 45.50^{b}	75.71 ± 5.70^{b}
3	25.45 ± 0.66^{cd}	3.31 ± 0.26^{a}	852.00 ± 46.80^{c}	65.88 ± 5.87^{c}
4	26.02 ± 0.73^{bcd}	3.43 ± 0.28^{a}	763.50 ± 50.60^{d}	65.63 ± 6.34^{c}
5	26.84 ± 0.87^{b}	3.46 ± 0.32^{a}	730.50 ± 57.50^{de}	67.79 ± 7.21^{bc}
6	28.37 ± 1.01^{a}	3.45 ± 0.37^{ab}	663.40 ± 66^{ef}	62.96 ± 8.27^{c}
≥7	29.49 ± 1.25^{a}	3.19 ± 0.44^{ab}	586.90 ± 78.70^{f}	66.60 ± 9.87^{bc}

Within a column, means that share a superscript are not significantly different ($p > 0.05$).

increases in levels of SCC with advancements in the level of parity (5.774 ± 0.193cells/ml, 5.895 ± 0.119cells/ml and 5.972 ± 0.109cells/ml for 1st, 2nd and 3rd parity groups respectively). In other species such as dairy sheep, Oravcová *et al*. (2018) reported an increase in SCC levels with advance in the level of parity (5.04 ± 0.04ml^{-1}, 5.11 ± 0.04ml^{-1} and 5.38 ± 0.04ml^{-1} for 1st, 2nd and 3rd lactation dams respectively). This suggests that there is a possibility that parity effects on SCC levels are similar in goat and sheep species. Both past and present findings entail that levels of SCC found in milk increase as parity level advances.

Average lactation urea concentration decreased from 1st to 2nd lactation; thereafter, followed by a pick-up in yield from 3rd to ≥7th parity lactation where peak concentration is reached. Dams in ≥7th and 2nd lactations yielded the highest and least average urea respectively (29.49 ± 1.25mg/dl and 25.28 ± 0.63mg/l). According to Capuco *et al*. (2001) and Carnicella *et al*. (2008) as age progresses, the intake of nutrients also increases. Various studies investigating the effects of crude protein (CP) content on milk urea concentration have been previously carried out (Giovanetti *et al.,* 2019; Nousiainen *et al*., 2004). Indeed, there is sufficient evidence that dietary crude protein levels are the most ideal indicator of milk urea concentration, with correlation between the two reported to be high and positive. Thus, values in the current study may be due to increases in dietary crude protein intake in older animals.

Trend for P decreased from 1st to 3rd lactation, with peak value observed in 1st parity dams (103.87 ± 5.83%); thereafter, followed by a fluctuating trend from 4th to ≥7th parity while least persistency value estimated in the 6th parity animals (62.96 ± 8.27%). According to Ruvuna *et al*. (1995) lactation curves are a representative of the relationship between milk yield and time after parturition. Current observations compare well with production patterns reported in literature by past studies. In dairy cattle, Glauber (2007) reported highest lactation persistency value in first calving groups. For an Egyptian Damascus goat population, Ayasrah *et al*. (2013) observed the highest lactation persistency value in first time kidding groups compared to those with high number of lactations. Weller *et al*. (2006) stated that persistency declines with advancements in lactation order because during 1st parity the lactation curve is flatter. Persistency values obtained in the present study may be a result of young animals having fewer lactations, as well as a flat lactation curve compared to older groups. Thus, resulting in greater persistency values.

Net returns decreased with an increase in the level parity. Highest and least NR were estimated in 1st and ≥7th parity groups (R1084.60 ± 46.50 and R586.90 ± 78.70 respectively). The current study is the first of its kind to investigate significance of parity on NR in dairy goat populations. Thus, comparable literature does not exist.

Current results also differed from the findings of Giaccone *et al*. (2010), who reported increases in urea levels from 1st to 2nd parity; thereafter, followed by a decline in ≥3rd parity groups (41.09 ± 0.52mg/dl, 45.03 ± 0.33mg/dl and 44.43 ± 0.33mg/dl for 1st, 2nd and ≥3rd parity dams respectively). Yoon *et al*. (2004) detected least and highest average urea in 6th and 5th parity groups respectively (15.82 ± 0.84mg/dl and 17.51 ± 0.47mg/dl respectively). Variation in values between current and past studies may have been influenced by differences between breeds and management practices applied (especially feeding practices related to CP levels). In crosses of Galla and East African with Toggenburg and Anglo Nubian goats, Ruvuna *et al*. (1995) reported increases in persistency values with advances in dam parity. For second lactation groups in a Turkish Saanen population, Pala and Savaş, (2005) found highest persistency when evening milk tests were used. Breed differences, the use of evening tests and 2nd lactation records probably influenced differences in results obtained between current and past studies.

4.5.2. Litter size effects

Average lactation milking performances of MY, FY, PY and LY; their respective standard errors and mean separations across various litter size levels are shown on Table 4.3. Dam litter size highly influenced ($p < 0.01$) average lactation milking performances of MY and LY as shown in Appendices 7.1 and 7.4 respectively. While its effects were not significant ($p > 0.05$) on FY and PY (Appendices 7.2 and 7.3 respectively). Average lactation milking performances of both MY and LY were statistically the same ($p > 0.05$) between groups that kidded twins and triplets. Average lactation PY increased from 1st to 2nd litter size level, followed by a decline in the 3rd level. Least and highest average PY lactation yields were observed in single and double litter kidding groups respectively (27.24 ± 1.41kg and 27.88 ± 1.41kg respectively). Average lactation milking performances of MY, FY and LY increased with advancements in dam kidding prolificacy, with highest yields reported in triple litter kidding dams (977.20 ± 41.50kg,

Table 4.3 Average lactation milking performances of milk yield (Kg), fat yield (kg), protein yield (kg) & lactose yield (kg), their respective standard errors and mean separations for dams that gave birth to singles, twins and triplets

Litter size	Milk yield	Fat yield	Protein yield	Lactose yield
1	939.60 ± 40.90^{b}	36.38 ± 1.65^{a}	27.24 ± 1.41^{b}	40.96 ± 1.99^{b}
2	969.20 ± 41.10^{a}	36.74 ± 1.65^{a}	27.88 ± 1.41^{a}	42.23 ± 1.98^{a}
3	977.20 ± 41.50^{a}	36.89 ± 1.67^{a}	27.70 ± 1.43^{ab}	42.32 ± 2.00^{a}

Within a column, means that share a superscript are not significantly different ($p > 0.05$).

36.89 ± 1.67kg and 42.32 ± 2.00kg for MY, FY and LY respectively). While single litter kidding dams gave least lactation yields (939.60 ± 40.90kg, 36.38 ± 1.65kg and 40.96 ± 1.99kg for MY, FY and LY respectively).

Litter size effects on milk production traits together with components have been widely investigated in the past. According to Rabasco *et al*. (1993) multiple litter kidding goats produce 11% more milk compared to single litter kidding groups. Results from the current study are close to the findings of past comparable literature reported in other dairy goat populations such as U.S Alpine (Browning *et al*., 1995), Red Sokoto (Akpa *et al*., 2002), Mexican Saanen (Torres-Vasquez *et al.,* 2009), Bangladesh Black Bengal (Mia *et* al., 2014), Draa (Ibnelbachyr *et al*., 2015) and Polish dairy goat population (Bagnicka *et al*., 2015). Both past and present results suggest that milk production increases as kidding prolificacy advances. These observations are explained by variation in quantity of hormones (placental lactogen, progesterone and prolactin) responsible for stimulation of the mammary gland during gestation.

Current results are in contradiction with the findings of previous studies that reported non-significant effects of litter size on lactation milking performance of lactose yield (Torres-Vasquez *et al*., 2009) and content (Bagnicka *et al*., 2016). The use of only the first lactation records (Torres-Vasquez *et al*., 2009), as well as breed differences (Bagnicka *et al*., 2016) in past investigations probably influenced differences in reported values.

Average lactation milking performances of urea, SCCI, NR and P; their respective standard errors, as well as mean separations across various litter size levels are shown on Table 4.4. Litter size significantly influenced ($p < 0.05$) lactation milking performances of all mentioned traits as shown in Appendices 7.4 to 7.8. While average lactation NR increased as prolificacy advanced, variation in NR between single and double litter kidding groups was not significantly different ($p > 0.05$). Both urea and SCCI levels followed similar trend to PY. While P decreased with advancements in kidding prolificacy.

Twin litter kidding dams gave the highest lactation yields for both SCCI and urea concentration (3.28 ± 0.27cells/mL and 27.10 ± 0.71mg/dl respectively), while triple and single litter kidding groups yielded least (26.46 ± 0.74mg/dl and 3.00 ± 0.28cells/ml for urea and SCCI respectively). The current study is the first of its kind to investigate significance of dam kidding prolificacy on lactation milking performances of NR and

Table 4.4 Average lactation milking performances of urea concentration (mg/dl), somatic cell count index(cells/ml), net returns (rands) and persistency (%); their respective standard errors and mean separations for dams with singles, twins and triplets

Litter size	Urea concentration	Somatic cell count index	Net returns	Persistency
1	26.73 ± 0.72^{ab}	3.00 ± 0.28^{b}	775.10 ± 49.80^{b}	74.55 ± 6.24^{a}
2	27.10 ± 0.71^{a}	3.28 ± 0.27^{a}	778.50 ± 49.20^{b}	70.28 ± 6.16^{b}
3	26.46 ± 0.74^{b}	3.15 ± 0.28^{ab}	843.70 ± 50.70^{a}	73.07 ± 6.36^{ab}

Within a column, means that share a superscript are not significantly different ($p > 0.05$).

SCCI in South African dairy goat populations. Therefore, comparable literature does not exist presently. Although there may be no comparable literature on SCCI, studies have been previously conducted to investigate significance of litter size on both SCC and SCS. Present findings on SCCI compare well with the findings of Poonia *et al*. (2018) who detected least and highest SCC levels in single and multiple litter kidding groups respectively (5.885 ± 0.135cells/ml and 5.915 ± 0.155cells/ml for single and multiple litter kidding dams). Both current and past observations are probably due to increased udder volume in groups pregnant with multiple kids. Therefore, resulting in increased milk yield, as well as number of body cells found in milk.

Current estimations on lactation performance of urea are probably attributed to triple litter kidding groups using much of their dietary crude protein intake towards the maintenance of gestation period. Thus, resulting in less urea levels found in their milk. This observation varies from the findings of Giaccone *et al*. (2007) who reported non-significant effects of litter size on urea concentration. Feeding same levels of dietary crude protein in both groups could have influenced past results.

Triple litter kidding dams gave highest average lactation NR while least returns were estimated in single litter kidding groups (R843.70 ± 50.70 and R775.10 ± 49.80). Reason behind this observation could be attributed to triple litter kidding groups also attaining highest lactation milking performances of MY, FY and LY. Furthermore, having produced least lactation SCCI levels, medical costs for treating intra-mammary infections cases were probably least compared to the other groups. Highest and least average lactation P values were estimated in single and double litter kidding animals respectively (74.55 ± 6.24% and 70.28 ± 6.16%). Different result was obtained by Rojo-Rubio *et al*. (2016) who found highest average lactation persistency value in groups with twin suckled kids for Mexican dairy goat population.

4.5.3. Dam birth season effects

Average lactation milking performances of MY, FY, PY and LY; their respective standard errors as well as mean separations across various dam birth seasons are shown on Table 4.5. Dam birth season did not significantly influence ($p > 0.05$) average lactation milking performances of FY, PY and LY as shown in Appendices 7.2, 7.3 and 7.4 respectively. While its effects were significant ($p < 0.05$) on average

Table 4.5 Average lactation milking performances of milk yield (kg), fat yield (kg), protein yield (kg) & lactose yield (kg); their respective standard errors, as well as mean separations across various dam birth seasons

Birth seasons	**Milk yield**	**Fat yield**	**Protein yield**	**Lactose yield**
Winter	918.90 ± 37.40^{b}	36.07 ± 1.51^{a}	26.42 ± 1.30^{a}	39.75 ± 1.83^{b}
Spring	955.70 ± 35.60^{a}	35.17 ± 1.44^{a}	27.19 ± 1.24^{a}	41.06 ± 1.73^{a}
Summer	938.60 ± 40.90^{ab}	35.69 ± 1.65^{a}	26.83 ± 1.42^{a}	40.94 ± 2.01^{ab}
Autumn	1034.80 ± 82.20^{ab}	39.76 ± 3.31^{a}	30.01 ± 2.70^{a}	45.61 ± 3.83^{ab}

Within a column, means that share a superscript are not significantly different ($p > 0.05$).

lactation MY (Appendix 7.1). Both average lactation milking performances of LY and MY were not significantly different ($p > 0.05$) between groups born during autumn and summer seasons. Groups born during autumn season gave highest lactation milking performances of all traits mentioned (938.60 ± 40.9kg, 35.69 ± 1.65kg, 26.83 ± 1.42kg and 40.94 ± 2.00kg for MY, FY, PY and LY respectively). However, the variability in this season was very high due to few observations, as almost 80% of births in this population occurred during spring season (between August and October). Therefore, to achieve optimal lactation milking performances of these traits in the Sothern hemisphere, it is best to breed these animals for spring kidding (955.70 ± 35.60kg, 35.17 ± 1.44kg, 27.19 ± 1.24kg and 41.06 ± 1.73kg for MY, FY, PY and LY respectively). While breeding for winter kidding will result in least average lactation milking performances of MY (918.90 ± 37.4kg) and LY (39.75 ± 1.83kg).

According to Hanson *et al*. (2011) performance of adult animals may be influenced by permanent changes in the metabolism that are attributed to both pre-natal and post-natal environments. Furthermore, management practices such as level of feeding throughout can never be ignored irrespective of the animal's season of birth. Johnson *et al*. (2001) stated that forage harvesting date and other management practices influence forage quality. Susanto *et al*. (2019) found increases in lactation milk yield as season changed from dry to wet in first calving cows. Therefore, current estimations may have been influenced by quantity and quality of feed available in the respective seasons animals are born. Broucek *et al.* (2006) discovered possibility of animals calved between the period December and February yielding highest lactation milking performances due to higher persistency effects of the lactation curve that are attributed to increased photoperiod.

Average lactation milking performances of urea, SCCI, NR and P, their respective standard errors, together with mean separations across various dam birth seasons are depicted on Table 4.6. Dam birth season had no significant influence ($p > 0.05$) on both lactation milking performances of P and SCCI as shown in Appendices 7.6 and 6.7 respectively. While its effects were significant ($p < 0.05$) on average lactation urea and NR (Appendices 7.8 and 7.5 respectively). Average lactation milking performances of both NR and urea were statistically the same ($p > 0.05$) between groups born during winter and spring seasons. While variation in average lactation P and SCCI were also not significantly different ($p > 0.05$) between groups born during summer and autumn seasons.

Table 4.6 Average lactation milking performances of urea concentration (mg/dl), somatic cell count index (cells/ml), net returns (rands) & persistency (%); their standard respective standard errors and mean separations across various dam birth seasons

Birth seasons	**Urea concentration**	**Somatic cell count index**	**Net returns**	**Persistency**
Winter	26.08 ± 0.63^{b}	3.04 ± 0.25^{b}	734.40 ± 44.20^{b}	75.35 ± 5.53^{a}
Spring	26.26 ± 0.62^{b}	3.21 ± 0.24^{a}	747.70 ± 42.90^{b}	71.14 ± 5.37^{b}
Summer	28.08 ± 0.82^{a}	3.35 ± 0.32^{ab}	836.00 ± 56.20^{a}	76.96 ± 7.04^{ab}
Autumn	26.63 ± 1.43^{ab}	2.97 ± 0.53^{ab}	878.10 ± 96.10^{ab}	67.10 ± 12.00^{ab}

Within a column, means that share a superscript are not significantly different ($p > 0.05$)

Highest value for average lactation P was estimated in groups born during the summer season (76.96 ± 7.04%). This observation may be due to increased photoperiod during summer season (longer days and short nights). Moreover, because most parts of the country experience summer rainfall, current observations may have also been a result of increases in quality and quantity of forages during the wet seasons. Summer birth season yielded highest average lactation urea (28.08 ± 0.82mg/dl). Because dietary crude protein levels are one of the major indicators of milk urea concentration, the observation was probably influenced by availability of quality forages during this season.

Summer birth season further yielded highest average SCCI levels per lactation (3.35 ± 0.32 cells/ml). According to Godden *et al.* (2003) in housed and field environments, the load of pathogens leading to mastitis generally increase due to increases in both temperature and humidity. Therefore, present observations are probably due to increased temperatures and humidity during summer period leading to increased infestation of pathogens that result in intra-mammary infections. Highest and least average lactation NR were estimated in animals born during summer and winter seasons respectively (R836.00 ± 56.20 and R734.40 ± 44.20 respectively).

3.5.4. Dam birth year effects

Figure 1 shows average lactation milking performance trends of MY, FY, PY, LY, urea, NR, P and SCCI across 61 birth years (from 1955 to 2016) in the South African Saanen goat population. Dam birth year highly influenced ($p < 0.01$) all traits subjected to analysis as shown in Appendices 7.1 to 7.8. Initial recording in the herd included lactation MY and FY. Average lactation milking performances of MY and FY follow a similar fluctuating trend. Thus, suggesting that positive correlated responses to selection may exist between these traits. Dams born during the first 12 years (from 1955 to 1967) except for the period between 1956 and 1957 yielded averages above 1000kg and 35kg for MY and FY respectively. During this period 1 020 lactation records were available.

Between the years 1968 and 2000, 14 905 records were available, with almost all animals yielding lactation averages below 1000kg for MY, except groups born in the years 1978 (1090kg), 1980 (1014.4kg) and 1985 (1031kg). Furthermore, least

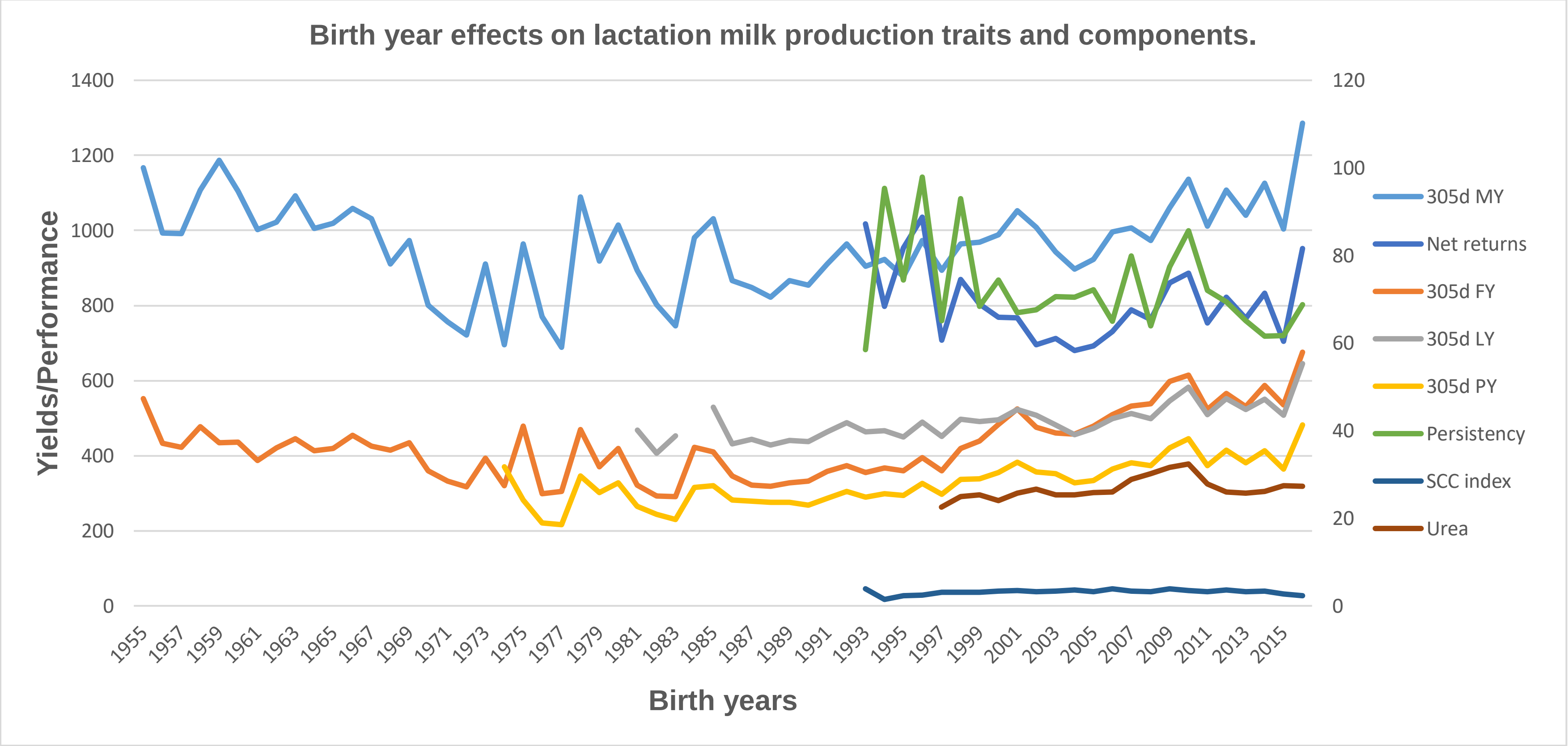

Figure 1. Yield trends for various milk production traits and components of does born across various years.

305d MY = lactation milk yield; 305d FY = lactation fat yield; 305d PY = lactation protein yield; 305d LY = lactation lactose yield; SCC index = somatic cell count index; urea = urea concentration lactation milking performance of MY between this period was observed in dams born during the year 1977 (688.7kg). Almost all animals born between the years 1971 and 1997 all yielded FY below 35kg per lactation.

The period between 2001 and 2016 saw a total 16 098 lactation performance records becoming available. Dams born particularly during the years 2003, 2004, 2005, 2006 and 2008 gave average lactation MY below 1000kg, while the rest yielded above 1000kg per lactation. All animals born during this period yielded average lactation FY above 35kg. Furthermore, groups born specifically in the years 2004 (896.9kg and 39.18kg) and 2016 (1285.8kg and 57.92kg) yielded least and highest respectively for average lactation MY and FY.

Official recording of average lactation PY and NR commenced during the years 1974 and 1991 respectively. Both average lactation milking performances of PY and NR follow a similar fluctuating trend to that of average lactation MY, suggesting possibilities of positive correlated responses to selection between these traits. Between the period 1974 and 2000, animals born during the years 1976 and 1974 yielded least and highest average lactation PY respectively (18.98kg and 31.8kg respectively). While animals born during the years 1991 and 1996 gave least and most NR per lactation (R618 and R1035.5 respectively).

All dams born between 2001 and 2016, except in the year 2005 (28.65kg) yielded average lactation PY above 30kg, with highest PY obtained in animals born during the year 2016 (41.31kg). During the same period, dams born in the year 2016 also gave the highest average lactation NR (R951.9).

Recordings of average lactation milking performances of LY and SCCI commenced in the years 1981 and 1991 respectively. Average lactation SCCI levels show an almost consistent trend from 1991 to 2016 with all dams except those born in the years 1991, 1994, 1995, 1996, 2015 and 2016 yielding above 3cells/ml per lactation. Recent reductions in SCCI levels may be attributed to intense selection methods applied against this trait in most herds. Average lactation milking performance of LY has not been consistent and shows a fluctuating trend that is almost similar to that of average lactation MY, with improved yields observed in dams born during recent years. Recent improvements in averages of lactation NR and other traits such as MY, FY and PY were probably due to the use of genetically superior animals for breeding in most herds, as a result of increased population size that may have also increased the intensity of selection.

Average lactation milking performances of urea and P were first recorded during the years 1997 and 1991 respectively. Trends for both average lactation urea and P have not been consistent over the years. Between the period 1991 and 2016, highest and lowest values for P were estimated in groups born during the years 1996 and 1993 respectively (97.9% and 58.5% respectively). This observation may have been a result of a majority of animals not reaching beyond 3rd parity in most herds during the period, as the lactation curve of animals in early lactations is usually flat. Furthermore, animals born particularly during the years 1997 and 2010 yielded least and most average urea concentrations per lactation respectively (22.54mg/dl and 32.388mg/dl). Given that milk urea concentrations indicate levels of dietary crude protein, variations in urea levels over the years may have been related to differences in feeding applied in herds over the years.

Generally, variation in lactation milking performances of various traits and components across various birth years may have been influenced by a host of factors. Differences in genetic composition of animals, climate and management practices applied in each year are probably among the factors that influenced current estimations. Bosman *et al.* (2015) observed high genetic variation between populations in the South African dairy goat population, with heterozygosity estimate ranges between 62.6% and 65% reported in the population. The increase in the size of population in recent years, as well as the level of heterozygosity in the population may have lowered chances of inbreeding depression in this population. Therefore, resulting in reduced inbreeding levels and improved yields in the herd.

4.5.5. Dam kidding season effects

Average lactation milking performances of MY, FY, PY and LY; their respective standard errors and mean separations across various dam kidding seasons are showed in Table 4.7. The effects were significant ($p < 0.05$) on average lactation milking performances of all mentioned traits except PY (Appendices 7.1 to 7.4). Lactation milking performances of both MY and LY were not significantly different ($p >$ 0.05) across winter, spring and summer kidding seasons. While average lactation

Table 4.7 Average lactation milking performances of milk yield (Kg), fat yield (Kg), protein yield (Kg) & lactose yield (Kg); their respective standard errors and mean separations across various dam kidding seasons

Kidding seasons	**Milk yield**	**Fat yield**	**Protein yield**	**Lactose yield**
Winter	1046.90 ± 25.60^{a}	38.10 ± 1.03^{a}	29.40 ± 0.97^{ab}	46.02 ± 1.35^{a}
Spring	1054.40 ± 24.10^{a}	36.88 ± 0.97^{b}	29.19 ± 0.94^{ab}	46.15 ± 1.29^{a}
Summer	1004.50 ± 39.50^{a}	38.82 ± 1.59^{ab}	30.23 ± 1.38^{a}	44.04 ± 1.93^{a}
Autumn	742.00 ± 129.00^{b}	32.90 ± 5.19^{ab}	21.62 ± 4.11^{b}	31.14 ± 5.85^{b}

Within a column, means that share a superscript are not significantly different ($p > 0.05$).

FY was also statically the between summer and autumn kidding groups. Highest average lactation milking performances of MY (1054.40 ± 24.10kg) and LY (46.15 ± 1.29kg) were both obtained in spring kidding groups, while summer kidding dams gave highest averages for both FY and PY per lactation (38.82 ± 1.59kg and 30.23 ± 1.38kg respectively). Least average lactation milking performances of all mentioned traits were observed in autumn kidding dams (742.00 ± 123.00kg, 32.90 ± 5.19kg, 21.62 ± 4.11kg and 31.14 ± 5.85kg for MY, FY, PY and LY respectively). From the shape of a lactation curve, it is well known that peak milk yield is reached during the first 60 days of lactation. Muller (2005) noted that majority (82%) of animals in the South African dairy goat population kid during spring season (between August and September). Therefore, current estimates may have been influenced by the availability quality fodder, as well as increased photoperiod.

Current estimates were similar to the result obtained by Ibnelbachyr *et al*. (2015) who found highest and least milking performance of total milk yield in animals that kidded during spring and autumn seasons respectively for a Draa indigenous goat population (80.4kg and 68.5kg respectively). In Saanen and Alpine goat populations, Mioč *et al*. (2008) reported highest protein content in groups that kidded during the summer season while least protein content was obtained in dams that kidded during the winter season (3.09% and 3.07% for summer and winter kidding seasons respectively). Abraham *et al*. (2018) discovered increases in average lactation milk yield as kidding seasons change from dry to wet (77.1 ± 1.39kg and 59 ± 1.77kg for wet and dry seasons respectively) in Ethiopian Begait dams. Furthermore, improvements in yields were reported to be attributed to availability of highly nutritive fodder during wet seasons.

Present findings did not concur with values reported by other comparable literature. In a population of Draa goats in Morocco, Ibnelbachyr *et al*. (2015) reported highest fat content in animals that kidded during summer season (5.46%), while highest contents for both protein and lactose were observed in groups that kidded during the autumn (4.81%) and summer (6.17%) seasons respectively. Variation in values obtained in the present study and those reported by Ibnelbachyr *et al*. (2015) may be due to farming systems (the previous study used records of goats raised under an intensive system of three kiddings in two years), breed differences (Saanen vs Draa), as well as the environment (South African climate vs Moroccan climate).

For a Croatian Saanen and Alpine goat populations, Mioč *et al*. (2008) observed better lactation milking performance in goats that kid early in the year compared to groups that kid during spring season (627.75kg vs 484.49kg, 3.48% vs 3.39% and 4.53% vs 4.51% for average milk lactation yield, as well as contents of fat and lactose respectively). Variation estimates between past and current investigations were largely influenced by differences in the environment (63% of animals in the previous study kidded during winter season), the inclusion of Alpine breed in analysis, as well as lactation length (animals with lactation length below 365 days were also included in the past study). In Czech White Shorthaired goat population, Ciappesoni *et al*. (2004) calculated highest milking performance of daily milk yield in groups that kidded during autumn season (2.733kg/day), while highest fat (3.89%) and protein (2.93%) contents were both observed in animals that kidded between winter and early summer kidding season (May - November).

Table 4.8 shows average lactation milking performances for urea, SCCI, NR and P, their respective standard errors, as well as mean separations across various dam kidding seasons. Kidding season highly affected (p < 0.01) average lactation NR and SCCI (Appendices 7.5 and 7.7 respectively), significantly influenced (p < 0.05) average lactation P (Appendix 7.6) but did not influence (p > 0.05) urea (Appendix 7.8). Autumn kidding dams performed highest for average P and urea (100 ± 16.7% and 29.94 ± 1.86 mg/dl respectively). While spring kidding season performed least for the two (60.44 ± 4.52% and 26.94 ± 0.53 mg/dl respectively). Summer kidding season yielded highest averages of NR and SCCI levels per lactation (889.70 ± 47.20rands and 3.90 ± 0.27cells/ml respectively), while least average lactation performances for the two were estimated in autumn kidding groups (746.00 ± 133.00rands and 2.18 ± 0.73cells/ml for NR and SCCI yield respectively).

The current study is the first to investigate significance of dam kidding season on lactation SCCI and NR in South African Saanen goat population. Thus, currently there is no comparable literature. However, current results on other components compare well with findings of Dahl *et al.* (2000) who found increases in milking performance of dairy cows with prolonged photoperiod. Other authors (Pesántez *et al*., 2014; Marete *et al*., 2014) found highest average lactation persistency in dairy goats that kidded during wet seasons compared to those kidding during dry seasons. According to Moran (2005) the persistency of milk can be influenced by feed quality

Table 4.8 Average lactation milking performances of urea concentration (mg/dl), somatic cell count index (cells/ml), net returns (rands) & persistency (%); their respective mean separations and standard errors across various dam kidding seasons

Kidding seasons	**Urea concentration**	**Somatic cell count index**	**Net returns**	**Persistency**
Winter	27.33 ± 0.52^{a}	3.15 ± 0.21^{c}	779.20 ± 36.70^{b}	61.26 ± 4.59^{bc}
Spring	26.94 ± 0.53^{b}	3.34 ± 0.20^{b}	781.80 ± 36.10^{b}	60.44 ± 4.52^{c}
Summer	27.85 ± 0.76^{ab}	3.90 ± 0.27^{a}	889.70 ± 47.20^{a}	68.64 ± 5.92^{ab}
Autumn	29.94 ± 1.86^{ab}	2.18 ± 0.73^{bc}	746.00 ± 133.00^{a}	100.00 ± 16.70^{a}

Within a column, means that share a superscript are not significantly different ($p > 0.05$).

and quantity offered post peak yield. As a result, both present and past observations may have been influenced by the presence of quality fodder during the wet seasons. Sandrucci *et al*. (2018) reported highest levels of SCC (5.93 cells/ml) in groups of animals kidding between spring and early summer (April - June). This observation was attributed to increases in temperature levels and humidity during this period.

The values estimated in the current study and those reported in comparable literature suggest that dairy goat production is seasonal. To achieve optimal lactation milking performance in dairy goat herds, it is necessary to exercise planned breeding. From the current study, spring kidding season gives a better lactation milking performance and highest herd NR per lactation compared to the rest. Variation in observations across various kidding season may be related to the availability of quality fodder during each season, as well as the length of photoperiod. However, further investigations are needed to determine the level at which kidding season influence the traits investigated by accounting for month within seasonal effects. Because the average gestation period of goats is 150 days (5 months), breeding during Autumn (March-April) season can yield positive results in the population. Summer kidding season gives the highest level of intra-mammary infections. This could have been due to the prevalence of pathogens under hot and wet conditions.

4.5.6. Kidding age effects and phenotypic correlation between milk production traits and dam kidding age

Phenotypic correlations between dam kidding age and milk production traits, together with components are shown on Table 4.9. As shown in appendices 7.1 to 7.8, dam kidding age significantly influenced ($p < 0.05$) lactation milking performances of all traits except NR, SCCI and urea. The present findings concur with findings of Mburu *et al*., 2014 and Ketto *et al*., 2014 who also found milk yield in goats to be highly influenced by kidding age of the dam.

Average lactation milking performances of all traits except SCCI (r_p= 0.189) decreased with increases in dam kidding age (r_p= -0.30, -0.004, -0.057, -0.051, -0.015, -0.265 and -0.271 for urea, MY, FY, PY, LY, NR and P respectively). Furthermore, the correlation between dam kidding age and MY was not significant ($P > 0.05$). Results obtained from the currents study suggest that SCCI levels in milk increase as age increases. Therefore, keeping old animals in herds will result in reduced lactation NR,

Table 4.9 Phenotypic correlation between kidding age and milk production traits together with components

	Kidding age	Urea	Milk yield	Fat yield	Protein yield	Lactose yield	Net returns	Persistency	Somatic cell count index
Kidding age	-								
Urea	-0.030**	-							
Milk yield	-0.004^{ns}	0.101*	-						
Fat yield	-0.057**	0.119**	0.891**	-					
Protein yield	-0.051**	0.136**	0.955**	0.947**	-				
Lactose yield	-0.015^{ns}	0.094**	0.982**	0.884**	0.946**	-			
Net returns	-0.265**	0.146**	0.886**	0.926**	0.933**	0.894**	-		
Persistency	-0.271**	-0.038**	-0.005^{ns}	0.145**	0.071**	0.047**	0.209**	-	
Somatic cell count index	0.189**	-0.029**	0.071**	0.027**	0.061**	0.007^{ns}	-0.019*	-0.157**	-

* = r_p significant at 5% level ($p \leq 0.05$)

** = r_p significant at 1% level ($p \leq 0.01$)

ns = r_p not significant ($p > 0.05$)

as well as lactation milking performances for MY, FY, PY, LY, urea and P in this population. Estimates on SCCI were probably due to older animals having more lactations therefore leading to increases in secretary parenchyma, teat and udder size. The mentioned increases in mentioned factors make older animals to be more prone to pathogens accumulated from lying on surfaces. In dairy cattle, Jingar *et al.* (2014) found reduction in lactation persistency levels as lactation order increased. Because parity and age are closely related, the lactation curve of animals with fewer lactations is usually flat, and this explains why lactation persistency is higher younger animals but declines with increasing age.

Phenotypic relationships between urea and SCCI, as well as between urea and P revealed low, negative correlated responses (r_p = -0.029 and -0.038 for SCCI and P respectively). Values obtained from the current study illustrate that, selecting for increased MY will result in highly favourable correlated responses of FY (r_p =0.891), PY (r_p = 0.955), LY (r_p = 0.982) and NR (r_p = 0.886), while associations between MY and SCCI (r_p =0.071), and MY and urea (r_p =0.101) are low and positive. Although low and negative correlated responses existed between MY and P (r_p = -0.005), the correlation was not significant ($p > 0.10$). PY was highly and positively correlated to LY (r_p = 0.946) and NR (r_p =0.933), while low and positive correlated responses existed between PY and P (r_p = 0.061), PY and SCCI (r_p = 0.071), as well as between PY and urea (r_p = 0.136). Selecting for increased LY would increase herd NR (r_p = 0.894), as well as improve lactation milking performances for P, SCCI and urea (r_p = 0.047, 0.007 and 0.094 for P, SCCI and urea respectively). To improve the levels of P, selection against SCCI has to be applied as the association between the two is negative (r_p = -0.157). High and positive associations exist between FY and PY (r_p =0.947), FY and LY (r_p =0.884), and FY and NR (r_p = 0.926). While correlations between FY and P, FY and SCCI and, FY and urea were all low and positive (r_p = 0.027, 0.145 and 0.119 for SCCI, P and urea respectively).

It is necessary to monitor and control SCCI levels in herds because abnormal levels would result in increased lactation milk yield losses that are due to increases in amounts of body cells. Furthermore, increases in SCCI levels would decrease both average lactation P and NR. The present estimates compare well with the findings of Muller (2005) who found high and positive phenotypic associations between MY and FY, MY and PY (r_p = 0.80 and 0.95 for FY and PY respectively) in the South African dairy goat population, while a high and positive estimate was also reported between FY and PY (r_p = 0.80). In a first lactation Mexican Saanen goat population, Torres-Vázquez *et al*. (2009) found high and positive correlations between MY and FY (r_p = 0.85), as well as between MY and PY (r_p = 0.95). Scholtens *et al*. (2018) reported high and positive correlated responses in both FY (r_p = 0.91) and PY (r_p = 0.97) arising from selecting for increased MY in New Zealand dairy goat population, while estimate between FY and PY was also reported to be high and positive (r_p = 0.93). Moreover, low and positive estimates were reported between SCC and FY (r_p = 0.10), and SCC and PY (r_p = 0.11). For Italian dairy cattle population, Roveglia *et al*. (2019) reported low and positive correlated responses in SCC that are due to selecting for improved FY (r_p = 0.10) and PY (r_p = 0.11), while a low and positive estimate was reported between MY and urea (r_p = 0.07).

Present results are also contradicted with the findings of Scholtens *et al*. (2018) who reported low and unfavourable correlated responses in MY (r_p = -0.10), FY (r_p = -0.13) and PY (r_p = -0.08) arising from selecting for increased SCS (-0.08) in New Zealand dairy goat population. Amin (2017) estimated moderate and negative associations between SCC and daily milk yield in Saudi dairy goat population (r_p = -0.36). In Jersey cows, Roveglia *et al*. (2019) found negative correlated responses in both MY (r_p = -0.20) and urea (r_p = -0.211) arising from selecting for increased SCC levels, while between LY and SCC a negative and high estimate was reported (r_p = -0.39). Generally, variations in estimates between past and present estimates were probably attributed to breed differences (different genetic merits of various breeds), the inclusion and exclusion of pedigree file in analysis, genotype by environment interaction (various genotypes respond differently to environments they are subjected to) and number of records.

4.6. Conclusion and Recommendations

Due to their significant effects on average lactation milking performances of various milk production traits and components, non-genetic factors determine to what extent the genetic potential of an animal expressed. Subsequently, these factors should be accounted for when comparing lactation milking performances in this population, by incorporating their effects in statistical models of genetic evaluations. Both parity and dam birth year effects are highly significant on lactation milking performances of all traits investigated. Average lactation milking performance increases between 1st and 6th parities with a better milking performance observed in 3rd parity groups. For optimal lactation milking performances and increased lactation herd NR, multiple kidding animals are preferred over single litter kidding groups. There have been improvements in lactation milking performances of milk production traits and components among animals born during recent years.

Recent improvements may have been a result of increased population size over the years that led to reduced genetic variability and increased selection intensity in the population. Therefore, reducing chances of inbreeding depression and increasing selection intensity. Animals born and kidding during spring season yield better per lactation compared to the rest of seasons. Availability of fodder and length of photoperiod in each respective season probably influenced variation in estimations across each season. The present findings further entailed that the traits and components studied can also be improved through phenotypic selection schemes. As a result, recording and inclusion of these traits in selection indices is essential. Selecting for improved MY will reduce P and result in highly favourable correlated responses of FY, PY, LY and NR. All production and components traits studied except SCCI decrease as dam kidding age increases.

The most ideal breeding season for this population is during Autumn season (March - April) to allow animals to kid during spring season. While selection for multiple kidding is also recommended over single kidding. All significant non-genetic factors should be considered by incorporating their effects in genetic evaluation models when estimating (co) variance components, heritabilities, as well as breeding values for this population.

CHAPTER 5

5.0 ESTIMATION OF GENETIC PARAMETERS FOR MILK PRODUCTION AND COMPONENT TRAITS IN THE SOUTH AFRICAN SAANEN GOAT POPULATION

5.1. Introduction

For a successful breeding program, knowledge on heritability estimates of various economic traits of importance as well as selection based correlated responses between them is essential in making effective herd selection decisions that are based on genetic predictions where selective breeding is applied. Prediction of direct and correlated responses to selection aids in developing selection indices for livestock populations (Castañeda-Bustos *et al*., 2014). For desired genetic gains and progress in herds, genetic characterization in selection programs for various traits of economic importance is essential (Rout *et al*., 2017).

According to Muller (2005) there are various non-genetic factors affecting milk yield and components in dairy goats. Effects of some of these factors on milk production and component traits were discussed in the previous chapter. Indeed, it is evident that these factors influence the production of these traits to a certain degree. Subsequently, these factors need to be adjusted for in statistical models for unbiased genetic predictions. Various methods are available for genetic parameter estimates in animal populations. According to Thompson (2008) unlike single-trait animal models, multi-trait models are preferred more for estimation of unbiased (co) variance components and genetic parameters in animal populations. However, Meyer *et al*. (2018) found that having single-trait estimations allows identification of any problems that may arise in later stages of the experiment and permits the reliability of results obtained in multi-trait animal models. In estimation of variance components, Gibbs sampling with multiple-trait animal models or restricted maximum likelihood (REML) methods are usually applied (Groenewald and Viljoen, 2003; Rupp *et al*., 2011).

The present study was carried out to estimate (co) variance components and direct heritability estimates of various milk production traits using uni-variate linear analysis, as well as direct and correlated responses to selection among them applying bi-variate linear analysis.

5.2. Rationale

One of the major problems experienced in genetic evaluations of dairy goats in developing and less-developed countries is the lack of enough lactation performance records that are linked to the pedigree. Generally, smallholder dairy goat systems in developing country are confronted by scarcity of longitudinal records (Desiere *et al*., 2015). The scarcity of records may be attributed to factors such as poor recording infrastructures and most farms not being involved in milk recording schemes.

Genetic parameters for MY, FY and PY have been carried out before for the South African dairy goat population (Muller, 2005) and other dairy goat populations across the globe (Rupp *et al*., 2011; Castañeda-Bustos *et al*., 2014; Bagnicka *et al*., 2015; Bagnicka *et al*., 2016; Scholtens *et al*., 2018). However, past estimations for the South African dairy goat population were not done using fully pedigreed lactation records, were based on relatively small dataset with only few animals having reached beyond three lactations while animals with incomplete lactation length (<305 days) were also included in analysis. Furthermore, recording of traits such as urea concentration and SCCI in the herd, commenced late compared to other traits such as MY, FY and PY. Therefore, genetic parameters for such traits and components have not yet been estimated.

Due to the forever changing environmental conditions over time, animals need to adapt for survivability and productivity. Increase in population size and improvements in genetic composition of animals with the progression of time are of advantage to livestock breeders as they increase the intensity of selection in herds. Therefore, as a result only genetically superior animals are used in breeding programs. Genetic characterization of this population is necessary in providing livestock breeders with intentions to acquire animals for breeding purposes with useful information that will aid in identifying genetically superior animals.

5.3. Objectives

The objectives were to estimate:

I. (Co) variance components and direct heritability estimates of lactation milk yield (MY), fat yield (FY), protein yield (PY), lactose yield (LY), urea concentration (urea), net returns (NR), persistency (P) and (SCCI) in the South African Saanen goat population using fully pedigreed lactation records.

II. Genetic and phenotypic correlations between lactation milk yield (MY), fat yield (FY), protein yield (PY), lactose yield (LY), urea concentration (urea), net returns (NR), persistency (P) and (SCCI) in the South African Saanen goat population using fully pedigreed lactation records.

5.4. Hypotheses

I. (Co) variance components and direct heritability estimates of milk yield (MY), fat yield (FY), protein yield (PY), lactose yield (LY), urea concentration (urea), net returns (NR), persistency (P) and (SCCI) are the same in the South African Saanen goat population.

II. There are no genetic ($r_g = 0$) and phenotypic ($r_p = 0$) relationships that exist between milk yield (MY), fat yield (FY), protein yield (PY), lactose yield (LY), urea concentration (urea), net returns (NR), persistency (P) and (SCCI) in the South African Saanen goat population.

5.5. Results and Discussion

5.5.1. Description of performance and pedigree data files

Average lactation milking performances, number of records and coefficient of variation (CV) for each trait are depicted on Table 5.1. The average values recorded were 1128.20 ± 7.51kg, 43.49 ± 0.32kg, 34.48 ± 0.23kg, 49.05 ± 0.32kg, 27.71 ± 0.13mg/dl, R834.87 ± 6.77, 68.41 ± 0.92% and 3.31 ± 0.04cells/ml respectively for MY, FY, PY, LY, urea, NR, P and SCCI respectively. The number of observations for all traits except urea were above 2 000. One of the reasons for low number of observations on urea in the South African Saanen goat population may be attributed to the fact that the recording of urea commenced late (1997) compared to other production traits and components. The coefficient of variation (CV) for milk production traits and components in the present study ranged between 18% and 65%.

5.5.2. Non-genetic effects

Dam litter size, parity, kidding age and the two-factor interaction between year-season of birth were tested for significance. The results from analysis are shown on Table 5.2. The two-factor interaction between year-season of birth effects did not significantly influence either of the traits investigated ($p > 0.05$). While kidding season effects were significant ($p < 0.05$) on lactation milking performances of MY, FY, PY, urea and P, its effects were not significant ($p > 0.05$) on other traits. All traits except LY were significantly influenced ($p < 0.05$) by kidding age. Parity significantly influenced ($p < 0.05$) P, while its effects were not significant ($p > 0.05$) on the rest of the traits. Lactation milking performances of MY, PY, LY and urea were all influenced by kidding prolificacy ($p < 0.05$), while the effects did not significantly influence ($p > 0.05$) other traits.

Table 5.1 Descriptive statistics for milk production traits and components

Trait	**Observations**	**Mean**	**Coefficient of variation (%)**
Milk yield	2 960	1128.20 ± 7.51	36
Fat yield	2 959	43.49 ± 0.32	40
Protein yield	2 959	34.48 ± 0.23	37
Lactose yield	2 904	49.05 ± 0.32	35
Urea concentration	1 612	27.71 ± 0.13	18
Net returns	2 352	834.87 ± 6.77	39
Persistency	2 352	68.41 ± 0.92	65
Somatic cell count index	2 074	3.31 ± 0.04	58

Table 5.2 Significance of non-genetic factors

Trait	**Year-season**	**DKS**	**Litter size**	**Parity**	**DKA**
Milk yield	ns	***	***	ns	***
Fat yield	ns	***	ns	ns	***
Protein yield	ns	***	***	ns	***
Lactose yield	ns	Ns	***	ns	Ns
Urea concentration	ns	***	***	ns	***
Net returns	ns	Ns	ns	ns	***
Persistency	ns	***	ns	**	*
Somatic cell count index	ns	Ns	ns	ns	***

* = $p \leq 0.05$; ** = $p \leq 0.01$; *** = $p \leq 0.001$; ns = not significant; Year-season = dam year-season of birth interaction; DKS = dam kidding season; DKA = dam kidding age

5.5.3. Univariate linear animal models under restricted maximum likelihood (REML) procedures

Log likelihood (LogL) values for different models applied on fixed factors and various milk production traits together with components are summarized in Table 5.3. Models with the highest LogL values were considered to fit the data best for all milk traits and components investigated. LogL values with a difference of not more than 2 units were regarded not to be significantly different ($p > 0.05$). Model 1 included only direct additive/animal genetic effects and was considered to fit all milk production and component traits best. Therefore, suggesting that in this population, milk production and component traits are largely influenced by average variations within genotypes rather than environmental variations within the genotypes.

5.5.4. (Co) variance components and ratios (± s.e.) estimated from univariate linear analysis

This study is the first of its kind to estimate (co) variance components and heritability values for SCCI and NR in South African dairy goat populations. Thus, comparable literature does not exist currently. According to Bagnicka *et al.* (2016) until recently, little information existed on genetic parameter estimates for lactose and SCC in dairy goat populations. This may have been a result of such traits being considered economically less important and excluded from selection indices compared to production traits such as lactation milk, fat and protein yields. Results on additive genetic variance, permanent environmental variance, phenotypic variance and direct heritability estimates; together with their respective ratios for various traits investigated in this study are presented on Table 5.4. Heritability values in the present study ranged from moderate to high, with estimates of 0.42 ± 0.03, 0.38 ± 0.03, 0.39 ± 0.03, 0.22 ± 0.03, 0.40 ± 0.03, 0.38 ± 0.03, 0.28 ± 0.05 and 0.20 ± 0.03 obtained for MY, FY, PY, LY, Urea, NR, P and SCCI respectively. Present results entail that genetic selection and improvement of these traits is possible if included in selection indices for this population.

Table 5.3 Log-likelihood (LogL) values obtained from uni-variate linear analysis for various models evaluated under each trait

Trait	FE	M1	M2	M3	M4	M5	M6
Milk yield	-9577.11	-9430.36	-9430.36	-9430.36	-9430.36	-9430.36	-9432.66
Fat yield	-8818.42	-8702.86	-8702.86	-8702.86	-8702.90	-8702.86	-8703.85
Protein yield	-9536.89	-9420.56	-9420.54	-9420.56	-9420.10	-9420.54	-9419.70
Lactose yield	-3276.13	-3240.77	-3240.77	-3240.77	-3238.89	-3240.77	-3238.44
Urea concentration	-8873.76	-8742.93	-8742.93	-8742.93	-8742.84	-8742.93	NC
Net returns	-4576.62	-4469.00	-4469.00	-4469.00	-4469.40	-4469.00	-4471.47
Persistency	-5253.79	-5235.89	-5235.89	-5235.89	-5235.91	-5235.89	-5235.90
Somatic cell count index	-2314.38	-2282.61	-2282.61	-2282.61	-2282.67	-2282.61	-2282.62

MY = milk yield; FY =fat yield; PY = protein yield; LY = lactose yield; Urea = Urea concentration; NR = net returns; P = persistency; SCCI = somatic cell count index; NC = not converged

Table 5.4 (co) variance components and direct heritability estimates of various traits; together with their respective ratios (± s.e) estimated from uni-variate linear model

Trait	**h^2 ± s.e**	**σ^2_A ± s.e**	**σ^2_C ± s.e**	**σ^2_P ± s.e**
Milk yield	0.42 ± 0.03	115 ± 9.05	157 ± 5.06	272 ± 8.08
Fat yield	0.38 ± 0.03	60 ± 5.03	98 ± 3.04	158 ± 05
Protein yield	0.39 ± 0.03	115 ± 10.02	180 ± 6.05	295 ± 9.05
Lactose yield	0.22 ± 0.03	5 ± 0.08	17 ± 0.08	22 ± 0.08
Urea concentration	0.40 ± 0.03	64108 ± 5560.01	97815 ± 3468.06	65 ± 5181.06
Net returns	0.38 ± 0.03	39139 ± 3825.09	63366 ± 2501.06	41 ± 3595.05
Persistency	0.28 ± 0.05	470 ± 88.06	1187 ± 73.01	1656 ± 73.04
Somatic cell count index	0.20 ± 0.03	1 ± 0.01	3 ± 0.01	3 ± 0.01

h^2 = direct heritability estimate; σ^2_A = additive variance; σ^2_C = environmental variance; σ^2_P = phenotypic variance.

According to Griffiths *et al*. (2000) high heritability values do not necessarily imply that the traits are not influenced by the environment. However, although environmental factors influence some of these traits. Majority of the variation in performance of animals is accounted for by variation in genetic composition of animals. Present results did not differ substantially with values obtained by other authors previously reported in literature. Although no information currently exist on genetic parameter estimates for SCCI in dairy goat populations. Several studies have been previously carried out to estimate heritability values, as well as (co) variance components for both SCC and SCS in dairy goat populations. Subsequently, previous estimates on the two can be used as a baseline to compare with current results obtained on SCCI.

Pizarro-Inostroza *et al.* (2020) found increases in heritability estimates of milk, fat, protein, lactose and SCC yields when the model including genotype effects was considered in analysis. Bagnicka *et al*. (2016) estimated moderate heritability value ($h^2 = 0.21$) for SCS in Polish White Improved (PWI) and Polish Fawn Improved (PFI) dairy goat populations. While an estimate of 0.20 has been reported for SCS in a New Zealand dairy goat population (Morris *et al*., 2011). For French Saanen and Alpine dairy goat populations, Rupp *et al*. (2011) estimated a moderate heritability value of 0.24 for SCS. In a New Zealand dairy goat population, Apodaca-Sarabia *et al*. (2009) found increases in heritability values of SCS (0.12 - 0.25 from early to late lactation) as lactation length increased.

Using sire model, Boichard *et al*. (1989) reported high heritability values for lactation milk yield and percentages of both fat and protein ($h^2 = 0.31$, 0.47 and 0.41 for milk yield, fat and protein percentages respectively) for first lactation Saanen goats participating in the French milk recording scheme. Iloeje *et al*. (1981) also applied sire model and found a high estimate of 0.53 for milk yield. In Jersey cows, Poulsen *et al*. (2015) reported a moderate genomic heritability value for SCC ($h^2 = 0.18$). While high genomic heritability values were also reported on protein, fat and urea yields in both Jersey cows ($h^2 =0.66$, 0.38 and 0.80 for protein, fat and urea respectively) and Holstein populations (0.40 for protein, 0.33 for fat and 0.29 for urea). Applying the REML approach, Hermiz *et al*. (2002) obtained a high heritability value for milk yield in an Iraqi local goat population ($h^2 = 0.46$). While Kala and Prakash (1990) estimated high heritability values for milk yield applying both sire and ANOVA models in Jamunapari and Barbari goat populations ($h^2 = 0.40$ and 0.36 for Jamunapari and

Barbari populations respectively). Castañeda-Bustos *et al*. (2014) obtained high heritability estimates of 0.37 and 0.38 for milk and protein yields respectively in US dairy goat population. Rout *et al*. (2017) used records of 140 and 305 days in lactation and obtained high heritability values of 0.28 and 0.25 respectively for total milk yield in a Jamunapari goat population.

Heritability values obtained in the current study vary from estimates obtained by Brito *et al*. (2011) who reported values of 0.19 for milk yield, 0.10 for fat yield, 0.12 for protein yield and 0.15 for lactose yield in Alpine and Saanen goat populations. Variation in estimates between current and past results may have been pertained to the differences in lactation length (305d vs 270d), breed (Saanen and Alpine vs Saanen), partitioning of animals into genetic groups based on breed composition (not done in the current study) and number of kidding orders accounted for (6 vs 7). Using 90 days milk yield records, Rout *et al*. (2017) reported heritability estimate of 0.15 for total milk yield in a Jamunapari goat population. In Kenyan low input smallholder systems, Bett *et al.* (2012) estimated a low heritability value of 0.15 for SCC. Variation in management practices applied in each system may have influenced difference in results obtained.

Torres-Vázquez *et al*. (2009) calculated moderate heritability values for lactation milk, fat and protein yields (h^2 = 0.17, 0.19 and 0.17 respectively) in a Mexican Saanen goat population. The use of only first lactation records, as well as genotype by environment effect could have contributed to difference in values obtained between present and past study. Poulsen *et al*. (2015) found high genomic heritability values of 0.32 and 0.49 for SCC and lactose in Holstein cows. The difference in methods of analysis between the two studies (quantitative vs molecular genetics) may have influenced variation in values obtained. For the South African dairy goat herd, Muller (2005) reported moderate heritability values of 0.21 for milk yield, 0.19 for fat yield and 0.20 for protein yield. The use of fully pedigreed lactation records in the present study, changes in genetic composition of animals as well as environmental conditions across various production years, differences in lactation length (≥ 305d vs ≥ 60d records) probably influenced variation in results obtained between the two studies

5.5.5. Genetic and phenotypic correlations obtained from bi-variate linear analysis

Results on genetic and phenotypic correlations between various traits are presented on Table 5.5. Genetic correlation between SCCI and all traits except LY (r_g = 0.004) were in a negative direction and ranged from low to moderate (r_g = -0.23, -0.13, -0.25, -0.09, - 0.22 and -0.37 for MY, FY, PY, urea, NR and P respectively). Furthermore, all correlation coefficients were not significant ($p > 0.05$), while their respective phenotypic correlation estimates were significant ($p < 0.05$). Phenotypic correlated responses were negative and low between SCCI and P (r_p = -0.19), as well as between SCCI and LY (r_p = -0.02). While very low and positive correlations existed between SCCI and other traits (r_p = 0.02, 0.07, 0.02, 0.07 and 0.006 for MY, FY, LY, urea and NR respectively). High and positive genetic correlations existed between MY and other traits (r_g = 0.97, 0.94, 0.95, 0.74 and 0.99 for FY, PY, urea, P and NR respectively) except LY (r_g =0.03), with genetic relationship between the two not significant ($p >$ 0.05). While phenotypic correlation estimates between MY and all traits investigated were positive and significant ($p < 0.05$). Most notably, phenotypic correlation estimates between MY and other traits except SCCI (r_p = 0.02) and P (r_p = 0.33) were very close to their respective genetic correlation values (r_p = 0.95, 0.91, 0.03, 0.92 and 0.92 for FY, PY, LY, urea and NR respectively). Therefore, suggesting that phenotypic selection of these traits may have similar efficiency as genetic selection.

Fat yield was negatively correlated to LY (r_g -0.03), while the genetic relationship between the two was also not significant ($p > 0.05$). Genetic correlation between FY and other traits were all significant ($p \leq 0.05$), with high values in a positive direction (r_g = 0.95 for PY, 0.96 for urea, 0.99 for NR and 0.74 for P) estimated between these traits. Phenotypic correlation estimates between FY and these traits were both in a positive direction and significant ($p \leq 0.05$. Furthermore, similar to the case of MY, phenotypic correlation coefficients between FY and other traits except P (r_p = 0.26) were also close to their respective genetic correlation coefficients (r_p =0.94, 0.02, 0.96 and 0.97 for PY, LY, urea and NR respectively). A very low and positive genetic correlation existed between PY and LY (r_g = 0.001), while correlation between the two was not significant ($p > 0.05$).

Table 5.5. Genetic (above diagonal) and phenotypic (below diagonal) correlations obtained from bi-variate linear model

Traits	**Milk yield**	**Fat yield**	**Protein yield**	**Lactose yield**	**Urea concentration**	**Net returns**	**Persistency**	**Somatic cell count index**
Milk yield	-	0.97**	0.94*	0.03^{ns}	0.95**	0.99**	0.74*	-0.23^{ns}
Fat yield	0.95***	-	0.95**	-0.03^{ns}	0.96**	0.99**	0.74*	-0.13^{ns}
Protein yield	0.91***	0.94**	-	0.001^{ns}	0.96**	0.92**	0.52*	-0.25^{ns}
Lactose yield	0.03*	0.02*	0.004*	-	-0.01^{ns}	0.11*	0.17^{ns}	0.004^{ns}
Urea concentration	0.92**	0.96**	0.98**	0.002**	-	0.92**	0.58*	-0.09^{ns}
Net returns	0.92**	0.97**	0.87**	0.07*	0.88**	-	0.76*	-0.22^{ns}
Persistency	0.33*	0.26*	0.16*	0.03*	0.17*	0.35*	-	-0.37^{ns}
Somatic cell count index	0.02*	0.07*	0.02*	-0.02*	0.07*	0.006*	-0.19***	-

* = $p \le 0.05$; ** = $p \le 0.01$; *** = $p \le 0.001$; ns = not significant

Positive genetic correlated responses ranging between moderate and high existed between PY and NR ($r_g = 0.92$), PY and P ($r_g = 0.52$), as well as between PY and urea ($r_g = 0.92$). Phenotypic correlation values between PY and other traits, except SCCI ($r_p = 0.02$) and P ($r_p = 0.16$) were also close to their respective genetic correlation estimates (r_p =0.04 for LY, 0.98 for urea, 0.87 for NR). A low, negative and significant ($p < 0.05$) genetic relationship existed between LY and urea ($r_g = -0.01$), while correlations with other traits and components were all not significant ($p > 0.05$), in a positive direction and very low ($r_g = 0.11$ and 0.17 for NR and P respectively). Phenotypic association between urea and P was significant ($p < 0.05$), in a positive direction and low ($r_p = 0.17$). While a high and positive phenotypic relationship existed between urea and NR ($r_p = 0.88$). High and positive genetic correlated responses existed between urea and P ($r_g = 0.58$), and between urea and NR ($r_g = 0.92$). Genetic correlation between NR and P was high and in a positive direction ($r_g = 0.76$), while phenotypic correlation between the two was positive and moderate ($r_p = 0.35$).

Present study is the first of its kind to estimate correlations between production traits (MY, FY, PY, LY), components (urea and SCCI) together with lactation NR and P in the South African Saanen goat population. Current results suggest that selecting for an increased lactation MY, either through phenotypic or genetic selection schemes will improve lactation milking performances of FY, PY, LY, urea and P. Therefore, also increasing herd lactation NR. Furthermore, genetic selection for improvement of all traits investigated will not significantly ($p > 0.05$) influence lactation SCCI yield. While selecting for an increased lactation LY will not significantly ($p > 0.05$) influence responses in both lactation P and NR.

Present results did not differ substantially with the findings of other authors (Boichard *et al*., 1989; Muller, 2005; Torres-Vázquez *et al*., 2009; Brito *et al*., 2011) who calculated genetic correlation values close to their respective phenotypic and also concluded that selecting for increased lactation milk yield would result in highly favorable correlated responses of both fat and protein yields. Morris *et al*. (2011) estimated negative genetic correlations ranging from low to moderate between SCC and other milk production traits in a New Zealand Saanen goat population ($r_g = -0.29$, -0.18 and -0.24 for lactose yield, protein yield and fat yield respectively). While a moderate genetic and phenotypic correlation values between milk yield and SCC were reported (r_g and $r_p = -0.27$ and -0.24 respectively).

Between SCS and other milk production traits (yields for milk, fat and protein), Scholtens *et al*. (2018) reported low and negative genetic (r_g = -0.02, -0.06 and -0.04 for milk, fat and protein respectively) and phenotypic (r_p = -0.10, -0.13 and -0.08 for milk, fat and protein respectively) relationships in a New Zealand mixed breed dairy goat population. Jeretina *et al.* (2017) stated that in order to improve herd management, it is essential to take into consideration both the dynamics and peaks in levels of somatic cell count that are attributed with daily milk yield losses during lactation period. Furthermore, SCCI can reliably be used as an indicator of intra-mammary infections (IMI) because it has the potential to allow a mutual comparison of milk yield losses that are attributed to levels of SCC across dams. Therefore, monitoring of these levels is essential for herd productivity.

In other species, König *et al.* (2008) estimated high genetic correlation value, in a positive direction between milk yield and milk urea nitrogen (r_g = 0.44) in Holstein cows. Otwinowska-Mindur and Ptak (2015) stated that one of the most important characteristics in measuring persistency is its correlation with lactation milk yield (305d milk yield). When using records of first, second and third parity records, Shokri-Sangari *et* al. (2019) obtained high and positive genetic correlation values between lactation milk yield and lactation persistency in Holstein cows (r_g = 0.63, 0.75 and 0.70 for first, second and third parity records respectively).

Current results are also in contrast with past findings reported in literature. Brito *et al*. (2011) reported high and positive genetic correlation values between yields for milk and lactose (r_p = 0.98). Genetic grouping of animals in the past study, difference in lactation length (270d vs 305d), genotype by environment interaction, as well as variation in number of breeds studied (Saanen and Alpine vs Saanen) may have influenced variations between past and current estimates. Pizarro-Inostroza *et al*. (2020) obatined moderate and negative correlations between milk yield and fat yield when genotype was included as a fixed effect in the model of analysis (r_g and r_p = -0.42 and -0.41 respectively). While a low genetic correlation value, in a positive direction was estimated between yields for milk and protein (r_g = 0.09). A moderate phenotypic correlation, in a negative direction was reported between the two (r_P = -0.48). A low and positive phenotypic association was reported between milk yield and lactose yield (r_p = 0.12), while a low genetic correlation value, in a negative direction was reported between the two (r_G = -0.07). The inclusion of genotype (dominance, additive and epistatic factors) as a fixed effect in the past study could have led to difference in estimates. In a study on crosses between Anglo Nubia and Criolla goat populations, Pesátez *et al*. (2014) calculated a phenotypic correlation value of 0.20 between total milk yield and lactation persistency. While Siqueira *et al*. (2017) reported an estimate of 0.39 between the two. Čobanovič *et al*. (2019) found a negative genetic association (r_g = -0.18) between daily milk yield and urea in a Saanen goat population. Difference in values obtained between past and current investigations were probably influenced by categorizing of animals based on dietary crude levels fed in the past study (feeding levels are uncertain in the current study). According to Silva-del-Rio, (2011) milk urea concentration levels can be reliably used as a tool to monitor dietary crude protein levels in dairy herds. Therefore, because the levels of urea concentration are highly variable across dairy herds, the best approach is to assess groups within herds and based on dam to dam variation within a group. Bagnicka *et al*. (2016) obtained high and genetic correlation values between daily milk yield and SCS (0.59) in Polish White Improved (PWI) and Polish Fawn Improved (PFI) populations. Breed differences, as well as genotype by environment interaction could have influenced variation in results obtained. For a Spanish Murciano-Granadina goat population, scientists Pizarro- Inostroza *et al*. (2020) obtained low and negative genetic correlation between SCC and lactose yield when genotype was included as fixed effect (-0.22).

5.6. Conclusion and Recommendations

Present study estimated genetic parameters for lactation milking performances of various economically important traits in the South African Saanen goat population. Heritability estimates obtained ranged from moderate to low and compared well values previously reported in literature. Therefore, genetic selection and improvement of these traits can be achieved through their inclusion in selection indices for the population. Lactation MY and SCCI had the highest heritability values amongst all traits investigated. This is probably because more intense selection for and against these traits, aimed at increasing MY while reducing SCCI has been rapidly applied in the population. Genetic correlation between lactation MY and other traits (FY, PY, urea, NR and P) are all high and positive indicating favorable correlated genetic responses to selection in these traits arising from selecting for increased MY. Furthermore, phenotypic correlation coefficients between MY and these traits except

P are close to their respective genetic correlation values. Therefore, on farm phenotypic selection of animals with better lactation milking performance can lead to genetic progress.

More efforts need to be made in making dairy goat farmers realize the importance of participating in official milk recording schemes. Furthermore, recording systems should be more improved and easily accessible for the convenience of farmers and allow more precise recordings of herds and pedigree profiles. Genetic parameter estimates obtained in this study should be further used for estimation of breeding values of these traits.

CHAPTER 6

6.0. General Discussion, Conclusions and Recommendation

6.1. General Discussion

The difference in results obtained from analyses for non-genetic significant effects between non-pedigreed and fully pedigreed lactation records from this study highlighted the powers of including genetic effects in statistical models of analysis, sample size and data pruning. Although there were similarities in some instances, results from analysis of non-pedigreed records on non-genetic significant effects are probably more logical due to large sample size. Chances of observing extreme values were reduced in the experiment, while observed values for the statistic probably grouped more closely to sampling distribution mean. Therefore, the sample variance probably estimated the population variance with more precision compared to the other analysis due to large number of observations in the experiment.

Results from both experiments revealed high and positive phenotypic correlations between MY and FY, MY and PY, and MY and NR. While phenotypic correlation coefficients between MY and SCCI from both analyses were significant, low and positive. Both analyses suggest that selecting for increased lactation MY would result in favourable correlated responses of FY, PY and LY, while also increasing herd lactation NR. These estimates were close to values reported in literature by previous authors (Muller, 2005; Scholtens *et al.,* 2018; Roveglia *et al*. (2019), who also found high relationship between these traits. Although currently no comparable literature exists on genetic and phenotypic relationships between SCCI and other traits. The increases in lactation SCCI levels arising from selecting for improved lactation MY were probably attributed to increases in number of body cells as milk production increases.

Phenotypic correlation coefficients obtained from both analyses showed low and negative association between P and SCCI. Jingar *et al.* (2014) reported decreases in lactation persistency as lactation order increases. Because high levels of SCC are usually found in older animals, P will reduce as age increases due to lactation curve in young animals being flatter than in older animals. Although MY, FY and PY were all positively correlated to urea in both analyses, values obtained from analysis of non-pedigreed data were all low. While fully pedigreed data analysis results showed high and positive relationships. Phenotypic correlation coefficients between LY and urea from both analyses were positive and low. Results from analysis of fully pedigreed records showed a negative association between MY and urea, while a low and positive relationship between the two was revealed by analysis of non-pedigreed lactation records. Results from analysis of non-pedigreed lactation records revealed negative association between MY and P, while estimates obtained from analysis of fully pedigreed records revealed a moderate, positive and significant relationship between the two.

FY, PY and LY were positively correlated to P in both analyses, with low coefficient estimates obtained. A low and negative phenotypic relationship between SCCI and NR was obtained in analysis of non-pedigreed lactation records, while estimate found in analysis of fully pedigreed data was also not far (very low and positive relationship). Increases in levels of SCCI will lead to a decline in the quality of milk. Therefore, as a result herd lactation NR will also decrease probably due expenses attributed to treatment of positive cases, etc.

Heritability values obtained suggest that inclusion of these traits in selection indices for the population can result in genetic progress. Genetic correlation coefficients between lactation MY and FY, MY and PY, MY and urea, as well as between MY and NR obtained in this study indicate favorable correlated response to genetic selection in these traits as a result of selecting for increased lactation MY. Furthermore, because phenotypic correlation coefficients between MY and these traits are also close their respective genetic correlation values. These traits can also be improved and selected through phenotypic selection schemes. Thus, recording and inclusion of these traits is essential in selection programs. Although the correlation coefficients were not significant, increases in levels of intra-mammary infections during lactation will result in reduced lactation yields for all traits except LY while also reducing enterprise NR per lactation.

6.2. Conclusions of the study

In this population, most of the variation in lactation milking performances of these traits were attributed to variation in genotypes rather than environmental variation within genotypes. There have been some improvements in yields during recent years in the population. These improvements are probably a result of more intense selection methods that are based on genetic predictions being applied in most herds, whereby only genetically superior animals are used for breeding. Animals born and kidding during spring season give highest lactation milking performances of these traits compared to the rest of the seasons. Majority of animals in this population (80%) kid during spring season. Thus, dairy goat production in the country is seasonal and planned breeding should be applied. Subsequently, investments in large scale processing and preserving facilities in the industry are essential to warrant a sufficient annual supply of goat milk together with its by-products to the markets.

Dams beyond 6th lactation produce less quality milk, while 3rd parity dams give highest lactation milking performances. Multiple litter kidding animals have a better lactation milking performance compared to single litter kidding groups. Selection for increased MY would result in favourable correlated responses of other traits such as FY, PY and P thus, leading to increased herd NR. Furthermore, because genetic correlation estimates between these traits are close to their respective phenotypic correlation values. Genetic progress can be achieved through phenotypic selection schemes. Therefore, phenotypic recording of these traits is essential.

6.3. Recommendations and scope for further study

More efforts need to be put in to educate dairy goat farmers about the importance of participating in official milk recording schemes as this would lead to more pedigree and performance data becoming available, to allow more precise genetic and phenotypic characterizations. With advancement in lactation order, SCCI levels increase while the quality of milk tends to decrease. This leads to reduced enterprise lactation NR and thus, animals beyond 6th parity are not recommended for optimal lactation milking performance. Multiple litter kidding groups are preferred over single litter kidding animals for optimal lactation milking performance. The most ideal breeding season for this population is during Autumn season (March – April) to allow animals to kid during spring season. Phenotypic correlation estimates can be reliably used in place of genetic correlations where their respective estimates are close and pedigree data that is linked to performance data is unavailable.

Selecting for increased lactation MY is recommended as it would increase lactation NR in herds, as well as improve lactation milking performances of other traits such as

FY, PY and P. Investigations based on the current data need to be conducted using pedigree information from either the dam, sire or both to compare with the current results. Moreover, breeding values should be estimated for these traits and components using the current genetic parameter estimates to compare with previous studies.

CHAPTER 7

7.0. References and Appendices

7.1. References

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7.2 Appendices

7.2.1. Analysis of variance (ANOVA) table for non-pedigreed data used

Appendix 7.1: Analysis of variance for non-genetic factors affecting lactation milk yield (MY) in the South African Saanen goat population.

Source of variation	DF	SS	MS	F-Value	P-Value
Kidding age (months)	1	1029337	1029337	8.13	0.004
Birth Season	3	1209742	403247	3.18	0.023
Birth Year	61	63877253	1047168	8.27	0.000
Kidding Season	3	1103953	367984	2.91	0.033
Parity	6	31298502	5216417	41.19	0.000
Litter Size	2	2003621	1001810	7.91	0.000
Error	9107	1153237785	126632		
Lack of Fit	7715	1071666056	138907	2.37	0.000
Pure Error	1392	81571730	58600		
Total	9183	1256911541			

DF = degree of freedom; SS = sum of squares; MS = mean of squares

Appendix 7.2: Analysis of variance for non-genetic factors affecting lactation fat yield (FY) in the South African Saanen goat population.

Source of variation	DF	SS	MS	F-Value	P-Value
Kidding age (months)	1	4841	4841.29	23.56	0.000
Birth Season	3	1071	357.06	1.74	0.157
Birth Year	61	424238	6954.72	33.85	0.000
Kidding Season	3	1655	551.55	2.68	0.045
Parity	6	30163	5027.15	24.47	0.000
Litter Size	2	346	173.02	0.84	0.431
Error	9106	1871093	205.48		
Lack of Fit	7714	1748471	226.66	2.57	0.000
Pure Error	1392	122623	88.09		
Total	9182	2505141			

DF = degree of freedom; SS = sum of squares; MS = mean of squares

Appendix 7.3: Analysis of variance for non-genetic factors affecting lactation protein yield (PY) in the South African Saanen goat population

Source of variation	DF	SS	MS	F-Value	P-Value
Kidding age (months)	1	3095	3094.44	24.54	0.000
Birth Season	3	635	211.69	1.68	0.169
Birth Year	44	129686	2947.41	23.38	0.000
Kidding Season	3	627	209.02	1.66	0.174
Parity	6	21816	3635.98	28.84	0.000
Litter Size	2	562	280.76	2.23	0.108
Error	8784	1107521	126.08		
Lack of Fit	7404	1032793	139.49	2.58	0.000
Pure Error	1380	74728	54.15		
Total	8843	1289461			

DF = degree of freedom; SS = sum of squares; MS = mean of squares

Appendix 7.4: Analysis of variance for non-genetic factors affecting lactation lactose yield (LY) in the South African Saanen goat population.

Source of variation	DF	SS	MS	F-Value	P-Value
Kidding age (months)	1	1761	1761.10	6.89	0.009
Birth Season	3	1662	554.10	2.17	0.090
Birth Year	35	84523	2415	9.44	0.000
Kidding Season	3	2327	775.70	3.03	0.028
Parity	6	44737	7456.10	29.16	0.000
Litter Size	2	2856	1427.90	5.58	0.004
Error	8194	2095416	255.70		
Lack of Fit	7014	1945786	277.40	2.19	0.000
Pure Error	1180	149629	126.80		
Total	8244	2234274			

DF = degree of freedom; SS = sum of squares; MS = mean of squares

Appendix 7.5: Analysis of variance for non-genetic factors affecting lactation net returns (NR) in the South African Saanen goat population.

Source of variation	DF	SS	MS	F-Value	P-Value
Kidding age (months)	1	91963	91963	0.83	0.363
Birth Season	3	1067484	355828	3.20	0.022
Birth Year	24	20537908	855746	7.69	0.000
Kidding Season	3	1434869	478290	4.30	0.005
Parity	6	12050859	2008477	18.05	0.000
Litter Size	2	2314031	1157016	10.40	0.000
Error	4058	451454961	111.251		
Lack of Fit	3698	420557363	113726	1.33	0.000
Pure Error	360	30897598	85827		
Total	4097	541548779			

DF = degree of freedom; SS = sum of squares; MS = mean of squares

Appendix 7.6: Analysis of variance for non-genetic affecting lactation persistency (P) in the South African Saanen goat population.

Source of variation	DF	SS	MS	F-Value	P-Value
Kidding age (months)	1	7086	7086	4.06	0.044
Birth Season	3	12597	4199	2.41	0.065
Birth Year	24	217365	9057	5.19	0.000
Kidding Season	3	19001	6334	3.63	0.012
Parity	6	412498	68750	39.38	0.000
Litter Size	2	14408	7204	4.13	0.016
Error	4057	7082284	1746		
Lack of Fit	3697	6458662	1747	1.01	0.465
Pure Error	360	623622	1732		
Total	4096	8871151			

DF = degree of freedom; SS = sum of squares; MS = mean of squares

Appendix 7.7: Analysis of variance for non-genetic factors affecting lactation somatic cell count index (SCCI) in the South African Saanen goat population.

Source of variation	DF	SS	MS	F-Value	P-Value
Kidding age (months)	1	0.70	0.6797	0.21	0.650
Birth Season	3	19.90	6.6490	2.02	0.109
Birth Year	24	473.90	19.7459	5.99	0.000
Kidding Season	3	68	22.6671	6.87	0.012
Parity	6	275.90	45.9825	13.94	0.000
Litter Size	2	52.80	26.4138	8.01	0.000
Error	3677	12125.70	3.2977		
Lack of Fit	3355	11299.80	3.3680	1.31	0.001
Pure Error	322	825.90	2.5650		
Total	3716	14104			

DF = degree of freedom; SS = sum of squares; MS = mean of squares

Appendix 7.8: Analysis of variance for non-genetic factors affecting lactation urea concentration (urea) in the South African Saanen goat population.

Source of variation	DF	SS	MS	F-Value	P-Value
Kidding age (months)	1	9.20	9.246	0.43	0.512
Birth Season	3	232.60	77.534	3.61	0.013
Birth Year	19	4922.90	825.90	36.59	0.000
Kidding Season	3	165.90	55.301	2.58	0.052
Parity	6	1017.70	169.618	7.90	0.000
Litter Size	2	159.30	79.669	3.71	0.025
Error	2952	63364.20	21.465		
Lack of Fit	2685	59732.40	22.247	1.64	0.000
Pure Error	267	3631.80	13.602		
Total	2986	82514.10			

DF = degree of freedom; SS = sum of squares; MS = mean of squares