

**Genetic Parameter Estimates for Milkability Traits in South**

**African Holstein Cattle**

**By**

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## DECLARATION

I, Thendo Stanley Tshilate, declare that this dissertation is my original work and has not been submitted for any degree at any other university or institution. The dissertation does not contain other persons' writing unless specially acknowledged and referenced accordingly.

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## ABSTRACT

Milkability, or ease of milking, is the rate at which milk can be completely drawn from a cow's udder. It is an important functional trait with regard to milking costs as well as udder health. Milkability traits have not been included in the breeding objectives of South African dairy cattle and their genetic parameters in the population have not been estimated. The primary objective of the study was to estimate genetic parameters for milkability traits in South African Holstein cattle. Data consisted of production and milkability records of 1 532 Holstein cows, from 6 herds, participating in the South African National Dairy Animal Recording and Improvement Scheme during the period 2015 to 2016 . Measures of milkability were average milk flow (AMF), maximum milk flow (MMF) and milking time (MT). Genetic parameters were estimated by a multi-trait sire model using the Restricted Maximum Likelihood (REML) procedure. Means for AMF, MMF and MT were 1.99 kg/min, 3.02 kg/min and 5.50 min, respectively. Non-genetic factors affecting variation in milkability traits were herd-year-season of calving, parity and milk yield. Heritability estimates for AMF, MMF, and MT were  $0.23 \pm 0.09$ ,  $h^2 = 0.41 \pm 0.12$  and  $h^2 = 0.36 \pm 0.11$ , respectively. Genetic correlations between the three milkability traits were medium to high, ranging from  $-0.35 \pm 0.23$  between AMF and MT to  $0.79 \pm 0.09$  between AMF and MMF. Correlations were positive between AMF and MMF and negative between MT and the other two traits. There was an increase in the mean EBV for AMF of 0.002 kg/min (0.0001 kg/min per year) during the period 2002 to 2014. Maximum milk flow also showed an increasing genetic trend of 0.04 kg/min (0.0003 kg/min per year) over the same period. The genetic trend for MT was undesirable, as it increased by 0.0003 kg/min. There is scope for improving milkability through selection, in South African Holstein cattle, as indicated by the moderate to high heritability estimates. The favourable genetic correlations among milkability traits imply that selection on one trait will result in a correlated improvement in the others. Results of the current study provide a basis for including milkability traits in the breeding objective for South African Holstein cattle.

**Keywords:** Genetic parameters, average milk flow, maximum milk flow, milking time, genetic trends.

## DEDICATIONS

This dissertation is dedicated to my late Mom and my family as a whole who has always been the light for me and there for me. You have always wished the best out of me, you are the best family and this is for you.

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## ABBREVIATIONS

AMF	Average milk flow
ARC	Agricultural Research Council
BLUP	Best linear unbiased prediction
CV	coefficient of variation
EBV	Estimated breeding value
$h^2$	Heritability
HYS	Herd-year-season
MMF	Maximum milk flow
MT	Milking time
REML	Restricted maximum likelihood
$r_g$	Genetic correlation
$r_p$	Phenotypic correlation
SD	Standard deviation

## CHAPTER 1 INTRODUCTION

### 1.1. Background

Milkability or ease of milking is defined as the rate at which milk is completely drawn from a cow's udder (Banga, 2009; Heringstad and Bugten, 2014). It measures the cow's ability to let down milk and to be completely milked. It is characterised by average milk flow (kg/min), maximum milk flow (kg/min) and milking time (min) which provide valuable information about the efficiency and capability of milk release (Zucali *et al.*, 2009). Good milkability is achieved when the milking machine removes milk from the udder gently, quickly and completely (Lee and Choudhary, 2006; Carlstrom, 2014). Generally, the milkability of a cow is expressed as a function of milking speed and milking time, which can be measured by either manual scoring or using specially designed instruments (Lee and Choudhary, 2006).

Milkability is an important functional trait with regard to udder health as well as labour efficiency (Gade *et al.*, 2007; Antalík and Strapák, 2010). Slow milking cows delay the milking process of the herd, particularly in milking parlours (Mijic *et al.*, 2007; Strapák *et al.*, 2011). On the other hand, an increase in milking speed results in decreased milking labour time, leading to lower labour costs and reduced costs for electrical power and weariness of milking equipment (Lee and Choudhary, 2006; Gray *et al.*, 2012; Vosman *et al.*, 2014). Milk flow disorders cause an economic loss because of an increased risk of mastitis (Querengasser *et al.*, 2002). There is, however, evidence that faster milking cows could be more susceptible to udder health problems (El-Awady and Oudah, 2011; Lee and Choudhary, 2006).

Inclusion of milkability in the breeding objective requires knowledge of its genetic variation as well as its relationship with other traits. Studies show heritability estimates for milkability traits in the ranges of 0.55 to 0.56 for maximum milk flow, 0.14 to 0.55 for average milk flow and 0.17 to 0.44 for milking time, with genetic correlations between -0.20 and 0.98

among these traits (Luttinen and Juga, 1997; Zwald *et al.*, 2005; Lee and Choudhary, 2006; Gade *et al.*, 2007; Guler *et al.*, 2009). The genetic correlation estimates between milkability traits and somatic cell score (SCS) were moderate to high (0.22-0.89) and the genetic correlation between milkability and clinical mastitis were negative, ranging from -0.5 to almost zero (Luttinen and Juga, 1997; Rupp and Boichard, 1999)

The evaluation of milkability traits is important in connection with establishing the efficiency of milk ejection (Strapak *et al.*, 2011). Milkability traits are currently not included in the national genetic evaluation programme for South African dairy cattle. The primary objective of this study was to estimate genetic parameters required to incorporate milkability in the breeding objective for the South African Holstein cattle. Genetic correlations between milkability traits were determined in order to enable a combined evaluation of these traits in a multiple trait analysis. Such an approach will help to increase the accuracy of selection and simultaneous improvement of milkability.

## **1.2. Research Problem**

Milkability is an important functional trait and is increasingly being included in dairy selection objectives worldwide (Zwald *et al.*, 2005; Lee and Choudhary, 2006; Gade *et al.*, 2007; Dodenhoff and Emmerling, 2008). Cows with high genetic merit for milkability have, however, been found to be more susceptible to mastitis. Milkability traits have not been included in the breeding objectives of South African dairy cattle and their genetic parameters have not been estimated. Genetic parameter estimates are, however, a prerequisite to estimating the breeding values of a trait as well as its inclusion in the breeding objective. This study's aim was to produce estimates of genetic parameters for milkability traits and their correlations. The information will enable selection for improvement of both milkability and udder health traits in Holstein cattle in a way that will maximize overall economic gain. Therefore, the study will benefit dairy farmers particularly those utilizing the Holstein breed.

### **1.3. Objectives of the study**

#### *1.3.1. Overall objective*

The overall objective of the study was to estimate genetic parameters of milkability traits in South African Holstein cattle.

#### *1.3.2. Specific objectives*

The specific objectives were to estimate the following parameters for South African Holstein cattle:

- i) Heritabilities of average milk flow, maximum milk flow, and milking time.
- ii) Genetic correlations among milkability traits.
- iii) Genetic trends for milkability traits.

### **1.4. Hypotheses**

The null hypotheses tested in the study were:

- i) There is no significant genetic variation in average milk flow, maximum milk flow, and milking time.
- ii) There are no relationships among milkability traits.
- iii) There is no genetic trend for milkability traits.

## CHAPTER 2 LITERATURE REVIEW

### 2.1. Introduction

The goal of any dairy farmer is to deliver a high quality product that has consumer demand (Jones, 2009). High milk production, increased milking speed, limited milking time and healthy udders are priority traits at milking farms (Mijic *et al.*, 2007). Compromised milkability traits (average milk flow, maximum milk flow and milking time) and udder health (absence of mastitis) cause significant economic losses on dairy farms. Economic losses include reduced milk production, lower milk quality, culling cost, labour cost and veterinary services (Zwald *et al.*, 2005; Lee and Choudhary, 2006; El-Awady and Oudah, 2011; Samore *et al.*, 2011).

In recent years, genetic evaluations of udder health have received increasing attention (El-Awady and Oudah, 2011), while milkability traits receive limited attention in dairy cattle breeding (Lee and Choudhary, 2006). In South African Holstein cattle, dairy breeding objectives comprise of milk yield and somatic cell score (Banga *et al.*, 2014); milkability is not considered during selection. This study focused on genetic evaluation of milkability traits and determining the relationship between milkability traits and udder health traits in South African Holstein cattle. This chapter will review some of the studies on milkability and udder health traits.

### 2.2. South African dairy industry

Milk production is an important part of many farming enterprises (MPO, 2015). In South Africa the contribution of milk production makes approximately 0.5% to the world milk production (DAFF, 2012; SA Yearbook, 2013/14). It is also the fifth largest agricultural industry in the country (SA Yearbook, 2013/14). It comprises of organizations that play different roles and these include Milk South Africa, Milk Producers' Organisation (MPO), and Agricultural Research Council (SA Yearbook, 2009/10). Milk South Africa coordinates the

matters related to the South African dairy industry, while the MPO is a voluntary, democratic organisation founded by milk producers to protect general interests and serve as their mouthpiece (SA Yearbook, 2009/10). The Agricultural Research Council (ARC) contributes fully in the Multiple Across-Country Evaluation for all dairy breeds in South Africa. Milk South Africa manages industry matters and is financed by statutory contributions. The National Recording and Improvement Scheme, managed by the ARC, ensures the efficient and economic sustainability of livestock production. It also provides scientific and technical assistance to contributors to assist in making the right decisions (SA Yearbook, 2009/10).

The global industry trend for dairy production is increasing herds with larger numbers of cows (Calstrom, 2014). In South Africa between the year 2001 and 2007 the number of cows per herd has increase while the number of dairy farmers during the same period decreased by 30%. Between the year 2003 and 2007 the average herd size increased from 70 to 138 cows (Scholtz and Grobler, 2009). Correspondingly, in the year 1997 there were about 7077 milk producers in South Africa, in the year 2011 that number had decreased to 4 000 herds (DAFF, 2012).

Dairy farming contributes to the supply of animal protein through the production of milk and other dairy products such as cheese and yoghurt (Kgole, 2013). Total milk production for the whole of South Africa during the year 2011 was 260 000 kg from approximately 890 000 dairy cows (DAFF, 2012). The suitable areas for milk production in South Africa is coastal areas because of mild temperatures as well as good rainfall ensuring good quality natural and planted pastures. The inland production areas are generally climatically less favourable for milk production. Western Cape contribute 27% of the total milk produced in South Africa followed by Eastern Cape and KwaZulu–Natal which contribute up to 24% each, Free State contribute 13%, North–West 5%, Mpumalanga 4%, Gauteng, Northern Cape and Limpopo shared the 3% (DAFF, 2012).

The Holstein is the most popular dairy breed across the world and in South Africa. It is white and black in colour and is a large-framed breed. It is one of four major South African dairy breeds that undergo routine genetic evaluation by the Agricultural Research Council's (ARC) Animal Production Institute (Mostert, 2007; Kgole *et al.*, 2012).

### **2.3. Automatic milking system**

The main reason for advancing the idea about a fully automated milking process into reality was influenced by the fact that labour cost was increasing in the 1970s (Carlstrom *et al.*, 2013; Carlstrom, 2014). An automatic milking system (AMS) provides objective, frequent and accurate measurements of several important traits (Heringstad and Bugten, 2014). It allows each cow to be milked on an individual basis and at a place from which the animal can see its herd, which reduces milking-related stress. Several authors (Edwards *et al.*, 2014; Lee and Choudhary, 2006) have highlighted that, it is important that animals have a positive experience at milking time and do not mind using the AMS. The milking machines currently used allow cows to freely choose the time of milking and to dynamically adjust the inter-milking interval throughout lactation as well as throughout the day (Carlstrom *et al.*, 2013). An AMS allows farmers to monitor milking speed, milking flow and milking duration, which offers opportunities to improve their levels and hence provides a greater potential for profitable dairy production (Gray *et al.*, 2012; Edwards *et al.*, 2014; Sitkowska *et al.*, 2015).

Electronic mobile milk flow meters enable investigators to study in detail milk flow during milking. Data from electronic milk meters that routinely measure milking duration provide a valuable source of information on milking speed and other milking characteristics such as flow rate. Average milk flow and maximum milk flow have been proposed elsewhere as measures of milking efficiency among animals (Gray *et al.*, 2012; Samore *et al.*, 2011).

Good milk flow curve shapes depend on a good balance among man, machine and physiological/anatomical characteristics of the cow and are considered to be related to good milk production, short milking time and good udder health. Studies of milk flow during milking

provide useful information for enhancing the efficiency of the milking process, avoiding some common mistakes, and protecting teat integrity and udder health (Sandrucci *et al.*, 2005; Tamburini *et al.*, 2007).

#### **2.4. Non genetic factors affecting milkability traits**

Knowledge of factors affecting milkability traits is an important pre-requisite for proper use and accurate interpretation of milkability traits data. Non genetic factors affecting milkability traits are environmental factors that can be classified as factors with measurable effects (milking conditions, lactation stage, herd test day, year and age at calving, season and year of calving) and factors with immeasurable effects (infectious diseases, parasitic infestations) (Tancin *et al.*, 2006; M'hamdi *et al.*, 2012).

Milking routine and milking machine affect the shape of milk flow curves. Milk flow rate is maximized when calm cows are milked with a consistent routine at every milking. Proper cow handling and udder preparation will decrease unit on-time. Routines should be consistent from one milking to the next and from one milker to the next (Jones, 2009). First calving cows have been found to be stressed during milking due to close contact with humans (Zucali *et al.*, 2009). The longest main milking phase duration and total milking time with the lowest peak and average milk flow was observed in the cows without prestimulation (Sandrucci *et al.*, 2005; Sandrucci *et al.*, 2007; Salamon *et al.*, 2011). Therefore, prestimulation of cows before the start of milking should be applied to ensure fast and complete milk removal and to maintain proper udder health. Salamon *et al.* (2011) reported that, better udder preparation resulted in greater milk yield per milking, greater peak milk flow rate, shorter total milking time, shorter time of incline phase, and lesser bimodality compared with poorer preparation.

Many researchers (M'hamdi *et al.*, 2012; Guler *et al.*, 2009; Cho *et al.*, 2004) have reported that the effect of calving season on 305 days milk yield was significant and indicated that milk flow rate was higher in autumn and winter. In contrast, Aydin *et al.* (2008)

reported that effect of calving season on milking time and milk flow rate was non-significant. The effect of calving season on milkability traits was significant and milking time was longest in cows calving in winter (M'hamdi *et al.*, 2012). Gade *et al.* (2007) tested the effect of age of calving and found that the different ages of calving within parity do not influence milkability traits.

Parity and stage of lactation has been reported to influence all milkability traits (Guler *et al.*, 2009). Naumann and Fahr (2000) and Guler *et al.* (2009) observed that increasing parity was associated with decreasing average milk flow. Strapak *et al.* (2011) noted that, in relation to parity the highest milk flow rates were measured in second lactation dairy cows. The highest average and maximal milk flow rates were measured in the group of cows in second lactation (M'hamdi *et al.*, 2012). Milking time reported was longest in the first month of lactation and decreased as lactation advanced (Povinelli *et al.*, 2003; Aydin *et al.*, 2008; Guler *et al.*, 2009). Aydin *et al.* (2008) noted that the decrease of milking time on the lactation was about 27.2% below milking time at peak lactation. Povinelli *et al.* (2003) and Tancin *et al.* (2006) stated that milkability traits, or at least one of them vary during lactation. Milk flow rate was relatively stable with slight reduction after 2<sup>nd</sup> month of lactation (Tancin *et al.*, 2006; Aydin *et al.*, 2008). Gade *et al.* (2006) also noted that lactation curve for milk flow rate for dairy cows showed a descending pattern throughout the lactation.

Results of these studies indicate that milkability traits are affected by environmental factors. These factors should be taken into account when interpreting milkability traits results (Sandrucci *et al.*, 2007). Most of the factors affecting milkability traits were caused by herd management factors.

## 2.5. Definition of traits

Genetic parameters such as heritability and phenotypic and genetic correlations are statistical parameters used to measure the genetic component of a trait (Rupp and Boichard, 2003). Milkability traits (average milk flow rate, maximum milk flow and milking time) are traits that are economically important in dairy farming (Erdem *et al.*, 2010, Gray *et al.*, 2012). Average milk flow is defined as the average milk yield measured within a time interval of one minute and the average main milking process per minute. Maximum milk flow is defined as the peak milk flow rate within a time interval of one minute. Milking time is defined as the total milking time, being the time taken from the beginning till the end of the milking process (Tancin *et al.*, 2006; Edwards *et al.*, 2014).

## 2.6. Milkability

Milkability is defined as the average speed with which milk is drawn from the udder and is determined by measuring total milk yield and milking time (Heringstad and Bugten, 2014). Milkability belongs to a group of functional, cost-saving traits in dairy cattle in addition to health, fertility and labour efficiency (Gade *et al.*, 2006; Wiggans *et al.*, 2007; Erdem *et al.*, 2010; Strapak *et al.*, 2011). Milkability of a cow is also measured as milking speed and milking time that can be measured either by manual scoring or with the help of an instrument specially designed for studying milkability traits (Lee and Choudhary, 2005; Gray *et al.*, 2012).

### 2.6.1. Descriptive statistics for milkability traits

Different studies have reported different phenotypic mean values for milkability traits in their studies. These were determined to compare the phenotypic variations of milkability traits of various studies. Literature on descriptive statistics for milkability traits is shown in table 2.1.

Table 2.1. Descriptive statistics for milkability traits in the literature.

	AMF (kg/min)	MMF (kg/min)	MT (min)
Antalik & Strapak, (2010)	1.76	3.08	4.34
Bobic <i>et al.</i> (2014) <sup>Holstein</sup>	2.40	3.60	7.26
Bobic <i>et al.</i> (2014) <sup>Simmental</sup>	1.65	2.56	7.96
Carlstrom <i>et al.</i> (2009) <sup>Swedish Holstein</sup>	3.86	5.58	
Carlstrom <i>et al.</i> (2009) <sup>Swedish Red</sup>	3.03	4.53	
Gade <i>et al.</i> (2007)	2.30	4.0	12.9
Gade <i>et al.</i> (2006)	2.50	3.80	5.7
Jepertiene <i>et al.</i> (2007)	1.50	2.51-4.00	5.00-6.00
Laureano <i>et al.</i> (2014)	2.36		
Lucic <i>et al.</i> (2013)	2.31		
Muller <i>et al.</i> (2011)	2.00		
Povinelli <i>et al.</i> (2003)	1.82		5.85
Sprengel <i>et al.</i> (2001) <sup>Austria</sup>	1.98		
Sprengel <i>et al.</i> (2001) <sup>Baden-Wattenberg</sup>	1.77		
Sprengel <i>et al.</i> (2001) <sup>Bavaria</sup>	1.74		

AMF= average milk flow, MMF= maximum milk flow, MT= milking time

In previous studies, phenotypic mean of AMF ranged from 1.50 to 3.86 kg/min (Jepertiene *et al.*, 2007; Carlstrom *et al.*, 2009; and Bobic *et al.*, 2014). Jepertiene *et al.* (2007) report the lowest phenotypic mean from Polish Red and white cattle, while Carlstrom, (2000) reported high phenotypic mean on Swedish Holstein cattle. In literature herd management, milking equipment, breed and environmental conditions have been reported to cause variation in the milkability traits. Gade *et al.* (2006 & 2007) reported their results which they collected from the research herds, which is likely to operate under standardized conditions.

Phenotypic mean of MMF range from 2.51 to 5.58 kg/min (Jepertiene *et al.*, 2007; Carlstrom *et al.*, 2009; Antalik & Strapak, 2010; Gade *et al.*, 2007). Carlstrom *et al.* (2009) reported the higher phenotypic mean of MMF from both Swedish Red and Swedish Holstein

cattle data recorded from 19 commercial dairy herds using automated milking system. Bobic *et al.* (2014) and Jepertiene *et al.* (2007), reported the lower phenotypic mean of MMF from Simmental cattle and Polish Red and white cattle.

Milking time phenotypic mean reported by previous studies ranges from 4.34 to 12.90 minutes (Antalik & Strapak, 2010; Gade *et al.*, 2007). Lower phenotypic mean for milking time was reported by Antalik & Strapak, (2010) on Slovakia Holstein cattle, while, Gade *et al.* (2007) reported higher phenotypic mean on Germany Holstein cattle.

### *2.6.2. Heritability estimates for milkability*

The heritability estimates of milkability traits have been reported by several authors. Most of these heritability estimates were reported by authors who were comparing milkability traits and other traits like SCC, milk yield and udder type traits. Literature estimates of heritability of milkability traits are shown in Table 2.2.

Table 2.2. Heritability estimates for milkability traits in the literature.

	AMF	MMF	MT	Milkability
Aydin <i>et al.</i> (2008)	0.37		0.37	
Calstrom <i>et al.</i> (2009) <sup>Swedish Holstein</sup>	0.29			0.23-0.32
Calstrom <i>et al.</i> (2009) <sup>Swedish Red</sup>	0.49			0.34-0.60
Calstrom <i>et al.</i> (2013)	0.37-0.48			
Calstrom, (2014)	0.27-0.54		0.33-0.44	
Dodenhoff and Emmerling, (2008)	0.21 - 0.41			
Edwards <i>et al.</i> (2014)				0.27
Gade <i>et al.</i> (2007)	0.42	0.56	0.38	
Gade <i>et al.</i> (2006)	0.55	0.55	0.39	
Gray <i>et al.</i> (2012)	0.27	0.11		
Guler <i>et al.</i> (2009)	0.21		0.23	
Heringstad and Bugten, (2014)				0.11
Laureano <i>et al.</i> (2012)	0.23-0.32			
Luttinen and Juga, (1997) <sup>Ayrshire</sup>				0.24
Luttinen and Juga, (1997) <sup>Holstein</sup>				0.16
Povinelli <i>et al.</i> (2003)	0.24		0.19	
Rupp and Boichard, (1999)				0.17
Samore <i>et al.</i> (2011)		0.41		0.1-0.4
Vicario <i>et al.</i> (2006)	0.20			
Zwald <i>et al.</i> (2005)			0.17	

AMF= average milk flow, MMF= maximum milk flow, MT= milking time

In previous studies, heritabilities ranging from 0.1 to 0.6 were estimated for milkability traits based on serial data for automated milking systems (Zwald *et al.*, 2005; Rupp and Boichard, 2003; Edwards *et al.*, 2014; Carlstrom *et al.*, 2009). Low heritability estimates averaging 0.16 were reported by Luttinen and Juga, (1997) in Finnish Holstein cattle. Rupp and Boichard (2003) and Carlstrom *et al.* (2009) reported moderate heritability estimates ranging from 0.23 to 0.60 in both Swedish Holstein and Swedish Red cattle.

Most reported heritability estimates for average milk flow and maximum milk flow are moderate, ranging from 0.21 to 0.55 and 0.55 to 0.56, respectively (Gade *et al.*, 2006; Gade

*et al.*, 2007; Aydin *et al.*, 2008; Guler *et al.*, 2009). Gade *et al.* (2006, 2007) studied the genetic parameters for milkability traits from German Holstein cattle and reported moderate to high heritabilities ranging from 0.38 to 0.56. Guler *et al.* (2009) observed moderate heritability for average milk flow and milking time traits from Turkey Holstein Friesian cows, while Aydin *et al.* (2008) observed moderate heritabilities of average milk flow and milking time Brown Swiss data. Dodenhoff and Emmerling. (2008) and Calstrom, (2014) reported heritabilities of AMFin different lactations were ranging from 0.21 to 0.41, 0.28 to 0.37 and 0.21 to 0.36 for lactations 1, 2 and 3, respectively.

Heritability estimates for milking time were low to moderate ranging from 0.17 to 0.39 (Gade *et al.*, 2006; 2007; Zwald *et al.*, 2005; Guler *et al.*, 2009). Moderate heritabilities were found by Gade *et al.* (2006, 2007) in German Holstein cattle, while low heritability estimates were observed by Zwald *et al.* (2005) in American Holstein cattle. There is no information available on South African cattle.

### 2.6.3. Genetic correlation among milkability traits

Table 2.3 shows estimates of genetic correlations among three milkability traits.

Table 2.3. Genetic correlations among three milkability traits (average milk flow, maximum

	AMF and MMF	AMF and MT	MMF and MT
Gade <i>et al.</i> (2006)	0.98	-0.89	-0.86
Gade <i>et al.</i> (2007)	0.91	-0.77	-0.84
Erdem <i>et al.</i> (2010)		-0.47	
Guler <i>et al.</i> (2009)		-0.63	
Laureano <i>et al.</i> , (2011)	0.33	-0.04	-0.22
Edwards <i>et al.</i> (2014)	0.95	-0.79	-0.81
Samore <i>et al.</i> (2011)			-0.41

milk flow and milking time).

AMF= average milk flow, MMF= maximum milk flow, MT= milking time

Table 2.3 presents estimates of genetic correlations of milkability traits among three lactations. Genetic correlations among milkability traits were near unity. Genetic correlations ( $r_g$ ) between average milk flow and maximum milk flow ranged from 0.89 to 0.91 (Gade *et al.*, 2006; 2007). Negative genetic correlations between average milk flow and milking time have been reported in the literature (Gade *et al.*, 2006; 2007; Erdem *et al.*, 2010). A moderate genetic correlation between the average milk flow and milking time was obtained in the Italian Holstein cattle by Samore *et al.* (2011).

Table 2.4. Genetic correlations between the first three lactations and milkability traits (average milk flow, maximum milk flow and milking time).

	AMF	MMF	MT
Lactation 1-2	Gade <i>et al.</i> (2007) 0.991	Gade <i>et al.</i> (2007) 0.97	Gade <i>et al.</i> (2007) 0.93
Lactation 1-3	Gade <i>et al.</i> (2007) 0.88	Gade <i>et al.</i> (2007) 0.93	Gade <i>et al.</i> (2007) 0.92
Lactation 2-3	Gade <i>et al.</i> (2007) 0.95	Gade <i>et al.</i> (2007) 0.98	Gade <i>et al.</i> (2007) 0.97
All lactations	Antalik and Strapak, (2010) 0.69; Carlstrom, (2014) 0.97-0.98	Antalik and Strapak, (2010) 0.42	Samore <i>et al.</i> (2011) 0.62-0.91 Carlstrom, (2014) 0.93-0.99

AMF= average milk flow, MMF= maximum milk flow, MT= milking time

High genetic correlations between milkability traits in different lactations were reported by Gade *et al.* (2007). The correlations obtained among milkability traits in different lactations were very high compared to estimates obtained by Antalik and Strapak (2010) and Samore *et al.* (2011). High genetic correlations for milkability traits among different lactations were obtained between lactations 2 and 3, while low genetic correlations were obtained between lactation 1 and 3 (Gade *et al.*, 2007). Carlstrom. (2014) reported higher genetic correlations for average milk flow and milking time among lactations compared to estimates obtained by Antalik and Strapak (2010). Moderate genetic correlations were obtained by Antalik and Strapak. (2010) among maximum milk flow in all studied lactations. There is no such data available in South Africa. There is therefore a need to estimate genetic correlations between milkability traits in different lactations, to point out any differences in South African Holstein cattle.

## 2.7. Genetic trends

Genetic trends for milkability traits reflect the level of milking speed over a given period in the herd. As expected, reports in literature show different trends (Gade *et al.*, 2006; Gade *et al.*, 2007; Vicario *et al.*, 2006). Vicario *et al.* (2006) observed a genetic improvement in milkability that amounted to about half a standard deviation in 10 years in Italian Simmentals. Gade *et al.* (2006, 2007) observed the genetic trends on Germany Holstein cattle and reported that for milkability traits, the mean BVs of the sires indicated a selection gain insofar as the bulls showed the genetic disposition for higher milk flow and shorter milking duration. Genetic trends for milkability traits in South African Holstein cattle have not been estimated, therefore, there is a need to conduct such studies to ensure that farmer's selection decisions are advancing their herd in the direction that they intend.

## 2.8. Conclusions

Literature review findings generally reflect moderate heritability of milkability traits. The genetic correlations among milkability traits have been estimated in other countries around the world, while in South Africa they have not been estimated. The primary objective of this study is to estimate genetic parameters required to incorporate milkability in the breeding objective for the South African Holstein cattle.

## CHAPTER 3: MATERIALS AND METHODS

### 3.1. Data

Cow performance data were obtained from six different dairy farms around Gauteng and Eastern Cape provinces. The data collected includes average milk flow rate, maximum milk flow rate, milking time, milk yield, age in months, calving date, birth date, lactation number, and days in milk. The total number of milk records, collected from January 2016 to September 2016, were 3024.

### 3.2. Milkability traits

The automatic milking systems in the sampled herds provided information about three milkability traits, namely average milk flow (AMF) (kg/min), maximum milk flow (MMF) (kg/min) and total milking time (TMT) (min). Data used in this study were recorded from different milking parlour designs, namely herringbone, tandem and rotary milking parlours. On three of the dairy farms that contributed the data, cows were milked twice a day and traits were recorded at every milking using afimilk automated units (Afifarm Dairy Farm Management Software). The other farmers were using ALPRO-De Laval automated units, milking their cows three times (one farmer) a day, and twice (two farmers) a day. Pedigree data were obtained from the Integrated Registration and Genetic Information System (INTERGIS) for Holstein cows participating in the National Milk Recording and Improvement Scheme (NMRIS) and farmers not participating in the NMRIS provided the pedigree records for their animals.

### 3.3. Data editing

Milking data comprised of daily milking records and session milking records. The session milking records were averaged into daily values. Records with average milk flow less than 0.1kg/min or greater than 4.0 kg/min were deleted, following the editing procedure of Carlstrom *et al.* (2009). Animal records without data on any of the milkability traits were also deleted.

Two calving seasons were defined as summer (October – March) and winter (April - September) (Dube *et al.*, 2008; Mostert *et al.*, 2004). Contemporary groups were created according to herd, year and season of calving. Contemporary groups with animals less than 5 were deleted, in order to reduce the prediction error variance and to increase the accuracy of the estimation of breeding values.

The pedigree file was prepared with consideration of animals with milkability records. Animals with unknown birth dates and sires were excluded from the pedigree. The pedigree was prepared with consideration of three generations of the studied animals. After editing, the data set for (co)variance estimates consisted of records on 1 532 animals from six herds sired by 207 different sires and 994 different dams. The pedigree diagram for animals is shown in Figure 3.1.

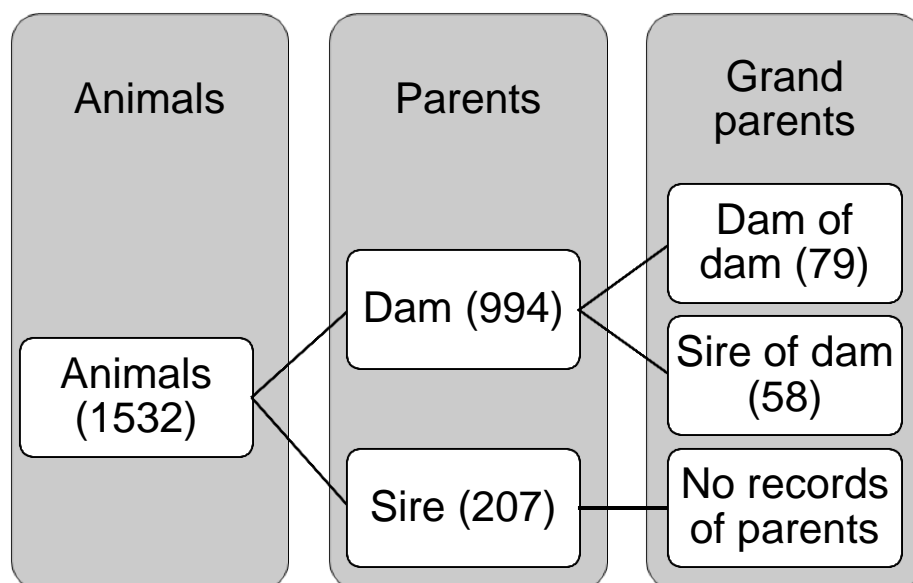


Figure 3.1: Animal pedigree information diagram

### 3.4. Statistical analyses

#### 3.4.1. Non-genetic factors affecting milkability traits

Descriptive statistics for milking time, average and maximum milk flow were computed using the *Proc means* procedure of the statistical analysis system (SAS 9.4, 2012). To determine non-genetic factors affecting these traits, an analysis of variance (ANOVA) was performed using the General Linear Models (GLM) procedure of SAS (SAS, 2012). The following model equation (Equation 1) was used to test for effects to include in models used in the analyses of milkability traits.

$$y_{ijklm} = \mu + \beta MY + HYS_i + P_j + DIM_k + (PDIM)_l + \varepsilon_{ijklm} \quad [1]$$

Where:

$Y_{ijklm}$  = Observation for milkability traits [Average milk flow (kg/min) or maximum milk flow (kg/min) or milking time (min)],

$\mu$  = is the population mean,

$(HYS)_i$  = fixed effect of the  $i^{\text{th}}$  herd-year-season of calving,

$(P)_j$  = fixed effect of the  $j^{\text{th}}$  parity,

$DIM$  = the  $k^{\text{th}}$  of the days in milk,

$MY$  is milk yield,

$\beta$  is the regression coefficient of milk yield on AMF, MMF or MT

$(PDIM)_{jk}$  = the interaction effect of days in milk by parity,

$\varepsilon_{ijklmn}$  = is the vector of random residuals errors.

### 3.4.2. Estimation of genetic parameters

The (co) variance components for milkability traits were estimated by the restricted maximum likelihood (REML) procedure using ASReml software (Gilmour *et al.*, 2006). At first, the animal model was attempted to estimate the (co)variance components; however due to the structure of the data a sire model had to be used.

The sire model equation was:

$$y = Xb + Zs + e \quad [2]$$

Where:

$y$  is the vector of observations (average milk flow, maximum milk flow and milking time);

$X$  is the incidence matrix relating observations to fixed effects;

$b$  is the vector of fixed effects (herd-year-season, parity and milk yield);

$Z$  is the incidence matrix relating observations to random sire effects;

$s$  is the vector of random sire effects of the animal;

$e$  is the vector of random residual effects.

The (co) variance structures of the model are:

$$\text{Var} \begin{bmatrix} s_i \\ s_j \\ e_i \\ e_j \end{bmatrix} = \begin{bmatrix} A\sigma_s^2 & A\sigma_{s_{ij}}^2 & 0 & 0 \\ A\sigma_{s_{ij}}^2 & A\sigma_s^2 & 0 & 0 \\ 0 & 0 & I\sigma_e^2 & I\sigma_{e_{ij}}^2 \\ 0 & 0 & I\sigma_{e_{ij}}^2 & I\sigma_e^2 \end{bmatrix} \quad [4]$$

$$\text{Var} \begin{bmatrix} y_i \\ y_j \end{bmatrix} = \begin{bmatrix} Z_i A Z_i' \sigma_s^2 + I\sigma_e^2 \\ Z_j A Z_j' \sigma_s^2 + I\sigma_e^2 \end{bmatrix} \quad [5]$$

Where:  $A$  is the numerator relationship matrix;  $I$  is an identity matrix,  $\sigma_s^2$  is the sire variance,  $\sigma_e^2$  is the residual variance,  $\sigma_{s_{ij}}^2$  is the sire covariance between trait  $i$  and trait  $j$  and  $\sigma_{e_{ij}}^2$  is the residual covariance between trait  $i$  and trait  $j$ .

It was assumed that covariance between sire effects and residual errors was equal to zero. It was further assumed that the residual errors were independent, identical and normally distributed with variance  $I\sigma_e^2$ .

The solution to the mixed model equations is given by equation 6 (Henderson, 1984).

$$\begin{bmatrix} X'X & X'Z \\ Z'X & A^{-1}\alpha \end{bmatrix} \begin{bmatrix} b \\ s \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix} \quad [6]$$

$$\text{Where, } \alpha = \frac{\sigma_e^2}{\sigma_s^2} = \frac{(1-h^2)}{h} \quad [7]$$

The heritability ( $h^2$ ) were estimated as follows:

$$h^2 = \frac{4\sigma_s^2}{\sigma_p^2} \quad [8]$$

$$\sigma_p^2 = \sigma_s^2 + \sigma_e^2 \quad [9]$$

Where:  $h^2$  is the heritability estimates of average milk flow, maximum milk flow or milking time.

$\sigma_s^2$  is the sire variance,

$\sigma_p^2$  is the phenotypic variance,

$\sigma_e^2$  is the residual variance.

Phenotypic correlations ( $r_p$ ) were estimated using equation 10:

$$r_p = \frac{Cov_{pij}}{\sigma_{pi}\sigma_{pj}} \quad [10]$$

Where:

$r_p$  is the phenotypic correlation between traits i and j;

$Cov_{pij}$  is the phenotypic covariance between traits i and j;

$\sigma_{pi}$  is the phenotypic standard deviation for trait i;

$\sigma_{pj}$  is the phenotypic standard deviation for trait j.

Genetic ( $r_g$ ) correlations were estimated using equation 11:

$$r_g = \frac{Cov_{gij}}{\sigma_{gi}\sigma_{gj}} \quad [11]$$

Where:

$r_g$  is the genetic correlation between traits i and j;

$Cov_{gij}$  is the genetic covariance between traits i and j;

$\sigma_{gi}$  is the genetic standard deviation for trait i;

$\sigma_{gj}$  is the genetic standard deviation for trait j.

### 3.4.3. Genetic trends estimates

Genetic trends for milkability traits were estimated by first estimating the breeding values for each trait. Estimated breeding values (EBVs) for each of the milkability traits were estimated by solving Best Linear Unbiased prediction (BLUP) mixed model equation (equation 6) (Henderson, 1984) using the ASReml software (Gilmour, 2002). The EBVs were used to determine genetic trends by calculating mean EBVs per year of birth using the Statistical Analysis Software (SAS 9.4, 2012). Genetic trends show the change in average merit for the population over successive years.

## CHAPTER 4 RESULTS

### 4.1. Descriptive statistics

The phenotypic means and standard deviations for average milk flow (AMF), maximum milk flow (MMF) and milking time (MT) are shown in Table 4.1.

Table 4.1. Summary statistics for milkability traits.

Traits	Mean	SD	Minimum	Maximum	CV
Average milk flow (kg/min)	1.99	0.72	0.30	3.90	30.17
Maximum milk flow (kg/min)	3.02	1.16	0.40	7.20	30.82
Milking time (min)	5.50	2.09	0.30	13	29.9

SD = standard deviation, CV = coefficient of variation

The coefficient of variation of all studied milkability traits was similar, ranging from 29.9 to 30.82. The minimum average milk flow were slightly lower (with 0.1kg/min) than the maximum milk flow, while the maximum mean of average milk flow was lower by 3.3 kg/min. The difference between the mean for average milk flow and maximum milk flow was 1.03 kg/min. All milkability traits followed a normal distribution (Figure 4.1 to 4.3).

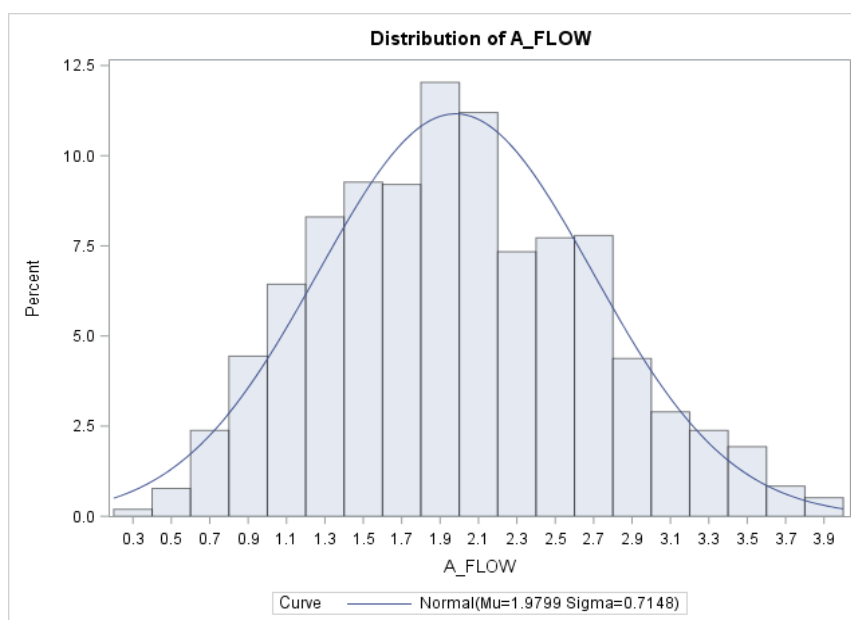


Figure 4.1: Frequency distribution of Average Milk flow.

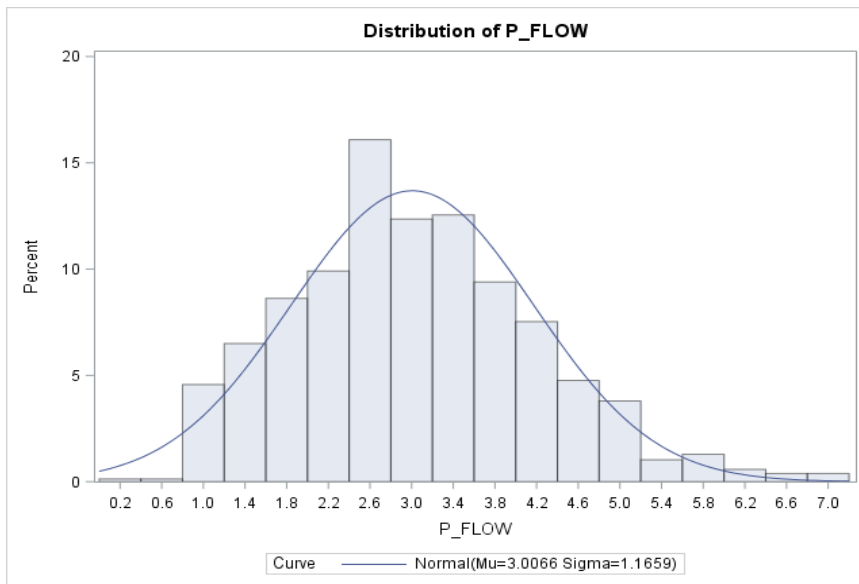


Figure 4.2: Frequency distribution of Maximum Milk Flow

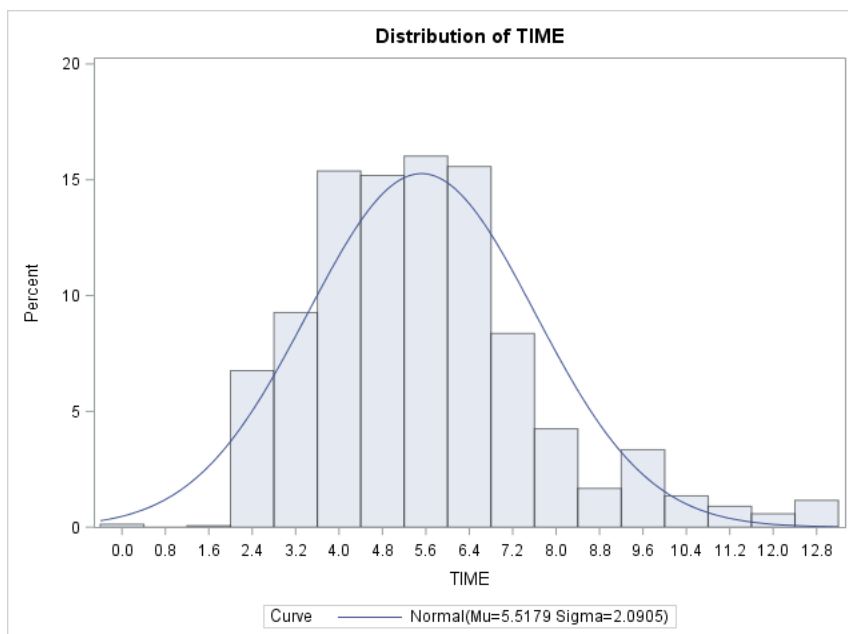


Figure 4.3: Frequency distribution of Milking Time.

#### 4.2. Non-genetic factors affecting milkability traits

The contribution to variation and significance in milkability traits by non-genetic factors affecting AMF, MMF and MT are shown in Table 4.2. The factors were herd-year-season (HYS), parity, milk yield, interaction effects of days in milk by parity and interaction effects of milk yield by parity.

Table 4.2. Effects of non-genetic factors on average milk flow, maximum milk flow and milking time.

Factors	Traits					
	AMF (R=0.38)		MMF (R=0.32)		MT (R=0.39)	
	Significance	Effect contribution (%)	Significance	Effect contribution (%)	Significance	Effect contribution (%)
Herd Year Season	***	48,3	***	38,8	***	78,3
Parity	***	4,6	***	3,4	***	2,9
Milk yield	***	42,2	***	51,3	***	13,2
Parity X days in milk	***	3,9	***	3,8	**	1,9
Parity X milk yield	NS	0,5	**	1,3	***	3,1

AMF= average milk flow, MMF= maximum milk flow, MT= milking time, \*\*p<0.01, \*\*\*p<0.001, NS= non-significant, %= Percentage.

Herd-year-season (HYS) (contemporary group) had the highest contribution to the variation in average milk flow (48.34%) and milking time (78.33%), followed by milk yield and parity, respectively. The highest contribution to variation in MMF was Milk yield (51.27%) followed by herd-year-season (HYS) and parity. The interaction effects of days in milk by parity had a minimal contribution to the variation in all milkability traits.

Herd-year-season (HYS), parity, milk yield and interaction effects of days in milk by parity had significant effects ( $p < 0.001$ ) on all traits. The interaction effects of milk yield by parity had significant effects on maximum milk flow ( $p < 0.001$ ) and milking time ( $p < 0.01$ ), while it had insignificant effects on the average milk flow ( $P > 0.05$ ).

### 4.3. Genetic parameters

#### 4.3.1. Heritability estimates

Estimates of heritabilities and standards errors for average milk flow, maximum milk flow and milking time are shown in Table 4.3.

Table 4.3. Estimates of variance components and heritability  $\pm$  standard error for Average milk flow (AMF), maximum milk flow (MMF) and Milking time (MT)

Traits	$\sigma_a^2$	$\sigma_e^2$	$\sigma_p^2$	$h^2 \pm SE$
AMF	0.10	0.41	0.44	0.23 $\pm$ 0.09
MMF	0.42	0.93	1.04	0.41 $\pm$ 0.12
MT	1.02	2.55	2.08	0.36 $\pm$ 0.11

$h^2$ =heritability estimate, SE = standard error,  $\sigma_a^2$  = additive genetic variance,  $\sigma_e^2$  = residual variance and  $\sigma_p^2$  = phenotypic variance.

The heritability estimates were moderate to high for average milk flow, maximum milk flow and milking time, ranging from 0.23 $\pm$ 0.09 to 0.41 $\pm$ 0.12. The residual variance for milking time was higher compared to the other milkability traits, which indicates that there might be factors affecting milking time that were not accounted for by the model used.

#### 4.3.2. Genetic and phenotypic correlations

Genetic and phenotypic correlations among milkability traits are shown in Table 4.5. The correlations show the degree of relationship among milkability traits in the South African Holstein cattle population.

Table 4.4. Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlations between milkability traits [Average milk flow (AMF), maximum milk flow (MMF) and Milking time (MT)]

Traits	AMF	MMF	MT
AMF		0.79±0.09	-0.35±0.23
MMF	0.86±0.01		-0.46±0.18
MT	-0.30±0.03	-0.32±0.03	

Genetic correlations between the three milkability traits were medium to high. The genetic correlation between average and maximum milk flow were positive and high (0.79±0.09). A negative and moderate genetic correlation (-0.35±0.23) was estimated between average milk flow and milking time and between maximum milk flow and milking time (-0.46±0.18).

Phenotypic correlations between the three milkability traits were also medium to high. The phenotypic correlation between average and maximum milk flow was positive and high (0.86±0.01). Negative and moderate phenotypic correlations were estimated between average milk flow and milking time (-0.30±0.03) and between maximum milk flow and milking time (-0.32±0.03).

#### 4.3.3. Genetic trends

Figures 4.4 to 4.6 show the genetic trends for milkability traits for Holstein cows that were born from 2002 to 2014. The estimated breeding values (EBVs) were averaged per year of birth. Genetic trends for average milk flow in Figure 4.2 show that the estimated breeding values increased at an average rate of 0.002 kg/min over the 12-year period, and at 0.0001 kg/min per year.

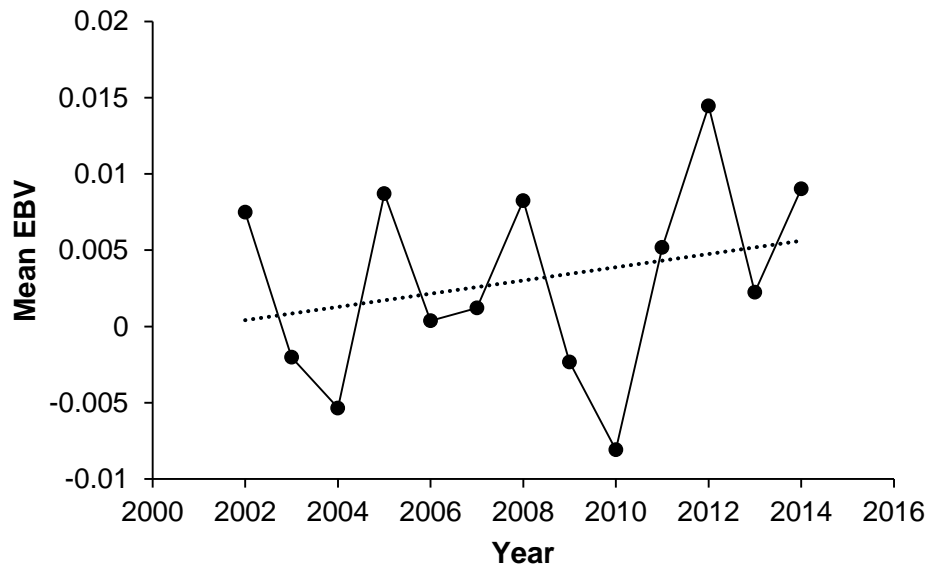


Figure 4.4: Genetic trends for average milk flow in Holstein cattle

The genetic trends for maximum milk flow (Figure 4.3) and milking time (Figure 4.4) show that the estimated breeding values for both traits increased at an average rate of 0.04 kg/min over the same period or roughly at 0.0003 kg/min per year. .

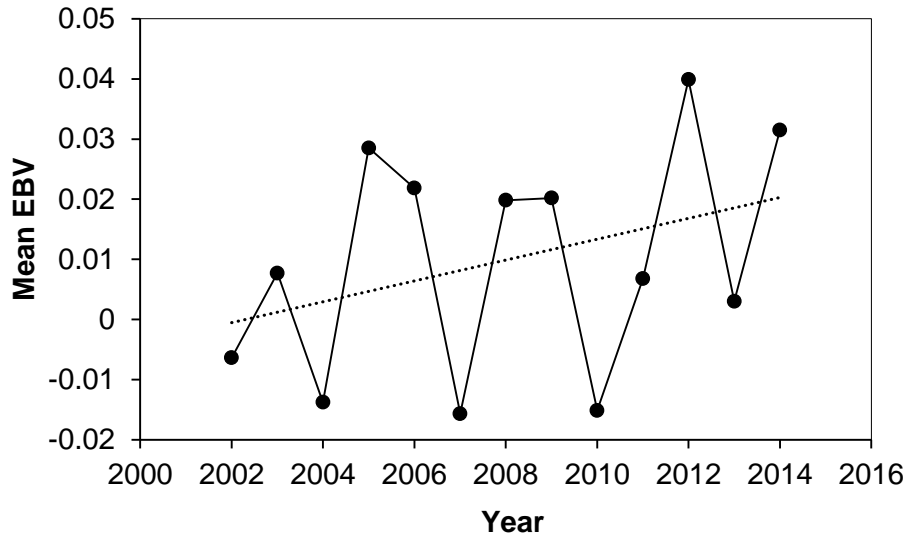


Figure 4.5: genetic trends for maximum milk flow in Holstein Cattle

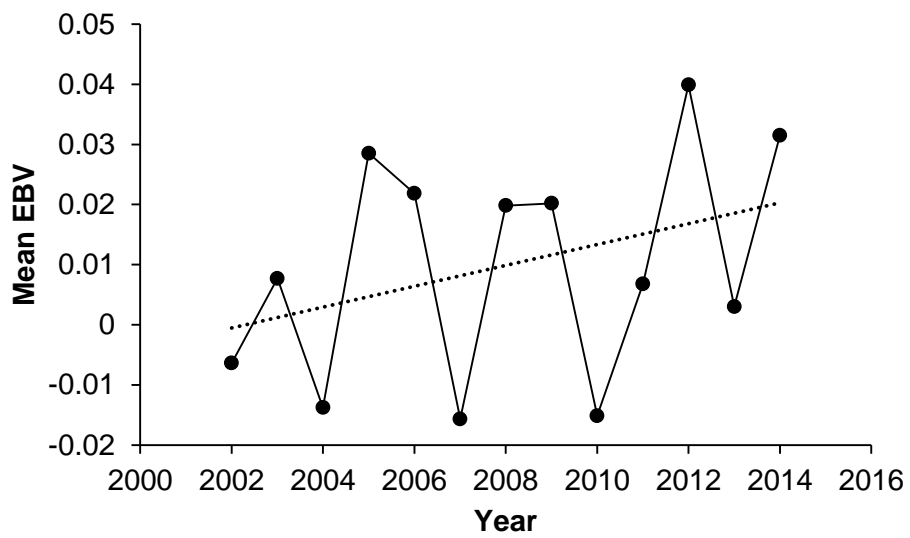


Figure 4.6: Genetic trends for milking time in Holstein cattle

## CHAPTER 5 DISCUSSION

### 5.1 Introduction

Milkability traits are gaining importance among dairy farmers worldwide. The main interest of a farmer is to minimize the total milking time of a cow and, hence, that of the whole herd, without affecting the total milk production (Povinelli *et al.*, 2003; Gade *et al.*, 2006&2007; El-Awardy and Oudah, 2011 and Samore *et al.*, 2011). Genetic improvement of milkability traits in South African Holstein cattle is hampered by a lack of the requisite genetic parameter estimates, for genetic evaluation.

Milkability traits from previous studies include: milk duration (milking time), peak flow rate (maximum flow rate) and average flow rate, as well as a division of the milking phase into time for increasing flow rate, time for maximum flow rate and time for decreasing flow rate (Gade *et al.*, 2006; Lee and Choudhary, 2006). In this study, traits used to measure milkability were average milk flow rate (AMF), maximum milk flow rate (MMF) and milking time (MT). These traits were measured automatically, during milking, using automated milking systems.

### 5.2. Descriptive statistics

Average milk flow is an important economic trait because it affects labour efficiency and production costs (Gade *et al.*, 2006; Povinelli *et al.*, 2003). An increase in average milk flow results in decreased labour working time and a decline in production costs, by reducing the electricity for operating the milking parlour. Horn (2004) indicated that an average milk flow of 2.0 kg/min was the goal for Hungarian Simmental cows.

The mean for AMF in the current study was 1.99 kg/min, which was higher than those reported previously by Povinelli *et al.* (2003); Jepertiene *et al.* (2007); Antalík & Strapák, (2010) and Bobić *et al.* (2014). On the other hand, Glade *et al.* (2006 & 2007); Müller *et al.* (2011); Lucić *et al.* (2013) and Laureano *et al.* (2014) found higher means (above 2.0 kg/min). The mean of 1.99 kg/min is, however, comparable to those reported by Spengel *et al.* (2001) in the German Simmental breed and Müller *et al.* (2011) in Germany Holstein cattle. It is also similar to the target value of 2.0 kg/min for Hungarian Simmental cows (Horn, 2004).

Maximum milk flow measures the rate at which high or peak milk flow is reached in the milking of a cow. The mean for MMF observed in this study was similar to those reported by Antalík & Strapark, (2010) and Jepertiene *et al.* (2007). Higher MMF values were observed by Carlstrom *et al.* (2009) on Swedish Holstein cattle and Gade *et al.* (2006 & 2007) on Germany Holstein cattle. Bobic *et al.* (2014) reported a slightly lower MMF rate for Simmental dairy cattle.

Milking time is economically important because it determines the total milking time of the cow in the milking parlour. An increase in milking time has a negative effect on production costs because it leads to an increase in labour time. Mean milking time observed in the current study was similar to values reported by Jepertiene *et al.* (2007); Gade *et al.* (2006) and Povinelli *et al.* (2003), but lower than those observed by Bobic *et al.* (2014) and Gade *et al.* (2007) which ranged from 7.26 to 12.9 minutes. Different milking parlours and herd management practices could have caused the variation in these results.

All the three milkability traits (AMF, MMF and MT) followed a normal distribution, when tested for normality. This indicates that the assumption of normality, made in the models used to analyse data for these traits was not broken.

Different herd management practices and improved breeds in other farms could be the cause of the disparity in the means for milkability traits among different studies. The study by Gade *et al.* (2006 & 2007) was conducted on commercial dairy farms involved in a project to develop a new data-recording scheme, where cows in one farm were milked thrice and cows in the other farm were milked twice a day. The current study was conducted on herds that voluntarily provided data and their herd management practices were different from each other. For example, farmers were using different milking parlours and milking schedules.

## **5.2. Non-genetic factors affecting milkability traits**

Non-genetic factors that had a significant effect on variation in the three milkability traits were herd-year-season of calving (HYS), parity, and milk yield. Contemporary group (i.e. HYS) had the highest contribution to variation in AMF (48.34%) and MT (78.33%). Carlstrom *et al.* (2009) and Gade *et al.* (2007) fitted HYS as a fixed effect in their models for genetic analysis of the milkability traits. Herd, year and season of calving have been used as non-genetic factors in other studies (Guler *et al.*, 2009; El-Awady and Oudah, 2011 and Povinelli

*et al.*, 2003). Different herd management practices such as feeding schedule, prestimulation time, and milking machine function affect milkability (Zucali *et al.*, 2009; Jones, 2009 and Salamon *et al.*, 2011). A study by M'hamdi *et al.* (2012) reported that milk flow rate was higher in cows calving in autumn and winter than in those calving in summer and spring, probably due to season effects on milk yield. On the other hand, cows calving in summer may have low milk flow due to their being subjected to high environmental temperatures in the first 3 or 4 months of lactation (Guler *et al.*, 2009; Cho *et al.*, 2004).

Milk yield had the highest contribution to variation in MMF (51.27%) and the second largest contribution to variation in AMF and MT. This supports previous findings by Carlstrom *et al.* (2009) who reported that high milk yield was observed from cows with high milk flow rate, using automated milking systems (AMS) data. This means that, when using the AMS with a timer (e.g. Afimilk rotary parlours) cows with higher milk flow will produce higher milk yield than cows with lower milk flow. This is due to the fact that slow milking cow do not milk out completely.

Parity had the lowest contribution to variation in milkability traits which is in agreement with previous results by Naumann and Fahr, (2000), Aydin *et al.* (2008) and Strapark *et al.* (2011). Naumann and Fahr (2000) and Guler *et al.* (2009) observed that increasing parity was associated with decreasing average milk flow. Strapak *et al.* (2011) and M'hamdi *et al.* (2012) reported that the highest milk flow rates were measured in second lactation dairy cows, due to animals adapting to the milking machines.

Herd-year-season, milk yield, and parity should be considered when analysing milkability traits. Neglecting these factors may increase errors in the estimation of genetic and phenotypic parameters.

### **5.3. Genetic parameters**

#### *5.3.1. Heritability estimates*

One of the specific objectives of this study was to estimate the heritability of milkability traits. This is important in determining the extent to which these traits are under genetic influence, as well as enabling them to be included in the selection objective. Differences in heritability values among different studies may be due to differences in the populations studied, as genetic parameters are population specific. Data for the current study were obtained from different commercial herds, while in previous studies by Gade *et al.* (2006 & 2007) data were recorded on a research farm with a more standardised

environment. The choice of model used for analysis also contributes to disparity in variance components estimates. For example, Laureano *et al.*, (2012) used a random regression model, while other studies (Gade *et al.* (2006 & 2007); Carlstrom *et al.* (2009) used a repeatability animal model. Vosman *et al.* (2014) used a sire model similar to the model used in the current study.

#### 5.3.1.1. Average milk flow

The heritability of AMF (mean value of current study) was moderate and comparable to values reported by Laureano *et al.* (2012). It was, however, slightly higher than estimates from other studies (Vicario *et al.*, 2006; Dodenhoff & Emmerling, 2008; Laureano *et al.*, 2012). On the other hand, Gade *et al.* (2006 & 2007) reported higher heritabilities, ranging from 0.42 to 0.55. The differences in the results may be attributed to the models used to analyse the data. For example, studies by Gade *et al.* (2006 & 2007) both analysed the data using an animal model, while the current study used a sire model.

#### 5.3.1.2. Maximum milk flow

The heritability estimate for MMF in the current study was moderate and similar to those obtained by Samore *et al.* (2011) and Carlstrom *et al.* (2009) in Swedish Red cattle. It was, however, lower than estimates by Gade *et al.* (2006 & 2007) and higher than the values reported by Gray *et al.* (2012) from a study on genomic selection in Italian Brown Swiss cows. Carlstrom *et al.* (2009) also obtained a slightly lower heritability in Swedish Holstein cattle. Differences in the populations studied and models used probably also account for the disparity in estimates among studies.

#### 5.3.1.3. Milking time

The heritability estimate for milking time observed in the current study was moderate and comparable to those obtained by Aydin *et al.* (2008) and Samore *et al.* (2011). It was, however, slightly lower than previous estimates by Gade *et al.* (2006 & 2007) and Carlstrom, (2014) and higher in comparison to those from studies by Povinelli *et al.* (2003) and Zwald *et al.* (2005). As with AMF and MMF, the various studies were conducted on different populations and disparate statistical modelling approaches were applied; hence the variation in estimates.

### 5.3.2. Genetic correlations

Another specific objective of this study was to estimate genetic correlations among the three milkability traits. Knowledge of the genetic relationships among these traits may help to improve accuracy of selection as well as enable their incorporation in an index of overall economic merit. Differences in estimates of genetic correlation among studies may be due to differences in the populations studied and the statistical models used.

#### 5.3.2.1. Average milk flow and maximum milk flow

The correlation between AMF and MMF (0.79) shows a strong association between these two traits, and is in agreement with other studies on Holstein cattle (Gade *et al.*, 2006 & 2007; Edwards *et al.*, 2014). It was, however, slightly lower compared to those reported by Gade *et al.* (2006 & 2007) and Edwards *et al.* (2014) in German and US Holstein cattle, respectively. Comparatively lower estimates were, on the other hand, reported for Brazilian Holstein cattle by Laureano *et al.* (2011) using a linear regression model.

The positive genetic correlation between AMF and MMF indicates that animals with a high genetic merit for average milk flow also tend to have high maximum milk flow. Therefore, improving either of these traits through selection would result in a correlated improvement in the other. Milking speed (AMF) can be calculated manually as milk yield (kilogram) divided by milking time (minutes); therefore, farmers without automated milking systems can also record and improve this trait through selection.

#### 5.3.2.2. Average milk flow and milking time

The moderate and negative genetic correlation between AMF and MT was according to expectation, since flow rate is a function of time. It confirms the fact that an increase in milk flow rate reduces milking time. Similar results have been reported in previous studies (Erdem *et al.*, 2010; Guler *et al.*, 2009). Lower genetic correlations were, however, obtained by Laureano *et al.* (2011) in Brazilian Holstein cattle; while higher estimates were reported by Edwards *et al.* (2014) and Gade *et al.* (2006 & 2007). The favourable genetic correlation between AMF and MT implies that improvement in AMF can be achieved through selection on MT. This is practical in situations without automated milking systems, where MT can simply be recorded using a stopwatch.

### 5.3.2.3. Maximum milk flow and milking time

Moderate and negative genetic correlations between MMF and MT obtained in the current study are favourable. Previous studies have consistently reported a negative genetic association between these two traits. Moderate genetic correlations between MMF and MT were also reported by Samore *et al.* (2011). Laureano *et al.* (2011), however, found a lower genetic correlation, while Gade *et al.* (2006 & 2007) and Edwards *et al.* (2014) obtained higher estimates. Selection for high MMF is thus expected to result in a correlated reduction in MT, thus improving labour efficiency and lower electricity costs.

### 5.3.3. Genetic trends

Genetic trends for milkability traits were determined to ascertain if there has been any genetic change in these traits in the South African Holstein cattle population over time. Such information helps in determining strategies for improving these traits within the population. There was an increase in genetic merit for AMF and MMF, which indicates an improvement. Gade *et al.* (2006 & 2007) also observed similar trends in the Germany Holstein cattle population over a 10 year period. The increase in genetic trend for MT (i.e. decrease in genetic merit) was unexpected, due to its favourable association with AMF and MMF. Since MT is the main trait of interest, this might mean there is a need to pay direct attention to it.

Milkability traits have been reported to be highly and positively correlated to milk yield (Gade *et al.*, 2006; Wiggans *et al.*, 2007; Erdem *et al.*, 2010; Strapak *et al.*, 2011). The genetic trends observed in the current study may partly be a correlated response to selection for higher milk yield. In German Holstein cattle, Gade *et al.* (2006 & 2007) observed an increase in genetic merit for milk yield together with milkability traits. In South African Holstein cattle, the genetic merit for milk yield has increased markedly during the same period of time (Ramatsoma *et al.*, 2014); hence the possibility of a correlated response in milkability.

## CHAPTER 6 CONCLUSIONS AND RECOMMENDATIONS

### 6.1. Conclusions

The conclusions of the current study were:

- 6.1. The mean for AMF, MMF and MT observed in the current study are comparable to those reported in the literature.
- 6.2. Non-genetic factors including herd-year-season of calving, parity and milk yield have a significant effect on AMF, MMF and MT. Therefore, these factors should be accounted for when analysing milkability data.
- 6.3. The heritabilities of AMF, MMF and MT are moderate to high, which indicates scope for improving them through selection.
- 6.4. Correlations among milkability traits (AMF, MMF and MT) are favourable and moderate to high, implying that selection on one of the traits will result in a correlated improvement in the others.
- 6.5. Increasing genetic trends were observed for AMF and MMF, which shows that these traits have been improving over time in South African Holstein cattle. While the increasing genetic trends for MT shows that, this trait was deteriorating. Therefore, there is a need to improve it due to its favourable association with AMF and MMF. Including milkability traits in the breeding objective for South African Holstein cattle will help to enhance this improvement.

### 6.2. Recommendations

The technology around milking cows is fast moving due to the increasing interest in robotic milking, worldwide. With such a development follows an increasing interest in using electronic recording of data for breeding cows with traits that are desirable for automatic milking. The importance of milkability worldwide has increased with the use of automated milking systems. The current study has observed moderate to high heritabilities for milkability traits, which indicates that there is scope for improving these traits through selection. An increase in milk flow has been reported to have an unfavourable effect on udder health. Therefore, selection for intermediate milk flow is optimum, as it will increase profit while not negatively affecting the udder health.

Milkability traits are currently not included in the breeding objective of South African Holstein cattle. Inclusion of these traits in the breeding program can help to reduce milking time, which will result in reduced production costs and an increase in herd profitability. Variance component estimates obtained in the current study provide the basis for including these traits in the breeding objective for South African Holstein cattle.

Before including milkability traits in the breeding objective, further information is needed, such as correlations of these traits to other economically important traits such as udder health, udder conformation and size and placement of teats.

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## APPENDIX 1. Informed consent form

### Informed Consent Form

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#### **Genetic Parameter Estimates for Milkability Traits in South African Dairy Cattle.**

Tshilate Thendo Stanley

University of Venda, Department of Animal Science

Private bag X5050

Thohoyandou

0950

073-663 9199

Date: \_\_\_\_\_

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Dear Sir/ Madam,

I hereby kindly request you to allow me as a student of University of Venda to come and collect data at your farm for my masters' research study. The results of the conducted study will benefit you by increasing the accuracy of selection and simultaneous improvement of both milkability and udder health and other dairy farmers particularly those utilising Holstein breed. In condition the end user of dairy products will also benefit from the study by consuming milk of high quality (low somatic cell count milk).

The purpose of this study is to estimate genetic parameters of milkability traits and correlations between milkability traits and udder health in the South African Dairy cattle.

#### **The study procedure is as follows:**

Milkability data (average milk flow rate, maximum milk flow and milking time) will be recorded at the milking parlour in the morning and afternoon using the automated milking herd management system. Somatic cell count and pedigree data will be obtained from the Integrated Registration and Genetic Information System (INTERGIS) for cows participating in the National Milk Recording and Improvement Scheme (NMRIS). These data will include relevant cow performance records, such as herd, birth date, calving date, lactation number and test date.

I therefore request the following data from your herd: parity, age in months, days in milk (DIM), milk yield, milk duration or time, average milk flow and maximum milk flow or Peak flow.

Kind regards

\_\_\_\_\_

Tshilate T.S

Researcher

I, the undersigned, confirm that (please tick box as appropriate):

1.	I have read and understood the information about the project, as provided in the Information Sheet dated: _____.	<input type="checkbox"/>
2.	I have been given the opportunity to ask questions about the project and my participation.	<input type="checkbox"/>
3.	I voluntarily agree to participate in the project.	<input type="checkbox"/>
4.	I understand I can withdraw at any time without giving reasons and that I will not be penalized for withdrawing nor will I be questioned on why I have withdrawn.	<input type="checkbox"/>
5.	The procedures regarding confidentiality have been clearly explained (e.g. use of names, pseudonyms, anonymisation of data, etc.) to me.	<input type="checkbox"/>
6.	If applicable, separate terms of consent for interviews, audio, video or other forms of data collection have been explained and provided to me.	<input type="checkbox"/>
7.	The use of the data in research, publications, sharing and archiving has been explained to me.	<input type="checkbox"/>
8.	I understand that other researchers will have access to this data only if they agree to preserve the confidentiality of the data and if they agree to the terms I have specified in this form.	<input type="checkbox"/>
9.	Select only <b>one</b> of the following: <ul style="list-style-type: none"> <li>• I would like my name used and understand what I have said or written as part of this study will be used in reports, publications and other research outputs so that anything I have contributed to this project can be recognized.</li> <li>• I do not want my name used in this project.</li> </ul>	<input type="checkbox"/>
		<input type="checkbox"/>
10.	I, along with the Researcher, agree to sign and date this informed consent form.	<input type="checkbox"/>

**Participant:**

\_\_\_\_\_

Name of Participant

\_\_\_\_\_

Signature

\_\_\_\_\_

Date

**Researcher:**

\_\_\_\_\_

Name of Researcher

\_\_\_\_\_

Signature

\_\_\_\_\_

Date