Genetic Variation of In-line Recorded Milkability Traits and Associations with Udder Conformation and Health in Swedish Dairy Cattle

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Cover: Caroline's grandmother Ruth Johansson, milking at the family farm, Bersebo, Östergötland, around year 1935
   (photo: Unknown)

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Abstract

Slow-milking cows lead to less efficient use of automatic milking systems (AMS) or may hold up the milking process when many cows are milked together in conventional milking parlours (CMP). Traditionally, genetic evaluations for milkability have been based on subjective observations, where the herdsmen have scored the animals once on a scale from slow to fast milking. This thesis aims at providing information useful for a genetic evaluation system based on in-line measured milkability traits. The aim was also to advance our understanding of the genetic relationships between milkability, udder conformation and udder health in order to evaluate opportunities of improving both milkability and udder health.

Milkability data from two different sources were used in the analyses: AMS and CMP data from commercial herds with Swedish Holstein and Swedish Red cows. Average flow rate (AFR), milking time (MT), box time (BT), handling time and proportion Attachment failures were used as most promising measures of milkability. The results showed that it is possible to use in-line measured information about milkability for genetic evaluation purposes. Moderate to high heritabilities and generally high repeatabilities were found for AFR, MT and BT in both breeds. High genetic correlations were obtained between AFR and the time traits. High genetic correlations between traits measured in the two systems showed that it should be possible to jointly use them in the genetic evaluation.

Shallow udders with short and thin teats were genetically associated to higher milking speed. High correlations of udder and teat conformation from in-line measured teat coordinates to corresponding traits scored by classifiers show the potential for future use of information from teat coordinates as a complement to classifications.

High milking speed was generally shown to be genetically correlated to worse udder health even though the results were somewhat inconsistent between the breeds. In the future, emphasis should be put on an udder health and milkability index aiming at improving both milkability and udder health.

Keywords: dairy cattle, milkability, flow rate, automatic milking system, conventional milking parlour, udder conformation, udder health, heritability, genetic correlation, genetic evaluation

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Oavsett om du tror att du kan eller inte kan, så får du rätt.
  Henry Ford

Contents

List of Publications

This thesis is based on the work contained in the following papers, referred to by Roman numerals in the text:

I Carlström, C., Pettersson, G., Johansson, K., Strandberg, E., Stålhammar, H. and Philipsson, J. (2013). Feasibility of using automatic milking system data from commercial herds for genetic analysis of milkability. *Journal of Dairy Science*, 96:5324-5332.

II Carlström, C., Strandberg, E., Johansson, K., Pettersson, G., Stålhammar, H. and Philipsson, J. (2014). Genetic evaluation of in-line recorded milkability from milking parlours and automatic milking systems. *Journal of Dairy Science*, 97:497-506.

III Carlström, C., Pettersson, G., Strandberg, E., Johansson, K., Stålhammar, H. and Philipsson, J. (2014). Genetic associations of teat cup attachment failures, incomplete milkings and handling time in automatic milking systems with milking speed, temperament and udder conformation (submitted).

IV Carlström, C., Strandberg, E., Johansson, K., Pettersson, G., Stålhammar, H. and Philipsson, J. Genetic associations of in-line recorded milkability traits and udder conformation with udder health (manuscript).

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Abbreviations

AFR	average flow rate
AMS	automatic milking system
AtF	proportion milkings with attachment failures
BT	box time
CM	clinical mastitis
CMP	conventional milking parlour
EBV	estimated breeding value
HT	handling time
IM	proportion incomplete milkings
LSCS	lactation average somatic cell score
MI	milking interval
MT	milking time
NAV	Nordic cattle genetic evaluation
NoM	number of milkings per day
PFR	peak flow rate
RR	random regression
SCS	somatic cell score
SH	Swedish Holstein
SR	Swedish Red

1 Introduction

Use of modern milking systems is rapidly increasing throughout the world and the Nordic countries are in leading positions for implementation of automatic milking systems (AMS). In Sweden, by September 2013, 31% of the dairy cows were milked in AMS, and another 26% in conventional milking parlours (CMP), while 43% were milked in stanchion barns (N-E Larsson, pers. comm., 2014-02-12). To ensure good economy with an AMS, the milking box needs to be efficiently utilized so that a maximum amount of milk is produced per robot per day. Slow-milking cows lead to less efficient use of milking robots or may hold up the milking process when many cows are milked together in conventional parlours. Consequently an increasing interest of the cows' milkability traits has followed and selection against slow-milking cows is of great interest. However, several early studies have shown unfavorable relationships between milking speed and udder health (i.e. Luttinen & Juga, 1997; Boettcher et al., 1998; Rupp & Boichard, 1999; Zwald et al., 2005).

Traditionally, genetic evaluations for milkability have been based on subjective observations, where the farmers or herdsmen have scored the animals once on a scale from slow to fast milking (Jakobsen, 2006). As the dairy herds increase in size, and less personnel time is spent per cow, the accuracy in genetic evaluations based on such subjective data will likely decrease. Modern milking systems provide an opportunity to capture repeated in-line measured milkability observations, and from AMS, especially, not only the traditional milking speed traits flow rate and milking duration are captured but also information about occupation time in the milking box, proportion of milkings with teat cup attachment failures and milking interval etc. However, the knowledge of how to handle in-line measured milkability from AMS data of commercial herds, but also from CMP, has been limited (Gäde et al., 2007; Byskov et al., 2012). Most results so far originate from experimental research herds (Gäde et al., 2006; Lovendahl, et al., 2011).

This thesis aims at providing information useful for development of a genetic evaluation system based on in-line measured milkability traits, by investigating the usefulness of AMS data and by estimating heritabilities for various milkability traits, genetic relationships between milking systems and between different measures of milkability. The aim was also to advance our understanding of the genetic relationships between milkability, udder conformation and udder health in order to evaluate opportunities of improving both milkability and udder health.

2 Background

2.1 Structural change of Swedish dairy production

There has been a dramatic change in the structure of dairy farms. The global industry trend for dairy production is increasing herd sizes with larger numbers of cows. This is true also in Sweden where the number of cows per herd has increased in an accelerating pace in the same time as the number of dairy herds has decreased dramatically. In the year 1970 the average herd size was 17 cows, in the year 2000 that figure was 34 and in the year 2013 the average number of cows per herd was 70. Correspondingly, in the year 1970 there were about 42,000 dairy herds in Sweden, in the year 2000 that number had decreased to 12,000 and in the year 2013 4,600 herds were left.

The possibility for increasing number of cows per herd is connected to the development of milking equipment and corresponding housing systems. The milking machine was first introduced in Sweden in the beginning of the 20th century. During the 1930s it developed into the tie stall system, where the milker bring the milking equipment to the tethered cow, kneel or squat to attach the equipment and the milk is collected in a pipeline system (A:sson Moberg, 1988). During the following decades development of milking parlour systems, and eventually also AMS, started.

Before 1970s only a few individual herds had loose housing systems in Sweden. In the year 1981 3% of the total number of herds had loose housing systems (Gjestang, 1983). But from the end of 1990s almost all new buildings is loose housing. In the year 2004 the figure was 19% of all herds and in 2013 35% of the herds, corresponding to 57% of all cows, were loose housing systems. The cows held in loose housing systems are either milked in CMP, where many cows are milked together, or in an AMS.

2.2 Automatic milking systems

In the 1970s the cost of labour was growing in many countries, which was the main trigger to start develop the idea about a fully automated milking process into reality. The development of cow identification systems was followed by automatic cluster removers, milk yield recording equipment and sensors to detect udder health problems, and finally what turned out to be the real challenging step, the development of automatic teat cup attachment systems. In 1992 the first robot was installed in a commercial herd in the Netherlands. And even if the adoption of the new technology was slow in the beginning it aroused much interest among dairy farmers and from the end of the 1990s it has been a rapid development, mainly in north-western Europe. (Meijering, de Koning, van deer Vorst, 2002) The Scandinavian countries are today in leading positions. In Sweden 21% of all dairy herds use AMS, corresponding to 31% of the cows are milked in AMS (September 2013).

In traditional tie stall barns the farmer spent much labour time together with the animals during milking. The introduction of AMS completely changed the nature of labour. To monitor individual cows and to control their feeding and milking processes data had to be collected and processed and a large number of sensors were therefore incorporated in the AMS. A management information system then makes the data available and interpretable. As a consequence a lot of the earlier physical labour was now substituted into management and supervision (Spahr and Maltz, 1997). This shift in type of labour appears to be one of the most important reasons why farmers decide to invest in AMS. A survey within the EU project 'Implications of the introduction of automatic milking on dairy farms' showed in a questionnaire from 107 herds in four countries (Belgium, The Netherlands, Denmark, and Germany) that two-thirds of the farmers stated social reasons, such as increased labour flexibility, improved social life and health concerns, as opposed to economic reasons, for investing in an AMS. (Meskens & Mathijs, 2002).

At the same time as the sensors act as the farmer eye during the milking process and, hence, make a more flexible lifestyle possible for the farmer, they have also another great advantage, which has so far not been fully utilized. They generate a huge amount of data that could be used as measurements of important traits. To be able to improve traits by breeding it is a prerequisite to have good measurements of the trait that you want to select for. With the AMS sensors we get in-line measurements of traits such as milk flow rate and occupation time in the milking box, milkability traits which indeed are of great interest for genetic improvement. To make the AMS economically efficient a key figure in Sweden, to aim for is 2000 litres of milk per day and robot. Milk flow rate, has together with the number of cows, been shown to be the most

important variable influencing the daily milk yield per AMS (Castro et al., 2012).

2.3 Milkability

Milkability measures the cow's ability to let down milk and to be completely milked (Larsson & Ekström, 2000). A good milkability is obtained when the milking machine removes milk from the udder gently, quickly and completely (Lee & Choudhary, 2005). The trait is affected by the milk yield, the resistance from the teat canal and the strength of the hormonal letdown reflex (Johansson & Rendel, 1963). It could be measured as average flow rate, peak flow rate, milking time or with a subjective score by the herdsmen.

Milkability was a trait of great interest early on in dairy cattle breeding. After the Second World War the use of milking machines became more and more common. At the same time labour costs led to higher demands for shorter milking times. Many research projects with the aim to develop methods for milkability observations, which could be used in genetic evaluations, were therefore carried out from the middle of the 1950s to the middle of the 1970s (Rendel, 2003). Different methods were developed and as time went by they were also simplified in such a way that results from the regular test milkings or interviews with the farmers, could be used (Philipsson, 1970; Josefsson & Philipsson, 1973). A general trend from all studies, regardless of breed and country, were that milkability, observed as flow rate or milking time, did not only show moderate to high heritabilities (0.2-0.5), but also the highest relative genetic variation among all observed traits in dairy cattle. In other words, there are big differences in milkability between cows within herds and a large proportion of these differences are genetically determined.

During the last decades before year 2000 milkability became a less important trait in the selection schemes for bulls and cows. This was partly depending on the fact that milkability seems to be an optimum trait and that the selection goal for cows that fitted in our relatively small herds in tie stall barns were reached. When the Swedish national breeding objectives were reviewed in year 1999, milkability was even deleted from the sire index since the breeding objectives on average was considered achieved for the trait. However, since then there has been a dramatic change in the structure of dairy production and coherent milking techniques. As discussed above the development towards large herds with CMP or AMS is fast. This requires, once again, large demands on the cows' milkability traits. Since year 2008 milkability is included in the Nordic Total Merit Index.

2.4 Main issues

To ensure good economy with AMS, the milking box needs to be efficiently utilized so that a maximum amount of milk is produced per robot per day. Slow-milking cows are not a problem only in milking robots though, they also hold up the milking process when many cows are milked together in CMP. Thus, selection against slow-milking cows is of great interest to save time and to make efficient use of expensive equipment. Generally, genetic studies about milkability have recently been based on subjective observations, where the farmers or herdsmen have scored the animals once in first lactation on a scale from slow to fast milking. Modern milking systems provide an opportunity to capture repeated in-line measured milkability observations. Furthermore, AMS data allow us to expand the milkability concept to include not only the traditional milking speed traits flow rate and milking duration, but also, for example, traits concerning the occupation time in the milking box, teat cup attachment failures as well as milking interval.

Routine genetic evaluations for milkability traits based on automatically recorded data have not been implemented so far in Sweden. It has been considered important to study the possible outcome of including such data by addressing a number of questions.

The first question is: How useful are automatically captured milkability data for genetic analyses? Is it at all possible to use data directly extracted from AMS databases, where data from every milking are recorded regardless of the quality of the milking?

The second question is: Is it possible to integrate milkability information from different kind of milking systems, i.e. AMS and CMP, in genetic analyses and eventually in the genetic evaluation? Whilst cows in AMS are milked on a voluntary basis, CMP is a system with strict milking intervals for all cows. Thus, AMS and CMP represent different ways of handling cows at milking. Moreover, data are captured automatically in both systems but the traits are differently defined and measured in the different systems. Furthermore, which trait(s) would be of most interest as measurements of milkability?

The third question concerns the associations of milkability to other important traits. For cows to suit an AMS, traits such as udder shape and size and placement of the teat are likely to be of interest. It may for example be difficult to automatically attach teat cups on cows with deep udders or too wide, or too close, teat placement. Furthermore, milkability seems to be undesirably correlated to udder health. Earlier studies have been reporting unfavorable genetic correlations between milkability and somatic cell count (e.g. Moore et al, 1981; Luttinen & Juga, 1997; Boettcher et al, 1998; Rupp and Boichard, 1999). However, much has happened as regards production

increase, management systems and focus on milkability. These changes might also influence the relationships between milkability and somatic cell count. Furthermore, the genetic associations to mastitis show contrasting results (Lund et al., 1994; Luttinen & Juga, 1997; Rupp & Boichard, 1999; Zwald et al., 2005; Gäde et al., 2007). Possible existence of non-linear relationships could be one explanation, and needs to be investigated. Thus, advice is needed on how both milkability and udder health could be improved for high yielding cows in modern milking systems.

3 Aims of the thesis

The overall aim of this thesis was to study the possibilities for a genetic evaluation system based on in-line measured milkability traits. The aim was also to develop models for maximum use of data for genetic evaluations and advise on how both milkability and udder health might be improved. More specifically, the aims were to investigate:

- ➢ the overall feasibility of using different measures of milkability from AMS data for genetic analysis purposes
- ➢ heritabilities and repeatabilities for different repeatedly measured milkability traits in AMS and CMP
- ➢ genetic correlations between different milkability traits as well as between milkability measured in different lactations and in different milking systems, i.e. AMS and CMP
- ➢ genetic correlations between milkability, udder conformation and udder health traits
- ➢ evaluate opportunities of improving both milkability and udder health

4 Summary of the studies

4.1 Materials

A summary of data and traits used in paper I-IV is found in Table 1. Milkability data from 19 commercial AMS herds were used in all papers (I-IV). Originally information from each milking from autumn 2004, or since the installation of the AMS, to spring 2009 was downloaded from local herd databases. The dataset included information from 5,115,363 milkings of 4,968 cows. In paper I a lot of effort was put into editing of this dataset since the AMS register information about every milking regardless of the quality of the milking. Restrictions were placed regarding what should be interpreted as complete and normal milkings and records clearly inconsistent with normal variation of the traits were excluded. After editing, the final dataset for genetic analyses included information from 1,063,951 milkings of 2,053 SH cows and 1,155,732 milkings of 1,749 SR cows in the first three lactations. On average, the analyses of average flow rate (AFR), peak flow rate (PFR), box time (BT), milking time (MT), handling time (HT) and milking interval (MI) included 340 and 392 observations per cow for first-lactation Swedish Holstein (SH) and Swedish Red (SR) cows, respectively. Corresponding figures for later lactations were 455 and 539 observations. Information about number of milkings per day (NoM) (Paper I), proportion milkings with attachment failures (AtF) and proportion incomplete milkings (IM) (Paper III-IV) came from the same original dataset, but was not edited in the same way as the rest of the milkability traits. Only first lactation data was included in the genetic analyses of AtF and IM, since preliminary analyses resulted in estimates with high standard errors, with observations from 1,647 and 1,467 SH and SR cows respectively.

Paper II-IV included also milkability observations for 74 herds with CMP. Data, from spring 2007 to spring 2011, were obtained from the national milk-recording scheme (Växa Sweden). The dataset included 474,755 monthly observations from 11,123 SH cows and 7,554 SR cows from the first three lactations.

In Paper III genetic associations of milkability traits with udder conformation and temperament were investigated. Information about udder conformation and temperament came from linear classifications of first lactation cows. Data were provided by the national milk-recording scheme (Växa Sweden), for all 93 herds with milkability information, in total 12,513 SH cows and 9,413 SR cows with classifications from year 2000-2011. Information of some udder conformation traits were available from AMS teat coordinates for 12 of the 19 AMS herd included in Paper I-IV. In total 1,418 SH and 962 SR cows with udder conformation information from teat coordinates were included.

Information about udder health (Paper IV) came from Växa Sweden and was extracted from the dataset used in the Nordic cattle genetic evaluation, for all 93 herds with milkability information. In total udder health data from year 1982 to 2013 were available for 51,103 SH cows and 37,710 SR cows.

For the milkability datasets complementary information was needed to connect each cow to a pedigree and each observation to a lactation number and stage of lactation. This information was provided by Växa Sweden. In all papers pedigree data contained sires and dams of cows in three generations.

*Table 1.*Summary of data and traits used in Paper I-IV

Trait	Milking system[1]	Lactation number	In Paper
Milkability			
Average flow rate (kg/min)	AMS	1-3	I-IV
Average flow rate (kg/min)	CMP	1-3	II-IV
Peak flow rate (kg/min)	AMS	1-3	I
Milking time (min)	AMS	1-3	I-IV
Milking time (min)	CMP	1-3	II-IV
Box time (min)	AMS	1-3	I-IV
Handling time (min)	AMS	1-3	III-IV
Milking interval (hours)	AMS	1-3	I
Number of milkings (no/day)	AMS	1-3	I
Proportion attachment failures (%)	AMS	1	III-IV
Proportion incomplete milkings (%)	AMS	1	III
Udder conformation + temperament			
Fore udder attachment (scale 1-9)	AMS + CMP	1	III-IV
Rear udder height (scale 1-9)	AMS + CMP	1	III-IV
Rear udder width (scale 1-9)	AMS + CMP	1	III-IV
Central ligament (scale 1-9)	AMS + CMP	1	III-IV
Udder depth (scale 1-9)	AMS + CMP	1	III-IV
Front udder depth (mm)	AMS	1-3	III-IV
Rear udder depth (mm)	AMS	1-3	III-IV
Udder balance (scale 1-9)	AMS + CMP	1	III-IV
Udder balance (mm)	AMS	1-3	III-IV
Front teat placement (scale 1-9)	AMS + CMP	1	III-IV
Front teat placement (mm)	AMS	1-3	III-IV
Rear teat placement (scale 1-9)	AMS + CMP	1	III-IV
Teat length (scale 1-9)	AMS + CMP	1	III-IV
Teat thickness (scale 1-9)	AMS + CMP	1	III-IV
Right and left teat placement (mm)	AMS	1-3	III-IV
Temperament	AMS + CMP	1	III
Udder health			
Lactation average SCS[2]	AMS+CMP	1-3	IV
Early lactation mastitis incidence (0/1)	AMS+CMP	1	IV
Late lactation mastitis incidence (0/1)	AMS+CMP	1	IV
Mastitis incidence (0/1)	AMS+CMP	2-3	IV

[1]AMS = Automatic milking system, CMP = Conventional milking parlour system
[2]SCS = somatic cell score transformed to a logarithmic scale with base 10 (expressed in 10,000 cells/ml)

4.2   Methods

Linear animal models were used (Paper I-IV). Estimation of (co)variances and predictions of breeding values (EBV) were performed using the DMU package for analysis of multivariate mixed models (Madsen and Jensen, 2007). Univariate models were used for all heritability estimations and bivariate models for all estimations of genetic correlations.

All models included a random genetic effect of animal and a random residual effect. All models for traits with repeated observations (i.e. all milkability traits with the exception of AtF and IM also included a random permanent environmental effect to account for repeated measurements within cow.

The final model for genetic analysis of AFR and MT (Paper II-IV) included the fixed effects of herd-year-season at observation, lactation number, lactation month, milking system (i.e. AMS or CMP) and a fixed linear covariate of milk yield nested within milking system. In Paper I models where stage of lactation was handled in different ways (i.e. lactation month, lactation week or days in milk) were compared, using R^2, residual error variance, heritability and log-likelihood values, before lactation month was chosen. In the same way it was tested whether a fixed linear covariate of milk yield or of milking interval should be included. In the analyses where only one kind of milking system was included (Paper I and II) the same model was used without the fixed effect of milking system. The fixed linear covariate of milk yield was then nested within lactation moth.

In paper II the repeatability model described above was compared with four different random regression (RR) models. The RR models included the same effects as the repeatability model but were extended by adding first, second, third or fourth order of Legendre polynomials for the random permanent environmental effect and the random genetic effect. For a comparison of the models, estimates of error variance and log likelihood, as well as Pearson product-moment correlations between breeding values, were used.

For AtF and IM (Paper III-IV) the included fixed effects were herd, year-month at calving and age at calving. For udder conformation traits and temperament from linear classifications, herd, lactation week, classifier-year at observation, month at observation, age at calving and hours after milking were included as fixed effects, whereas milk yield at the test day closest to the classification date was included as a fixed linear covariate (Paper III-IV). For udder conformation traits measured with AMS teat coordinates the model included the fixed effects of herd-year-month at observation, lactation number and lactation week as well as a fixed linear covariate of milk yield at observation (Paper III-IV).

For the udder health traits (Paper IV) in first lactation the model included the fixed effects of herd-year of calving, month at calving and age at calving. The same model was used for udder health traits in later lactations (two and three), without the effect of age at calving but with addition of the effect of lactation number and a random permanent environmental effect to account for repeated measurements. The linearity of the relationships between milkability on one hand and udder health on the other were tested by fitting linear and quadratic regressions of sire EBVs, phenotypes or residuals for the udder health traits on corresponding EBVs, phenotypes or residuals for milking speed.

4.3 Main findings

4.3.1 Heritabilities for the traits included in the thesis

A summary of heritability estimates for the traits included in Paper I-IV is presented in Table 2. Estimates of the heritability were moderate to high for AFR, MT and BT, ranging from 0.21 to 0.54 (Paper I-II). Higher estimates were obtained for AFR and MT compared to BT in SH cows, whereas the estimates were at same level in SR cows. Higher estimates were generally obtained when the data sources, i.e. AMS and CMP, were combined. HT showed the lowest heritability of the time-related traits (Paper III). Moderate heritability estimates were obtained for AtF, low to moderate for MI, whereas lowest heritability estimates out of the milkability traits were found for IM and NoM.

It was confirmed in Paper III that analysed udder conformation traits scored by linear classification, i.e. fore udder attachment, rear udder height, rear udder width, central ligament, udder depth, front teat placement, rear teat placement, teat length and teat thickness, show moderate to high heritabilities. In both breeds, teat length followed by udder depth and front teat placement showed the highest heritabilities (0.32-0.45). Also the trait general temperament was scored on a linear scale. The obtained estimates showed a breed difference, where the heritability in Swedish Red was almost twice as high as in Swedish Holstein. Udder conformation traits measured by teat coordinates showed heritabilities at the same level (udder balance and front teat placement) or higher (udder depth) than corresponding traits based on linear classifications (Paper III).

Paper IV confirmed a low heritability for CM (<0.03) and higher, but still low (~0.14), for somatic cell score.

Table 2. Heritabilities for traits included in Paper I-IV, genetic correlations across lactations for traits measured in multiple lactations and genetic correlations across milking systems for the milkability traits measured in both AMS and CMP

Trait	Milking system	Heritability	Genetic correlations between lactations	Genetic correlations between milking systems
Average flow rate (kg/min)	AMS + CMP	0.27-0.54	0.97-0.98	0.97-0.98
Milking time (min)	AMS + CMP	0.33-0.44	0.93-0.99	0.98-1.00
Box time (min)	AMS	0.21-0.44	0.94-1.00	
Handling time (min)	AMS	0.05-0.15		
Milking interval (hours)	AMS	0.09-0.26		
Number of milkings (no/day)	AMS	0.02-0.07		
Proportion Attachment failures (%)	AMS	0.21-0.31		
Proportion incomplete milkings (%)	AMS	0.02-0.06		
Udder conformation (scale -9)	AMS + CMP	0.18-0.45		
Udder conformation (mm)	AMS	0.15-0.52		
General temperament (scale 1-9)	AMS + CMP	0.08-0.15		
Lactation average SCS[1]	AMS+CMP	0.11-0.17		
Clinical mastitis incidence(0/1)	AMS + CMP	0.005-0.03		

[1]SCS = somatic cell score transformed to a logarithmic scale with base 10 (expressed in 10,000 cells/mL)

4.3.2 Use of different sources of data

The thesis is based on two different data sources of milkability observations, partly AMS-data and partly CMP-data. A main difference between the two sources was the process of data editing needed. Almost a quarter of the cows in the AMS were lost in the process due to incomplete or inconsistent identification information. This problem is however thought to be specific for this dataset, as the data were collected during a period with fast-increasing herd sizes and new milking systems (Paper I).

Both datasets were edited to exclude observations clearly inconsistent with the normal variation for the traits. That resulted in a much higher loss of observations from the AMS dataset (34%, Paper I) than from the CMP dataset (2%, Paper II), which reflects that the AMS saves information about every milking regardless of the quality of data or milking. More than enough accurate data is still available for analysis. Repeatability estimates within lactation were obtained from AMS and CMP respectively. The results showed high consistency, with repeatability estimates of 0.63 to 0.89 for the milkability traits AFR, MT and BT, mainly depending on which lactation and milking system was being considered. Higher estimates were obtained for first lactation than later lactations and for AMS-data than for CMP-data. The results imply

that it should not be necessary to collect all observations per animals to achieve accurate information on each cow. Observations from 30 to 250 days after calving are preferred due to somewhat higher heritability than in the very early or late lactation stages (Paper II).

The milking speed traits AFR and MT, as well as BT, were proven to stay, more or less, the same trait genetically across the lactations (Table 2). Information about AFR and MT were available from both AMS and CMP and high genetic correlations were estimated between corresponding trait measured in the different milking systems (Table 2).

Furthermore, there were high genetic correlations, over 0.9, between AFR, MT and BT (Table 3). In preliminary analyses of the AMS-data, also PFR was included. Between PFR and AFR the genetic correlations reached unity (0.99-1.00) and it was thus decided to only keep one of the flow traits; AFR. Out of the flow rate traits and time traits, HT had the lowest genetic correlation to the other traits.

Overall, the results indicated that it is possible to use data from different sources, i.e. AMS and CMP, jointly for genetic evaluations. Furthermore, it should be enough to include information only from the first lactation, and only from one of the traits, AFR or BT, used as measures of milking speed.

4.3.3 Comparison of statistical models for genetic analysis

Statistical models were in Paper I compared regarding how to best adjust for lactation stage. Furthermore, it was tested whether the observations should be adjusted for milk yield or milking interval. It was decided to use lactation month as a measure of lactation stage. However, according to comparisons of coefficients of determination and residual variances, it did not make a difference when compared to the other alternatives, i.e. lactation week or days in milk as a linear covariate. To include milk yield as a linear covariate turned out to have a much greater influence on R^2, the residual error variance and the log-likelihood, than milking interval, and was thus decided to be included in the model.

In Paper II comparisons were made between the repeatability model and random regression models mainly on the basis of estimates of error variance, log likelihood function, heritability estimates and Pearson correlations between cow EBVs. According to the formal model fit parameters, the random regression model with third order of Legendre polynomials was favored. However, the Pearson correlations indicated that the repeatability model would give almost the same results for practical genetic evaluation purposes. Hence, the preferred model, used for the further studies (Paper III-IV), was a repeatability model including the fixed effects of herd-year-season, milking

system, lactation number (based on the high genetic correlations of traits across milking systems and lactations respectively), lactation month and a fixed linear covariate of milk yield. The size of the regression coefficient for milk yield varied between AMS and CMP and, hence, milk yield was nested within the effect of milking system. Because the variance differed between systems and lactations, the data was preadjusted for heterogeneous variance between AMS and CMP, and between lactations.

Table 3. Range of genetic correlations between different trait combinations in Paper I-IV

Traits		Genetic correlation
Average flow rate	Milking time, Box time	0.93-1.00
Box time	Milking time	0.93-1.00
Average flow rate, Box time	Handling time	0.72-0.89
Average flow rate, Box time	Proportion attachment failures	0.18-0.46
Handling time	Proportion attachment failures	0.56-0.73
Average flow rate, Box time	Proportion incomplete milkings	0.42-0.98
Handling time	Proportion incomplete milkings	0.63-0.89
Average flow rate, Milking time	Udder conformation	0.08-0.39
Box time, Handling time	Udder conformation	0.16-0.40
Proportion attachment failures	General temperament	0.44-0.71
Average flow rate, Milking time	Lactation average SCS[1]	0.37-0.57
Box time	Lactation average SCS	0.29-0.41
Average flow rate, Milking time	Clinical mastitis incidence	0.18-0.48
Box time	Clinical mastitis incidence	0.24-0.50

[1]SCS = somatic cell score transformed to a logarithmic scale with base 10 (expressed in 10,000 cells/mL)

4.3.4 Associations of teat cup attachment failures with udder conformation and temperament

In Paper III results showed that a high proportion of milkings that contain some kind of teat cup attachment disturbance, either problems with the attachment of teat cups, or a kick-off of the teat cup(s) during milking, is genetically associated to udder shape as well as teat length and thickness, at least in SR cows. Furthermore, results revealed a clear genetic relationship between AtF and the classified trait general temperament in both breeds (Table 3), which imply that cows with high AtF are considered more nervous by the herdsmen.

4.3.5 Associations between milkability, udder conformation and udder health

Results showed that high milking speed is genetically associated to favorable shape of the udder, i.e. shallow udders, high rear udder attachment and close front teat placement, as well as to short and thin teats (Paper III). The levels of

the correlations are summarized in Table 3. Results were similar when (1) udder conformation was measured by teat coordinates or (2) based on linear classifications, naturally since the genetic correlations between corresponding traits measured by teat coordinates and linear scores, respectively, were between 0.91 and 0.98. Overall results imply that milking speed and udder conformation are more associated to each other in Swedish Red than in Swedish Holstein. In addition to already mentioned traits results show that high milking speed is associated to a strong central ligament, strong fore udder attachment as well as to a better udder balance in Swedish Red.

In Paper IV it was confirmed that better udder health is genetically correlated to a shallow udder, but also to a tight fore udder attachment and, at least in Swedish Holstein, to thin teats.

Results in Paper IV showed that high milking speed is genetically correlated to high lactation average SCS (Table 3). The results were consistent across breeds. The results for clinical mastitis showed the same trend for Swedish Holstein, i.e. higher milking speed was associated with higher risk for a mastitis incidence. In Swedish Red, however, the genetic correlations revealed opposite associations, with high milking speed being associated with lower risk for mastitis incidence in an early stage of the lactation. Fitted regressions of the phenotypic observations for udder health traits on phenotypic observations for milking speed imply that there is an unfavorable association between high milking speed on the one hand and high lactation average SCS and clinical mastitis on the other, but that it exist an optimum, and when the milking speed is lower than a certain threshold, lower milking speed is associated to worse udder health. There was, however, no evidence of non-linearity in the genetic relationships between milkability and clinical mastitis.

5 General discussion

5.1 Prospects for improved genetic evaluation of milkability

As measures of the cow's milkability, or milking speed as it sometimes is called, different traits have been used in various studies: milk duration, e.g., milking time, percentage of milk during the first 2 minutes of milking, 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. From the mid 1950s in Sweden, milkability was registered with quarter milking machines in some herds for progeny testing and selection of bull dams (Ral et al., 1988). From 1970 and for about 15 years, progeny testing of bulls was based on the objective measures from milkoscopes, milk duration and percentage of milk during the first 2 minutes of milking. However, in the early 1990s the linear classification system was introduced and since then milkability records reflect the herdsmen's assessment of the milking speed on a scale from 1 to 9. Most other countries with recording of milkability have traditionally also used some kind of subjective scoring on different scales, from 1-3 to 1-9 (Jakobsen, 2006). In the Nordic cattle genetic evaluation (NAV) Sweden and Finland still use subjective scores, whereas Denmark use objective measures, since 2011. Sweden is just in the process of including objective measures, partly depending on the promising results from this thesis.

In this thesis, the traits used as measures of milkability were the ones that are automatically measured during milking and possible to receive from either commercial AMS (paper I) or CMP (paper II) herds. From the AMS the traits AFR and PFR were recorded, but in preliminary analysis they gave almost identical results. Thus, only one measure, AFR, was used in further analyses as it is most widely used internationally. AFR is measured on udder quarter level, but it was decided to add the separate values together to a single value for the

whole udder. It means that flow rate was measured only during the time when each quarter actually was milked. In CMP on the other hand, only total milking time and milk yield were recorded and AFR was calculated as the ratio between them. These differences in calculation of AFR explain the higher means of AFR in AMS than in CMP (paper I-II). In the AMS the total milking time was not recorded, but was received as the ratio between milk yield and AFR for each udder quarter separately and, hence, in the same way also only reflect the time that each quarter actually was milked.

In AMS, information is also available about the occupation time in the milking box and besides the more traditional traits of flow rate and milking duration, two other traits more concerned with the milking efficiency were defined: box time (paper I) and handling time, i.e. the difference between box time and milking time (paper III). Box time is a very important parameter for the cow traffic and for the AMS to be economically efficient. As such, the trait has been studied phenotypically by several others (i.e., André et al, 2010; Castro et al., 2012), but has only been included in one other genetic study (Lovendahl, et al., 2011). It should be considered important to use this trait for further studies and maybe also for genetic evaluation purposes due to its direct economic importance.

5.1.1 Feasibility of in-line recorded milkability for genetic evaluation

The levels of the heritabilities estimated in the studies of this thesis indicate that in-line recorded milking speed data (Paper I-II) are suitable for genetic evaluation of milkability. Heritabilities for AFR and MT were at the same level, or slightly higher, as estimates from other studies based on objective measurements from CMP (e.g. Rensing & Ruten, 2005; Gäde et al., 2007; Dodenhoff & Emmerling, 2009; Byskov et al., 2012; Laureano et al, 2012), but lower compared to the studies based on AMS data (Gäde et al., 2006; Lovendahl et al., 2011; Byskov et al., 2012). However, comparisons of results with the other AMS studies are complicated. The studies by Gäde et al. (2006) and Lovendahl et al. (2011) are both based on data from research herds, which likely operate under more standardized environmental conditions. Furthermore, Byskov et al. (2012) did actually not study milk flow rate, but fat and protein flow. Studies based on subjective scores of milkability generally show lower heritability, between 0.10 and 0.25 (e.g. Meyer & Burnside, 1987; Lawstuen et al., 1988; Luttinen & Juga, 1997; Boettcher et al., 1998; Rupp & Boichard, 1999).

High genetic correlations were found between milking speed measured in different systems, i.e. AMS and CMP (Paper II). The high genetic correlations across systems might seem obvious. However, even though data are captured

automatically in both systems, it is different parameters that are measured, and in this thesis transformed to as similar traits as possible. Furthermore, AMS and CMP represent different ways of handling cows at milking, with CMP data referring to a system with strict milking interval and AMS data referring to a system based on voluntary milkings, usually 2-4 times a day. The results show the potential to use data from different systems jointly for genetic evaluation.

There were high genetic correlations between the milking speed traits AFR and MT (Paper II). The results were expected since flow rate is a function of time. Other studies confirm high genetic correlations, in the range of 0.8 to 0.9, between AFR and MT (Gäde et al., 2006; Gäde et al., 2007; Gray et al., 2011).

The results also showed high genetic correlations between AFR or MT on the one hand and BT on the other (Paper II). It implies that it should be enough to include only one of the traits in the genetic evaluation. BT is suggested to be the best measurement of milking speed for cows in AMS since the aim for improving milkability is to get cows faster through the milking parlour, hence making the BT per cow as short as possible, in order to serve as many cows as possible per milking box. In that perspective, the trait HT is also interesting, since it is totally disconnected from the difference in milk yield between cows. The lower heritability, compared to the milking speed traits AFR, MT or BT, makes the trait less interesting for genetic evaluation purposes. The trait also showed a high genetic correlation with BT (Paper III).

5.1.2 Choice of model

The preferred statistical model in this thesis, for genetic analysis of repeated milkability observations, was a repeatability model. Such a model assumes that variance components are constant during lactation. In Paper II, random regression models, which describe the correlation structure across lactation more accurately, was tested as well. The results showed that the heritability was quite constant during the main part of the lactation. Preliminary analyses showed the same results for the additive genetic variance. Thus, milkability does not have a pronounced lactation profile, like for example milk yield. Other studies (Dodenhoff & Emmerling, 2009; Laureano et al., 2011) have reported high genetic correlations between test-day milkability observations. Hence, they concluded that the possible advantage of using a random regression model may be smaller than for other traits, which confirms our results from the model comparisons.

An adjustment for milk yield at each milking was included in the model. It is well known that milk yield is affecting flow rate. It could be questioned whether an adjustment for yield should be done, as it may be genetically correlated to milkability. However, there are non-genetic factors that affect

flow rate through variation in milk yield. For AMS data this becomes especially important to consider since milk yield fluctuates a lot due to differences in milking interval and when during the day or night the cow is milked. Furthermore, preliminary analyses showed low genetic correlations between yield and milkability, especially flow rate.

5.2 Teat cup attachment failures

As previously mentioned, an advantage with AMS data is the possibility to obtain information of more milkability traits than the traditional milking speed traits. In this thesis one such trait was AtF (Paper III). The trait was based on non-intended automatically recorded teat cup removals. Unintentional teat cup removals will appear either depending on problems for the robot arm to attach the teat cups (i.e. during teat cup attachment), or depending on kick-offs during milking. Unfortunately, we could not separate observations due to the different reasons.

Results in Paper III showed the existence of a genetic association of AtF with general temperament. Kicking is likely to reflect the temperament of the cow and it could be speculated that a trait solely based on teat cup removals during the actual milking process would be higher genetically correlated to temperament. Such trait would be of much interest as a supplement to the subjective scores of general temperament used today. Correspondingly, removals solely due to attachment problems would perhaps result in higher genetic correlations to some udder shape and teat placement traits, and would then clarify the role of udder shape and teat placement for the AMS efficiency.

5.3 Udder conformation

The shape of the udder and size and placement of the teats were traits of great interest when the use of milking machines became broadly adapted (Johansson & Malven, 1960; Johansson, 1961). A similar raise in interest was seen with the introduction of automatic milking systems. It may, for example, be difficult to automatically attach teat cups on cows with deep udders or too wide, or too narrow, teat placement. Even though AMS have been proven efficient to milk a wide variety of udders one can easily imagine that udder shape and teat placement will affect the efficiency of the robot, i.e. the handling time and hence the box time will be affected.

Since 1993 udder conformation traits, together with other conformation traits, are recorded with a linear classification system in Sweden. The cow is described on a scale from 1 to 9, between two biological extremes, for each

trait, once in first lactation. Potential bull dams could be scored once more in second lactation. Today about 30% of all first lactation cows are scored, and the observations are mainly used to give bulls reliable EBVs (Jan-Åke, Eriksson, pers. comm.). With the linear classification system the evaluations became more descriptive than with earlier systems.

AMS use different techniques, ultrasonic systems, laser techniques or CCD camera systems, to localize the teats. The teat detection system creates a three-dimensional view, to help the robot arm to find the position of the teats (de Koning, 2011). Cartesian coordinates (x, y, z), used to specify the three-dimensional view for each teat, were in paper III used as records of some udder conformation traits. The coordinates were used to get the distance in mm between the front and rear teats respectively, and thereby measures of front and rear teat placement. In the same way the coordinates were used to get the distance between the floor and the teats, and thereby get measures of udder depth and udder balance. Additionally, distance between the front and rear teats in right and left udder half respectively were used as a measure of right and left teat placement.

The heritabilities for the udder conformation traits measured by teat coordinates were higher, or of the same level, compared with heritabilities for corresponding traits recorded with linear scores. The genetic correlations between the udder conformation traits measured by teat coordinates and corresponding traits recorded with linear scores were close to unity, over 0.9. The results imply that information from the AMS teat detection system would be useful in genetic evaluation of udder conformation. A similar study on Danish Holstein cows confirm the high genetic correlations between the teat coordinate traits and linear classification traits, and got even higher heritability estimates of the udder conformation traits measured by teat coordinates (Byskov et al., 2012). The latter could be explained by the fact that the Danish study used multiple registrations of teat coordinates whereas only one registration per cow was included in paper III. Even though the linear classification system is considered a rather accurate way of recording with experienced classifiers responsible for the scoring, the observations become more objective with teat coordinates measures and higher heritabilities are therefore expected.

The advantage of making use of teat coordinate measures is not only the objectiveness of the observations. It would also mean that it is possible to get information from more herds than those enrolled in linear classifications today, i.e. all herds with AMS. Moreover, today only a few cows are followed over lactations, teat coordinates make it easy to get information from multiple lactations to follow if the udder conformation changes over parities.

5.3.1 Genetic associations with milkability

There were genetic correlations significantly different from zero between milkability and udder depth, rear udder height, front teat placement, teat length and teat thickness, in such way that high milkability tended to be genetically associated with shallow udders, high rear udder attachment, close front teat placement and short and thin teats (paper III). In Swedish Red there were additional correlations between milkability and udder balance, central ligament and fore udder attachment.

Other studies confirm genetic correlations between udder conformation and milkability, but with some inconsistencies where some studies found associations of milkability to the majority of udder conformation traits (Boettcher et al., 1998; Wiggans et al., 2007), whereas others only found correlations with one, or a few traits (Zwald et al., 2005; Samore, et al., 2010). However, comparisons of results from different studies are difficult because of differences in which udder conformation traits that are included. Contrasting results in different populations could also probably be explained by considering the specific selection strategy practiced for type and production for each breed.

The general trend showed that for udder depth, front teat placement, teat length and thickness (as well as fore udder attachment and udder balance in Swedish Red) the levels of the genetic correlations were higher to the specific AMS-traits BT and HT than to the general milkability traits AFR and MT. The result supports the hypothesis that the shape of the udder and placement and size of the teats affect the efficiency of the robot by affecting the difficulties for the robot arm to attach the teat cups.

5.4   Genetic associations between udder health and milkability

For dairy farmers decreasing the cost of production is often as valuable, or even more valuable, than increasing the income. That is mirrored by the weight that functional traits today are given in the breeding goals together with production traits. Udder health is a very important functional trait. As Carlén (2008) stated there are many reasons, including economic losses, impaired animal welfare and ethical concerns, for why it is important to reduce the mastitis incidence. The heritability for CM is low, commonly reported between 0.01-0.04 (e.g. Rupp & Boichard, 1999; Heringstad et al., 2000; Carlén et al., 2004). Even so, it is possible to genetically improve the trait with selection since the low heritability is caused mainly by large environmental variation, while there is also a significant genetic variation of the trait (e.g. Philipsson et al., 1995; Zwald et al., 2004). Furthermore, high genetic correlations to SCS

(e.g. Sander Nielsen et al., 1997; Rupp & Boichard, 1999; Carlén et al., 2004) make it possible to improve the goal trait of better udder health, i.e. reduced CM also by indirect selection for SCS. Unfortunately though, udder health has previously been shown to be unfavorably correlated to the functional trait of main interest in this thesis, i.e., milkability. Both trait complexes are influenced by the anatomy of the teat canal, which makes an association possible. Though a wider teat canal and sphincter enable higher milk flow rate, it also facilitates access to pathogens (Persson Waller et al., 2003).

There were genetic correlations of 0.30-0.50 between LSCS and milkability (paper IV), meaning that fast-milking cows were found to have higher LSCS. The results were consistent over breeds and lactations. Other studies confirm this relationship, when milkability was recorded subjectively (Lund et al., 1994; Luttinen & Juga, 1997; Boettcher et al, 1998; Rupp & Boichard, 1999), as well as when milkability was objectively measured (Rensing & Ruten, 2005; Zwald et al., 2005; Gäde et al., 2007; Dodenhoff & Emmerling, 2009). The results imply that more selection pressure on milkability will lead to a deterioration of SCS, and hence, support the hypothesis by Persson Waller et al. (2003) that an easier way for the milk out of the udder also leads to an easier way in for pathogens.

The genetic correlations between milkability and CM were, however, not that consistent (paper IV). For Swedish Holstein the results were mainly consistent with LSCS, that is, fast-milking cows were found to have higher risk for clinical mastitis incidence. But, the opposite trend was seen for Swedish Red, hence, fast-milking cows were found to have lower risk for CM early in the lactation. Gäde et al. (2007) reported consistent results to those of Swedish Holstein (paper IV) for German Holstein cows. Previous studies, however, reported non-existent or favorable genetic correlations, i.e., consistent to the results of Swedish Red in paper IV (Lund et al., 1994; Luttinen & Juga, 1997; Rupp & Boichard, 1999, Sorensen et al., 2000; Zwald et al., 2005). According to Zwald et al. (2005), cows that have previously been infected with mastitis could have longer MT because of udder injury, which supports the results in Paper IV for SR cows. Furthermore, the last fraction of milk, during milking, contains much more cells than the foremilk (Miller et al., 1986). A suggested explanation for the inconsistency in correlations between milkability and SCS and CM is, hence, that higher milkability leads to a more complete draining of the udder and therefore to an increased SCS, at the same time as the complete draining helps to avoid CM (Rupp & Boichard, 1999; Rupp & Boichard, 2003).

It has been suggested that it might be a non-linear genetic relationship between udder health and milkability. On the phenotypic level, overall results

from Paper IV showed that too high a milking speed is associated with higher risk for CM. There is an optimum though, and when the milking speed is lower than a certain level, lower milking speed is associated with an accelerated risk for CM as well. The breed difference in level of milking speed, with lower values for SR (Paper I), could then contribute to the inconsistent results between breeds. However, no existence of non-linearity between CM and milking speed was found when fitting regressions of sire EBVs for CM on sire EBVs on milking speed. The results, with no existence of a non-linear genetic relationship between CM and milkability is supported by Zwald et al. (2005) and Gäde et al., (2007)

As results are not fully consistent, and may differ between breeds, it may be essential for future to continuously monitor milkability traits and risks for CM for each breed in order to take appropriate actions to maintain good udder health and milkability with a steadily increasing milk yield.

5.5   Selection index for udder health and milkability

Based on the results from Paper III-IV, an udder health and milkability selection index may be proposed as a way to improve milkability without deterioration of udder health, or even make an improvement in both milkability and udder health possible. Today the udder health index used for genetic evaluation in NAV includes CM and SCC together with the udder conformation traits udder depth and fore udder attachment. In this thesis a selection index was tested with SCS, CM, udder depth and BT included as index traits and CM and BT as goal traits. The selection index was based on data for SH in first lactation of 100 daughters per bull. The results showed that in order to force CM to remain constant, the economic weight set for CM would simultaneously lead to a reduction of 12% in selection response for BT measured as the sire selection efficiency (Table 4). If we would allow the response in BT to be even slower, a genetic gain in both udder health and milkability would be possible. Thus, even though this was a preliminary study of a possible selection index, it implies future possibilities for genetic improvement of both milkability and udder health.

Table 4. Responses from one round of sire selection in box time (BT), udder depth (UD), lactation average somatic cell score (LSCS) and clinical mastitis (CM), for alternative weighting of the goal traits BT and CM

Relative economic weights for CM[1]	Response in sire EBVs			
	BT (min)	UD (scores)	LSCS (10,000 cells/ml)	CM (incidence, 0/1)
-1	-0.95	0.15	0.05	0.02
-13	-0.84	0.30	0	0
-15	-0.80	0.32	0	0
-20	-0.68	0.36	-0.03	-0.01

[1]while keeping the economic weight for BT to -1

6 Conclusions

Automatically in-line measured data from AMS and CMP are useful for genetic evaluation of milkability, and high genetic correlations between traits measured in the different systems show that it is possible to jointly use them for accurate genetic evaluations of both bulls and cows.

AMS data requires extensive data editing but more than enough accurate data are still available for genetic analysis. Data from CMP milk meters requires less editing, but is on the other hand less extensive. However, high repeatabilities of milkability records indicate that it is sufficient with a few recordings for genetic evaluation purposes.

Due to high correlations between the different measures of milking speed, i.e. AFR, MT and BT, it is enough to choose one of the traits. BT is recommended to use in the genetic evaluation for AMS, because of its direct influence of number of cows possible to serve per robot.

A repeatability model is recommended for analysis of milkability data. Although model comparisons showed that genetic merit would be predicted most precisely with a random regression model, only small differences exist between the two different kinds of models in practice. Furthermore, it is recommended to include an adjustment for milk yield in the statistical model.

Records captured by AMS sensors can be used for genetic analysis of premature/unexpected teat cup removals, and the trait, AtF, is genetically correlated to general temperament, which implies that it could be used as an objective supplement for temperament observations in the future.

Udder conformation and teat placement traits measured with AMS teat coordinates show high heritabilities and high genetic correlations to corresponding traits scored by classifiers. Thus, it would be possible to use information from teat coordinates to replace, or be used as a supplement to, classifications for genetic evaluation of udder conformation and teat placement traits.

High milking speed is associated to high SCS. It seems to be a breed difference between milking speed and mastitis dependent on when mastitis occurred in the lactation. In order not to worsen udder health, if more pressure is put on selection against slow-milking cows, it is important to include milkability together with udder health in a selection index, with economic weights that maintain or improve udder health.

For future, it may be essential to continuously monitor milkability traits and risks of mastitis for each breed, as results may differ between breeds, in order to take appropriate actions to maintain good udder health and milkability with a steadily increasing milk yield.

7 Future research

The sensor technology around milking cows is fast moving due to the increasing interest in robotic milking, world-wide. With such a development follows not only an increasing interest in using in-line recordings of data for breeding cows with traits extra desirable for automatic milking, but also data for improved cow health and milk quality. In the near future, focus is suggested to be on the following objectives.

➢ Use of AMS sensor data as measurements of more traits that affect cow health and welfare as well as milk quality. Regarding milkability traits it would be especially interesting to expand the studies of teat coordinates to be able to estimate accurate breeding values for individual cows for udder conformation and teat size and placement traits. Furthermore, the temperament of the cow is important in AMS and it would be of great interest to find more objective ways to measure this trait.

➢ Use of AMS data for genomic selection. This thesis has shown that it is possible to use in-line recorded and repeatedly measured milkability traits for genetic evaluation, in order to obtain accurate breeding values for not only bulls but also for individual cows. Thus, the basis for future use of genomic selection for this trait is provided, with the possibility to include highly accurate breeding values of individual cows in a considerable expansion of the reference population, which normally consists of only bulls. With more experience of using teat coordinates as measurements of udder and teat conformation traits, it applies also to those traits.

➢ Continued studies of possible breed differences in the relationships between milkability and mastitis while considering the continuously increasing milk yield.

8 Genetisk variation i automatiskt registrerade mjölkbarhetsegenskaper och deras samband med juverexteriör och juverhälsa hos svenska mjölkkor

8.1 Bakgrund

Det sker stora strukturella förändringar inom mjölkproduktionen, såväl globalt som nationellt. Besättningsstorlekarna ökar samtidigt som antalet besättningar minskar. År 2013 fanns det 4600 mjölkkobesättningar i Sverige, med i genomsnitt 70 kor per besättning. Utvecklingen med ökande besättningsstorlekar har varit kopplad till utvecklingen av inhysnings- och mjölkningssystem. I början av 1980-talet hade enbart några procent av de svenska mjölkkobesättningarna lösdriftssystem. Men från slutet av 1990-talet är så gott som alla nybyggnationer lösdriftssystem och år 2013 hade siffran ökat till ca 35% (motsvarande 57% av korna). Av dessa använder 21% av besättningarna (31% av korna) automatiska mjölkningssystem (AMS), eller mjölkningsrobotar, som de också kallas. De skandinaviska länderna är idag i topp vad gäller användningen av mjölkningsrobotar. Att införa AMS innebär stora förändringar för mjölkföretagarna, på så vis att mycket av det tidigare fysiska arbetet ersätts med management- och tillsynsuppgifter. Sensorer i mjölkningsroboten övervakar mjölkningsprocessen, och möjliggör på så vis en mer flexibel livsstil för mjölkföretagaren. Samtidigt genererar sensorerna stora mängder data om mjölkningsprocessen, vilka skulle kunna användas som registreringar av viktiga egenskaper, som t ex mjölkflödeshastighet, något som ännu ej till fullo nyttjats.

Att mjölka kor har alltid varit ett tungt och tidskrävande arbete. Mjölkbarhet, som beskriver kons möjlighet att lätt släppa ner mjölken och bli urmjölkad, var därför tidigt en egenskap av stort intresse. Efter andra världskriget blev användningen av mjölkningsmaskiner allt vanligare och

samtidigt ökade arbetskostnaderna, vilket ledde till högre krav på kortare mjölkningstider, liksom på kornas juver- och spenexteriör. Flera lyckade forskningsprojekt med syfte att utveckla metoder för att registrera mjölkbarhet startades från mitten av 1950-talet i Sverige. Från 1970 och ca 15 år framåt baserades avkommeprövningen av tjurar, och testningen av tänkbara tjurmödrar, på objektiva registreringar av mjölkningstid och procent mjölk under mjölkningens 2 första minuter. Men i början av 1990-talet introducerades den linjära beskrivningen av exteriöregenskaper, mjölkbarhet och temperament. Djurskötaren bedömer varje enskild kos mjölkbarhet på en skala från 1 (långsam, trögmjölkad) till 9 (snabb, lättmjölkad). Samtidigt, under de sista decennierna på 1900-talet, minskade intresset för mjölkbarhet allt mer. Detta berodde delvis på att mjölkbarhet verkar vara en optimumegenskap och att ett urval då skett så att de flesta kor passade för de svenska förhållandena, med relativt små och uppbundna besättningar, hade nåtts. Vid avelsmålsrevideringen 1999 togs t.o.m. mjölkbarhet bort från tjurindexet. Men, som redan nämnts, har mycket hänt sedan dess vad gäller såväl besättningsstorlekar och mjölkningssystem där utvecklingen mot mjölkningsrobotar och konventionella gropsystem gått snabbt. Detta ställer återigen stora krav på kornas mjölkbarhetsegenskaper.

Syftet med den här avhandlingen var att undersöka om det vore möjligt att använda automatiska mjölkbarhetsregistreringar i avelsvärderingen. Det gjordes genom att analysera egenskaper från såväl mjölkningsrobotar som konventionella mjölkningsgropar, med avseende på hur stor arvbarhet de har och hur sambanden mellan egenskaper mätta i olika system ser ut, liksom sambanden mellan olika egenskaper som kan användas som mått på mjölkbarhet. Vidare undersöktes vilka genetiska samband det finns mellan mjölkbarhet, juverexteriör och juverhälsa i syfte att utvärdera möjligheten att förbättra såväl kornas mjölkbarhet som juverhälsa.

8.2   Sammanfattning av studierna

Resultaten visade att det är möjligt att använda automatiska registreringar från såväl mjölkningsrobotar som konventionella mjölkningsgropar för genetiska analyser, även om data som kommer direkt från roboten kräver mycket editeringsarbete eftersom robotens dator sparar information om varje mjölkning oavsett om mjölkningen har fungerat normalt eller ej. Analyserna visade att mjölkbarhet mätt som medelflödeshastighet, mjölkningstid eller som den totala tiden som kon uppehåller sig i mjölkningsboxen har en arvbarhet på 20-55%. Vidare visade höga upprepbarheter mellan registreringar, och starka samband mellan laktationer, att det bör räcka med några få

mjölkbarhetsregistreringar i första laktationen, per ko, för att skatta säkra avelsvärden på både tjurar och enskilda kor.

Mjölkningsrobot och konventionella mjölkningsgropar representerar två skilda sätt att hantera korna vid mjölkning, där det ena systemet bygger på frivillig mjölkning, vanligen 2-4 ggr/dygn, medan det andra bygger på strikta mjölkningsintervall som är lika för alla kor. Dessutom definieras, och mäts, egenskaperna på olika sätt i de olika systemen. De starka sambanden mellan systemen indikerar att det bör fungera bra att slå samman data från olika system i gemensamma analyser för avelsvärderingen. Dessutom var sambanden mellan de olika egenskaperna som användes som mått för mjölkbarhet starka, vilket betyder att det räcker att välja ett av måtten. För robotbesättningar föreslås att den totala tid som kon uppehåller sig i mjölkningsboxen är det bästa måttet på mjölkbarhet, tack vare egenskapens direkta påverkan på hur många kor som kan mjölkas per robot.

Delvis mot bakgrund av resultaten i avhandlingens första två studier, håller just nu automatiska registreringar på att implementeras i den svenska avelsvärderingen av mjölkbarhet.

Avhandlingen innehåller också analyser där spen-koordinater, vilka lagras i mjölkningsroboten och hjälper robotarmen att hitta spenarna, fungerade som registreringar av juverexteriör och spenplacering. De starka sambanden mellan de exteriöra egenskaperna registrerade på detta sätt och motsvarande egenskaper bedömda med linjär beskrivning indikerar en möjlig framtida användning av automatiska registreringar som tillägg till dagens linjära beskrivningar av juver- och spenexteriöra egenskaper. Vidare visade resultaten på samband mellan, å ena sidan, hög mjölkbarhet och, å andra sidan, väl anfästade juver, tät spenplacering fram, samt korta och smala spenar.

Sensorer i mjölkningsroboten registrerar också om spenkopparna släpper från spenarna innan mjölkningen är slut. Det kan dels hända under påsättningsprocessen, om robotarmen har problem att hitta spenen och tappar spenkoppen. Dels kan det hända om kon sparkar av spenkoppen under själva mjölkningen. Det visade sig finnas ett samband mellan högre andel mjölkningar där spenkopp fallit av en, eller flera, gåner och nervöst temperament hos kon. Resultaten antyder att det i framtiden kan finnas en möjlighet för automatiska registreringar också av temperament.

De genetiska sambanden mellan mjölkbarhet och juverhälsa visade en tydlig koppling mellan snabbmjölkande kor och högt celltal. Motsvarande samband mellan mjölkbarhet och mastit var dock mer svårtydda och visade på skillnader mellan SRB och Holstein. På fenotypisk nivå verkar det även här generellt finnas ogynnsamma samband mellan snabbmjölkande kor och högre risk att drabbas av mastit. Beroende på när i laktationen korna drabbats av

mastit finns det dock ett samband också mellan trögmjölkade kor och högre risk för mastit. Med andra ord verkar det finnas ett optimum för mjölkbarheten. Den skillnad som finns i nivå på mjölkbarhet mellan raserna, där SRB ligger på en något lägre nivå, framförallt tidigt under laktationen då mjölkbarheten ligger på en lägre nivå generellt, kan vara en förklaring till skillnaderna i resultaten mellan raserna. Holstein verkar ligga närmare gränsen att drabbas av mastit på grund av hög mjölkbarhet.

8.3 Kortfattade slutsatser

Automatiska registreringar, från såväl mjölkningsrobotar som konventionella system med mjölkningsgropar, kan användas vid skattning av avelsvärden för mjölkbarhet. Mjölkbarhet kan mätas på olika sätt, såsom flödeshastighet, mjölkningstid, och i robotsystem också som total tid som kon är i mjölkningsboxen. Det sistnämnda föreslås vara det bästa måttet för mjölkbarhet i AMS. Vidare räcker det med några få registreringar från första laktationen för att skatta säkra avelsvärden för mjölkbarhet på både tjurar och enskilda kor.

Det finns ogynnsamma genetiska samband mellan mjölkbarhet och juverhälsa. För att juverhälsan inte ska försämras i framtiden, om ett ökat tryck läggs på mjölkbarhet, så är det därför viktigt att inkludera mjölkbarhet tillsammans med juverhälsa och juverexteriör i ett selektionsindex. Eftersom det verkar finns skillnader mellan raserna är det viktigt att fortsatt kontinuerligt registrera såväl mjölkbarhet som mastit för respektive ras, för att kunna vidtaga lämpliga åtgärder för en bibehållen god juverhälsa och hög mjölkbarhet.

8.4 Framtidsfrågor

Med det ökade intresset för robotmjölkning följer ett ökat intresse att med hjälp av avel förbättra de egenskaper som är extra viktiga för att korna ska passa för robotmjölkning. Dessutom kommer sannolikt sensorer av olika slag, och som är knutna till robotmjölkningssystem, att ge utökade möjligheter att studera andra egenskaper som t.ex. kan påverka kons hälsa och välbefinnande liksom mjölkens kvalitet. Fortsatta studier om möjligheterna att använda spen-koordinater för att registrera juver- och spenexteriör är intressant, med målet att kunna skatta säkra avelsvärden för enskilda kor. Det vore även önskvärt att finna objektiva sätt att registrera kornas temperament med hjälp av robotdata. Vidare har studierna i den här avhandlingen visat att automatisk registrering av objektiva mått på kornas mjölkbarhet kan användas för att skatta säkra avelsvärden på både tjurar och enskilda kor. Därigenom har grunden lagts för

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References

André, G., Berentsen, P.B.M., Engel, B., de Koning, C.J.A.M. and Oude Lansink, A.G.J.M. (2010). Increasing the revenues from automatic milking by using individual variation in milking characteristics. *Journal of Dairy Science* 93, 942-953.

A:son Moberg, H. (1988). Jordbruket och maskinerna, omdanande utveckling. *Kungliga Skogs- och Lantbruksakademiens Tidskrift*, Suppl 20, 115-138.

Boettcher, P.J., Dekkers, J.C.M. and Kolstad, B.W. (1998). Development of an udder health index for sire selection based on somatic cell score, udder conformation, and milking speed. *Journal of Dairy Science* 81, 1157-1168.

Byskov, K., Buch, L.H. and Aamand, G.P. (2012). Possibilities of implementing measures from automatic milking systems in routine evaluations of udder conformation and milking speed. *Interbull Bulletin* 46, 28-32.

Carlén, E., Strandberg, E. and Roth, A. (2004). Genetic parameters for clinical mastitis, somatic cell score, and production in the first three lactations of Swedish Holstein cows. *Journal of Dairy Science* 87, 3062-3070.

Carlén, E. (2008). Genetic evaluation of clinical mastitis in dairy cattle. *Doctoral thesis. Swedish University of Agricultural Sciences*, Sweden.

Castro, A., Pereira, J.M., Amiama, C. and Bueno, J. (2012). Estimating efficiency in automatic milking systems. *Journal of Dairy Science* 95, 929-936.

De Koning, C.J.A.M. (2011). Milking machines: Robotic milking. *In: Fuquay JW editors. Encyclopedia of Dairy Science.* San Diego, CA: Academic Press. pp 952-958.

De Koning C.J.A.M., Van der Vorst, Y., Meijering, A. (2002). Automatic milking: experience and development in Europe. In: *Proceedings of the first North American conference on robotic milking*, Toronto, Canada, pp. 1-11.

Dodenhoff, J. and Emmerling, R. (2009). Genetic parameters for milkability from the first three lactations in Fleckvieh cows. *Animal* 3, 329-335.

Gjestang, K-E. (1983). Liggeplassens areal og utformning. In: Jamt, O. (red). *Nordisk Jordbruksforskning*. Nr. 4, pp. 585.

Gray, K.A., Vacirca, F., Bagnato, A., Samoré, A.B., Rossoni, A. and Maltecca, C. (2011). Genetic evaluations for measures of the milk-flow curve in the Italian Brown Swiss population. *Journal of Dairy Science* 94, 960-970.

Gäde, S., Stamer, E., Junge, W. and Kalm, E. (2006). Estimates of genetic parameters for milkability from automatic milking. *Livestock Science* 104, 135-146.

Gäde, S., Stamer, E., Bennewitz, J., Junge, W. and Kalm, E. (2007). Genetic parameters for serial, automatically recorded milkability and its relationship to udder health in dairy cattle. *Animal* 1, 787-796.

Heringstad, B. Klemetsdal, G. and Raune, J. (2000). Selection for mastitis resistance in dairy cattle: a review with focus on the situation in the Nordic countries. *Livestock Production Science* 64, 95-106.

Jakobsen, J. (2006). Results of survey for milkability and temperament. *International Bull Evaluation Service*, Uppsala.

Johansson I. (1961). Udder development and milking rate. pp 116-122 in *Genetic Aspects of Dairy Cattle Breeding.* University of Illinois Press, Urbana.

Johansson, I. and Malven, P. (1960). The influence of yield, udder pressure, size of teats and the teat orifice on the rate of milking. *Zeitschrift fur Tierzuchtung und Zuchtungsbiologie* 74, 1-13.

Johansson, I. and Rendel, J. (1963). Juverform, mjölkbarhet och mjölkavkastning. In: Ärftlighet och Husdjursförädling. LT:s förlag. pp 208-211.

Josefsson, G. and Philipsson, J. (1973). Intervjuundersökning som metod för kompletterande avkommebedömning av tjurar. Bearbetning av data från två seminstationer. *Lantbrukshögskolans meddelanden A204*, Institutionen för husdjursförädling, Uppsala.

Larsson, N-E. and Ekström, H. (2000). Exteriörhandboken, handledning och avelsvärdering för exteriöregenskaper. Svensk Mjölk, Hållsta.

Laureano, M.M.M., Bignardi, A.B., El Faro, L., Cardoso, V.L. and Albuquerque, L.G. (2012). Genetic parameters for first lactation test-day milk flow in Holstein cows. Animal 6, 31-35.

Lawstuen, D.D., Hansen, L.B., Steuernagel, G.R. and Johnson, L.P. (1988). Management traits scored by dairy producers. Journal of Dairy Science 71, 788-799.

Lee, D.H. and Chodhary, V. (2006). Study on milkability traits in Holstein cows. *Asian-Australasian Journal of Animal Sciences* 19, 309-314.

Lund, T., Miglior, F., Dekkers, J.C.M. and Burnside, E.B. (1994). Genetic relationships between clinical mastitis, somatic cell count, and udder conformation in Danish Holsteins. *Livestock Production Science* 39, 243-255.

Luttinen, A. and Juga J. (1997). Genetic relationship between milk yield, somatic cell count, mastitis, milkability and leakage in Finnish dairy cattle. *Interbull Bulletin* 15, 78-83.

Lovendahl, P., Lassen, J. and Chagunda, M.G.G. (2011). Genetic analysis of milkability, milking frequency, milk yield and composition in automatically milked cows. pp 80 in Book of Abstracts of *62nd Annual Meeting of the European Association for Animal Production, Stavanger, Norway.* Wageningen Academic Publishers.

Meskens, L. and Mathijs, E. (2002). Socio-economic aspects of automatic milking, motivation and characteristics of farmers investing in automatic milking systems. Deliverable D2 from EU project *Implications of the introduction of automatic milking on dairy farms* (QLK5 2000-31006), www.automaticmilking.nl

Meyer, K. and Burnside, E.B. (1987). Scope for a subjective assessment of milking speed. *Journal of Dairy Science* 70, 1061-1068.

Miller, M.H., Paape, M.J. and Acto, J.C. (1986). Comparison of milk somatic cell counts by coulter and fossomatic counters. *Journal of Dairy Science* 69, 1942-1946.

Moore, R. K., Higgins, S., Kennedy, B.W. and Burnside, E.B. (1981). Relationships of teat conformation and udder height to milk flow rate and milk production in Holsteins. *Canadian Journal of Animal Science* 61, 493-501.

Persson Waller, K., Westermark, T, Ekman, T. and Svennersten-Sjaunja, K. (2003). Milk leakage – an increased risk in automatic milking systems. *Journal of Dairy Science* 86, 3488-3497.

Philipsson, J. (1970). Förenklade mjölkbarhetsundersökningar. Försöksledarmöte, Uppsala.

Philipsson, J., Ral, G. and Berglund, B. (1995). Somatic cell count as a selection criteria for mastitis resistance in dairy cattle. *Livestock Production Science* 41, 195-200.

Ral, G., Berglund, B., Philipsson, J., Emanuelsson, U. and Tengroth, G. (1988). Juver- och mjölkbarhetsegenskaper samt mjölkavkastning och mastitförekomst - effecter av ras och ålder samt inbördes samband. Report, No 78. *Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics.*

Rendel, J. (2003). Mjölkningsteknik, mjölkbarhet och juverformer. In: *Från Byatjur till genteknik.* Kungl. Skogs- och Lantbruksakademien, Stockholm. pp 103-105.

Rensing, S. and Ruten, W. (2005). Genetic evaluation for milking speed in German Holstein population using different traits in a multiple trait repeatability model. *Interbull Bulletin*, 33, 163-166.

Rupp, R. and Boichard D. (1999). Genetic parameters for clinical mastitis, somatic cell score, production, udder type traits, and milking ease in first lactation Holsteins. *Journal of Dairy Science* 82, 2198-2204.

Rupp, R. and Boichard D. (2003). Review article: Genetics of resistance to mastitis in dairy cattle. *Veterinary Research* 34, 671-688.

Sander Nielsen, U., Aamand Pedersen, G., Pedersen, J. and Jensen, J. (1997). Genetic correlations among health traits in different lactations. In: Proc. International workshop on genetic improvement of functional traits in cattle; health. Uppsala, Sweden, June 1997; *Interbull Bulletin* 15, 68-77.

Samoré, A. B., Rizzi, R, Rossoni, A. and Bagnato, A. (2010). Genetic parameters for functional longevity, type traits, somatic cell scores, milk flow and production in the Italian Brown Swiss. *Italian Journal of Animal Science* 9, 145-152.

Sorensen, M. K., Jensen, J. and Christensen, L.G. (2000). Udder conformation and mastitis resistance in Danish firs-lactation cows: heritabilities, genetic and environmental correlations. *Acta Agriculturae Scandinavia, Section A – Animal Sciences* 50, 72-82.

Spahr, S.L., and Maltz, E. (1997). Herd management for robot milking. *Computers and Electronics in Agriculture* 17, 53-62.

Wiggans, G. R., Thornton, L.L.M, Neitzel, R.R. and Gengler, N. (2007). Short communication: Genetic evaluation of milking speed for Brown Swiss dairy cattle in the United States. *Journal of Dairy Science* 90, 1021-1023.

Zwald, N.R., Weigel, K.A., Chang, Y.M., Welper, R.D. and Clay J.S. (2004). Genetic selection for health traits using producer-recorded data. I. Incidence rates, heritability estimates, and sire breeding values. *Journal of Dairy Science* 87, 4287-4292.

Zwald, N.R., Weigel, K.A., Chang, Y.M., Welper, R.D. and Clay J.S. (2005). Genetic evaluation of dairy sires for milking duration using electronically recorded milking times or their daughters. *Journal of Dairy Science*, 88, 1192-1198.

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