Norwegian University of Life Sciences
Faculty of Biosciences
Department of Animal and Aquacultural Sciences

Philosophiae Doctor (PhD)
Thesis 2020:24

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SUPERVISORS

Prof. Bjørg Heringstad
Department of Animal and Aquacultural Sciences
Faculty of Biosciences
Norwegian University of Life Sciences
P.O. Box 5003, 1432 Ås
Norway

Dr. Morten Svendsen
Geno, Breeding and A.I. Association
P.O. Box 5003, 1432 Ås
Norway

EVALUATION COMMITTEE

Prof. Sven König
University of Giessen
Germany

Dr. Jarmo Juga
University of Helsinki
Finland

Dr. Laila Aass
Norwegian University of Life Sciences
Norway

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It is with great respect for the work all the Norwegian farmers are doing, and the demanding task of being a farmer today that I would like to thank all dairy farmers contributing data to our study. Thank you for the positive attitude towards sharing data with us.

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Kulokk

“Å kyri mi vene, å kyri mi !
Her sviv me no glade til sumartid;
i fjellet finn me dei finaste strå;
i dalen strøymer den stride å.
Og vinden stryker så ljuv og linn
som signande sus frå den klåre tind.

Å kyri mi gode, å kyri mi !
Her skal du vel trivast i grøne li;
her sildrar kjelda med surl og skval,
og graset er mjukt og skuggen sval.
Ja Nordanås-lii, der er det godt;
der gjeter huldri kvar einaste nott.

Å kyri mi snille, å kyri mi !
å ha det no godt, denne vesle ri !
Eg ormen skal jaga som bit din legg,
og fluge og mygg og stingande klegg.
Og dagen skal gå som den lette vals;
og vil du kvile, eg klår din hals.

Så lyder dei etter ditt klokkespel,
når heim me stundar ved solegladsbel;
då kjem du så god med ditt fulle jur
og slikkar ditt salt framved kjøken-mur.
Så vert du mjølka og gjeng i kve
og jortar og drøymer og søv ifred.

Å kyri mi vene, og kyri mi !
Drøym godt om meg og den grøne li !
Der sullar me sæle den sumar lang;
til hausten skal me på heimevang.
Då kjem du til gards som ei dronning, du,
og alle ropar: å nei, for ku !!”

Av Arne Garborg

Ås, 2020

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SUMMARY

The overall aim was to investigate several novel phenotypes recorded routinely for individual cows milked in automatic milking systems (AMS). Data were gathered from 77 Norwegian dairy farms, with additional data from the Norwegian Dairy Herd Recording System (NDHRS). Genetic parameters of new milkability, temperament, and udder health traits based on data from AMS were estimated for Norwegian Red (NR) cows.

Paper I aimed at evaluating whether traits subjectively assessed by farmers are the same genetically for cows in different milking systems. Milkability, temperament, and leakage were analyzed for AMS and other milking systems. NDHRS provided data for a total of 260,731 first parity NR cows scored by farmers from year 2009 to 2019. Results revealed strong genetic correlations across milking systems (0.86-0.99). Heritability for farmer-assessed temperament, milking speed, and leakage in AMS herds were 0.05, 0.22, and 0.04, respectively, and 0.09, 0.27, and 0.14 with data from cows milked in traditional milking systems. Lower heritability and phenotypic variation for cows in AMS suggest a need for alternative phenotypic data in future genetic evaluation.

In Paper II, new phenotypic data on milkability and temperament traits from AMS were investigated. Data from 77 herds equipped with milking robots from DeLaval and a total of 1,012,912 daily records from 4,883 NR cows were used in the analyses. Continuous traits such as boxtime, flowrate, and milking efficiency, measured as kg milk per

minute of boxtime, had high heritabilities (0.22-0.48). Also, traits with information of cows' behavior and temperament during milking were heritable (0.01-0.14). Reasonable and strong genetic correlations were estimated between many of the traits, and results confirm that there is a potential for using milkability and temperament traits from AMS in routine genetic evaluations.

In Paper III, data from the same herds were used to investigate novel indicator traits of udder health from AMS. Measurements on electrical conductivity (EC) at quarter level were available from all 77 herds and online cell count (OCC) of milk recorded at milking level were available from 24 herds. From OCC data, elevated mastitis risk (EMR) was calculated as a probability of mastitis on a continuous scale from 0 to 1. Estimated heritabilities ranged from 0.09 to 0.35, and EC-traits had largest heritability. No genetic correlation between OCC-based traits with EC-traits suggest EC to be less important as indicator trait. All AMS traits were genetically correlated (0.34-0.80) with lactation mean somatic cell score (LSCS), a trait used in the current genetic evaluation. Results shows that udder health indicators from AMS are heritable, and some of the traits have great potential for use in genetic evaluation for udder health.

The new milkability, temperament, and udder health traits investigated were heritable, and AMS provides highly accurate and objective information which is possible to use in the genetic evaluation. Traits with high repeatability and heritability can improve accuracies of estimated breeding values. The potential of using data from AMS for genetic evaluations are large, but routinely collection of data is needed. Also, further investigation of the genetic relationship with other important traits in the NR total merit index is necessary before implementation.

SAMMENDRAG

Det overordnede målet var å undersøke flere nye fenotypemål registrert rutinemessig på kyr melket i automatiske melkesystemer (AMS). Data ble hentet fra 77 norske melkekubesetninger, med tilleggsinformasjon fra Kukontrollen. Genetiske parametere ble beregnet for ulike egenskaper relatert til utmelking, lynne og jurhelse hos NRF, basert på data fra AMS.

I første artikkel var målet å undersøke om egenskaper vurdert av gårdbrukeren er de samme for NRF kyr i ulike melkesystem. Kyrnes utmelkingshastighet, lekkasje og lynne, slik de inngår i dagens avlsverdiberegning, ble analysert for besetninger med AMS og for besetninger med tradisjonelle melkesystemer. Kukontrollen bidro med data på totalt 260.731 NRF kyr i første laktasjon som var vurdert av produsenter i årene 2009 til 2019. Genetiske korrelasjoner mellom samme egenskap i ulike melkesystemer var høy (0.86-0.99). Arvbarheten for lynne, utmelkingshastighet og lekkasje var henholdsvis 0,05, 0,22 og 0,04, basert på data fra AMS besetninger og 0,09, 0,27 og 0,14 basert på data fra tradisjonelle melkesystem. Lavere arvbarheter og mindre fenotypisk variasjon for kyr i AMS indikerer at alternative fenotypemål bør vurderes for å beregne avlsverdier i framtida.

I andre artikkel undersøkte vi nye fenotypiske mål på utmelking og lynne målt i AMS. Data fra 77 gårder med melkerobot fra DeLaval, og 1.012.912 daglige registreringer fra 4.883 NRF kyr ble inkludert i analysene. De kontinuerlige egenskapene som bokstid, melkestrøm,

og melkingseffektivitet, målt som kg melk per minutt bokstid, hadde høye arvbarheter (0.22-0.48). Egenskaper med informasjon om kyrnes lynne og oppførsel under melking var arvelige (0.01-0.14). Logiske og sterke genetiske korrelasjoner ble estimert mellom mange av egenskapene, og resultatene bekrefter potensialet for å benytte utmelkings- og lynne egenskaper registrert i AMS som informasjon i avlsverdiberegningen på NRF.

I tredje artikkel ble data fra de samme gårdene benyttet for å undersøke nye indikatorer på jurhelse fra AMS. Målinger på elektrisk konduktivitet (EC) i melk på spenenivå var tilgjengelig fra alle 77 gårder, og celletall (OCC) på melkingsnivå var tilgjengelig fra 24 av gårdene. Fra OCC dataene ble et mål på forhøyet mastitt risiko (EMR) beregnet som en sannsynlighet for mastitt på en kontinuerlig skala fra 0 til 1. Estimerte arvbarheter varierte fra 0.09 til 0.35, og EC-egenskapene hadde høyest arvbarhet. Ingen genetisk korrelasjon mellom OCC-baserte egenskaper med EC indikerer at konduktivitet er mindre verdifull som indikator egenskap for jurhelse. Alle jurhelse-egenskaper fra AMS var genetisk korrelerte til gjennomsnittlig laktasjonscelletall (0.34-0.80) som benyttes i dagens avlsverdiberegning. Resultatene viser at jurhelseindikatorer fra AMS er arvbare, og at enkelte egenskaper har et stort potensial i avlsvurderingen av jurhelse.

De nye egenskapene relatert til utmelking, lynne og jurhelse var arvbare, og viser nytten av objektive data fra AMS til å beregne avlsverdier. Egenskaper med høy gjentaksgrad og arvbarhet kan øke sikkerheten på avlsverdiene. Potensialet for å benytte AMS data i avlsverdiberegning er stort, men rutinemessig innsamling av disse dataene må på plass. I tillegg bør de genetiske sammenhengene til andre viktige egenskaper for NRF undersøkes før en eventuell inkludering i avlsverdiberegningene.

LIST OF ABBREVIATIONS

A.I.	Artificial insemination
AMS	Automatic milking systems
BT	Boxtime (min)
BLUP	Best linear unbiased prediction
CM	Clinical mastitis
DIM	Days in milk
EBV	Estimated breeding value
EC	Electrical conductivity (mS)
ECmax	Maximum electrical conductivity (mS)
ECmean	Mean electrical conductivity (mS)
EMR	Elevated mastitis risk
FR	Flowrate (kg / min milking)
HT	Handlingtime (min)
IM	Incomplete milking (no.)
KO	Kick off (no.)
lnEMR	Log-transformed elevated mastitis risk
lnHT	Log-transformed handlingtime
lnOCC	Log-transformed online cell count

LSCS	Lactation-average somatic cell score
MEF	Milking efficiency (kg / min boxtime)
MF	Milking frequency
MI	Milking interval (hour)
NDHRS	Norwegian dairy herd recording system
NR	Norwegian Red
OCC	Online cell count (1000 cells / ml milk)
pIM	Proportion of incomplete milkings
pKO	Proportion of kick offs
pRM	Proportion of rejected milkings
pTNF	Proportion of teats not found
RM	Rejected milking
SCC	Somatic cell count
SCS	Somatic cell score
TMI	Total merit index
TNF	Teat not found

LIST OF PAPERS

I. Wethal, K. B., Svendsen, M., and Heringstad, B. 2020. Are farmer assessed temperament, milking speed, and leakage genetically the same traits in automatic milking system as in traditional milking systems? *Accepted by Journal of Dairy Science.*

II. Wethal, K. B., and Heringstad, B. 2019. Genetic analyses of novel temperament and milkability traits in Norwegian Red cattle, based on data from automatic milking systems. *Journal of Dairy Science 102:8221-8233.*

III. Wethal, K.B., Svendsen, M., and Heringstad, B. 2020**.** A genetic study of new udder health indicator traits with data from automatic milking systems. *Submitted to Journal of Dairy Science.*

1. GENERAL INTRODUCTION

1.1 Background

The dairy industry is a large contributor to the world's increasing demand for food, and 80% of the world population are consuming dairy products (FAO and GDP, 2018). The structural changes in developed countries towards larger herds continues, along with the reduction in number of dairy farms (Barkema et al., 2015). In the Nordic countries, dairy cows per unit have increased rapidly over several years, and individual cows are becoming more efficient and productive (Statistics Denmark, 2014, Tine, 2019, Swedish Board of Agriculture, 2018). Structural changes in the recent decades have increased automatization of dairy farms which has led to the invention of automatic milking systems (AMS) in the 1990s. The main driver for inventing the AMS was to improve milking efficiency and reduce dairy farmers physical workload (Rossing and Hogewerf, 1997). The first AMS was introduced in Norway in 2000, and since then the number of AMS have increased rapidly. The number of AMS have also increased in other Nordic countries. The system is still gaining popularity, and the proportion of cows on herds with AMS is especially high in Norway (Tine, 2019).

The AMS records vast amounts of data on many characteristics of individual cows. Because measurements are stored from every visit, the information is repeated and includes both milkings and visits in between milkings. These objective data can potentially be used for genetic evaluation, where objective data are beneficial and might increase accuracy of the breeding values. In addition, they might substitute subjective records of certain traits that are recorded routinely by farmers or advisors today in the routine genetic evaluation. Furthermore, there is potential for the AMS to contribute information on novel or additional traits, and to give extra information on current traits and possibly replace some of them in the future. For example, the current assessment of the cow's milking speed is scored subjectively once during first parity. The farmers score their cows on a 3-point scale. With records from AMS, accurate information on flow rate from each milking are available. Studies have shown that milkability and temperament traits in AMS have higher heritabilities (Carlström et al., 2016a). This is beneficial because larger heritability relates to increased genetic progress and selection response (Lynch and Walsh, 1998) and gaining larger selection response is of economic importance in a selection scheme.

High repeatability is reported for continuously recorded traits in AMS (Carlström et al., 2014), and both higher repeatability and heritability improves accuracies of estimated breeding values (Lynch and Walsh, 1998). Therefore, this study aimed at investigating genetic aspects of sensor data from AMS based on data from Norwegian dairy herds. The potential of using phenotypic data from AMS in routine genetic evaluations was the overall motivation of this thesis, and genetically interesting traits such as milkability, temperament, and udder health was the main focus. But first, an introduction including an overview of the dairy industry in Norway, and a brief introduction of the selection program of Norwegian Red (NR) dairy cattle is given.

1.2 The Norwegian Dairy Industry

1.2.1 Herd Size and Milking Systems

Dairy production in Norway is moving towards larger herds, and a rapidly increasing number of milking robots. In 2018, 45% of the Norwegian dairy cows were milked by an AMS (Tine, 2019). The first commercial Norwegian farm installed AMS 20 years ago, and the popularity of such systems has increased since. Figures from 2017 showed that the number milking robots in Norway were far above numbers in the other Nordic countries (Figure 1). The number of AMS in Norwegian herds have now reached 2,000 units (Vik et al., 2019). Almost 50% of the total Norwegian milk volume was produced by herds with milking robots in 2018, according to the Norwegian dairy herd recording system (NDHRS) (Tine, 2019).

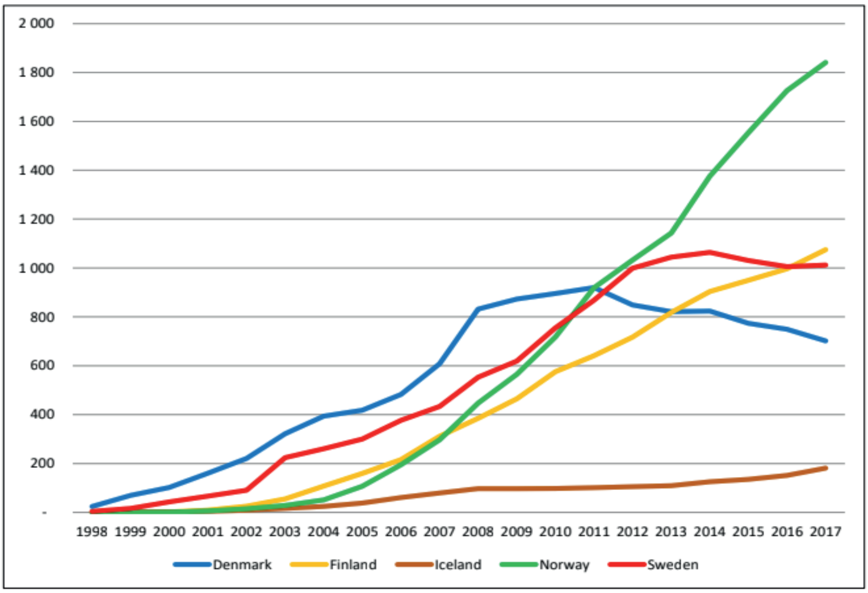

Figure 1. Number of automatic milking system units in Scandinavian countries by 2017 (Tine, 2017).

The picture is different looking at the percentage of farms, and in 2018 only 25% of Norwegian dairy farms were equipped with AMS (Figure 2), which is lower than the neighboring countries, Denmark and Sweden (Barkema et al., 2015). But because AMS herds on average are larger than others, they have a larger contribution to Norwegian milk production. A further increase in the number of herds with AMS is expected in the future due to restrictions in use of tiestall systems after 2034.

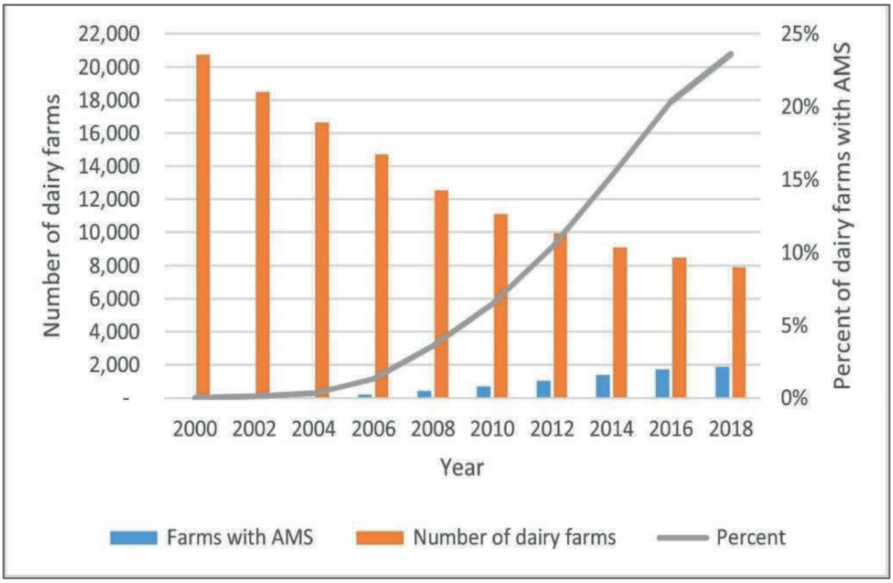

Figure 2. The number of Norwegian dairy farms with automatic milking systems (AMS) and the percentage of farms with AMS out of the total number of farms (Vik et al., 2019).

The economic margins of larger farms are probably smaller and expanding herd size is related to higher capital costs (Steeneveld et al., 2012). Automatization and installing AMS is costly, some farmers might compensate for this with increasing their income from milk thus expanding herd size. This strategy to handle increased expenses is one of the contributing factors that have moved Norwegian dairy farms towards larger herd-units and increased production level. Despite this, economical motives are less important than social motives for Norwegian farmers when investing in AMS (Vik et al., 2019). Farms with AMS have higher production, require more arable land, thus the investment might increase amount of work. Farmers’ reasons for investing in AMS might vary. Norwegian farmers' three main reasons for changing to these milking systems are reported by Vik et al., (2019); 1) AMS offers them flexibility at work, this means less strict working time and more opportunity for spending time with family and friends, 2) Less physical workload related to the milking process, 3) Motivations for technological development, and investment in the farm's future. Especially for young farmers, social time and time off work are probably very important. The AMS provide an opportunity to work during the daytime, while with the milking routines in traditional milking systems they must work late evenings at the expense of social life.

1.2.2 Regulations and Political Means

The technological change and increased production level on Norwegian dairy farms is, to some extent, driven by political motives that have influenced the change in National regulations (Vik et al., 2019). Dairy production is regulated, and this enables dairy farmers to maintain relatively stable incomes from milk production. Restrictions on the maximum production level is mainly to prevent units from becoming too large and keep the family-driven structure. Milk quotas apply only within certain areas, and act as political means against centralization of milk production (Norwegian Agriculture Agency, 2020). In 2014, the maximum milk production permitted per farm was doubled to 900,000 liters by the Norwegian government (Vik et al., 2019).

1.2.3 Cooperatives and Data Management

The large number of contributing herds in the NDHRS can be, in part, attributed to the long tradition of farmer-owned cooperatives and willingness to share data. The participation rate increased from 95% to almost 98% from 2002 to 2018 (Tine, 2019). The tradition of sharing data in the national database has been an important factor and has led to the establishment of both feeding advisory and the breeding organization, both of which are owned by the farmers. This has been a well-established system where both farmers and advisors play an important role in recording data in NDHRS. Sharing data is one of the cornerstones of the successful breeding program of NR. More than 90% of the cows included in NDHRS were of the NR breed in 2018 (Tine, 2019).

1.3 Breeding of Norwegian Red

The NR is a dual-purpose breed, and the breeding program started in 1935 (Geno, 2020). Individual health treatments have been recorded by veterinarians and are integrated in NDHRS with records on individual cows' health dating back to 1978 (Ruane et al., 1997). This made it possible to include health and fertility traits in the NR breeding program.

1.3.1 Traits of Norwegian Red

Historically a large number of traits have been included in the NR selection program. In the 1970s, both fertility and health traits were included in the total merit index (TMI), and these traits have received gradually more weight over the years (Figure 3). Currently the health and fertility traits are weighted with approximately 30%. Today, more than 40 different traits are included in the routine genetic evaluation.

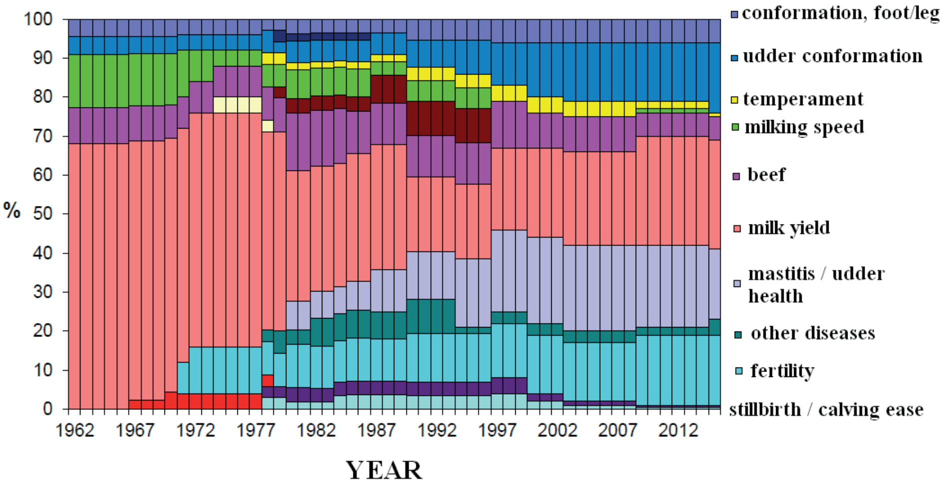

Figure 3. The development of the relative weight on trait groups included in the total merit index of Norwegian Red, percentage of weight on the y-axis and year on the x-axis (www.geno.no).

The breeding program for NR was based on daughter proven sires until 2015. Around 120 young bulls were tested each year and among these the 10-12 best bulls were selected to be elite sires after they were progeny tested. Sixty percent of inseminations were from elite sires and the other 40% were from young bulls.

After 2015, the selection of bulls changed from progeny testing to a breeding scheme based on genomic selection. Today, around 8,000 bull calves born each year are potential candidates for genotyping (Figure 4). Among these around 2,500 bull calves are genotyped and among these, the 150 bull calves with the best genomic breeding value (GEBV) are selected and bought by Geno. A phenotypic evaluation of traits such as conformation, growth performance, temperament, and semen characteristics are performed at the test station before 50-60 bulls are selected for A.I. each year. In addition to the selected bull calves, around 10,000 heifer calves born each year are potential candidates for genotyping; around 90 of these are bought by Geno and selected for embryo-production (Figure 4).

Single-step genomic prediction is used for calculation of breeding values for NR. This method combines all available phenotypic data with both pedigree and genomic information (Aguilar et al., 2010). Using the single-step method means that all NR animals, also animals that are not genotyped, receive a GEBV (Geno, 2019). With genomic selection, the number of tested bulls at the performance test station are decreased from 300 to 150 per year, but the number of elite sires increased to 50-60 per year due to the risk of inbreeding (Figure 4).

One of the main benefits of using genomic selection is the increased genetic gain due to shorter generation interval as this method enables bulls to be selected and bred at an earlier age (Geno, 2016). Even though genomic information from genotyped animals are available, it is important to have good phenotypic information on all traits in the selection scheme. Phenotypic information on the different traits are registered on dairy cows on commercial farms and available from NDHRS. Health traits and treatments are recorded by Veterinarians. Production and workability traits such as milk yield, milking speed, leakage, and temperament is recorded by the farmers, whereas conformation traits are assessed by classifiers.

This thesis mainly focused on use of data from the AMS to define new traits as a supplement or replacement for current traits in the breeding program. As a starting point we chose to investigate milkability, temperament, and udder health. Therefore, how these traits are recorded and used in the current genetic evaluation for NR is further explained below.

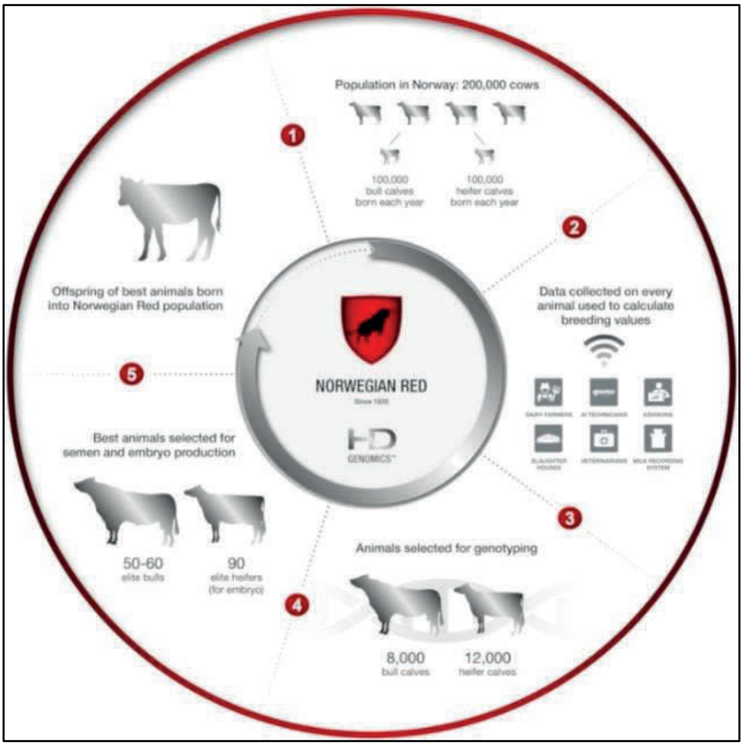

Figure 4. The breeding program of Norwegian Red, with 50-60 elite sires and around 90 elite heifers for embryo production being selected yearly. Selection relies on a genomic breeding value from single step-genomic prediction (Geno, 2019).

1.3.2 Workability

Workability traits such as temperament, milking speed and leakage are important as they might affect farmers' workload and profit. Currently, these three traits are recorded by the farmer, scored once on first parity NR cows on a categorical scale from 1-3, with a lower number being favorable.

Temperament has been included in the TMI for NR since 1978 and was originally scored by trained technicians in addition to the farmer's own assessment during milking. Since 2000, phenotypic records of these traits have been based on the farmer's own assessment, as cows milking temperament as 1 (extra nice), 2 (ordinary), and 3 (bad tempered). Farmers are instructed to assess this trait during milking, from day 30 in milk. Temperament of NR is weighted by 0.5% in the TMI and reported to have a heritability of 0.08 (Interbull, 2019a).

Milking speed and leakage were first included in the breeding goal for NR in 1960 and 1979, respectively. In the beginning both traits were measured by technicians. Milking speed were measured as milk flow in kg/min for the first two minutes of the milking, but since 1989 the farmer's own assessment of milking speed as 1 (fast), 2 (intermediate), and 3 (slow) are reported on each first parity cow. Leakage is reported on the same cows, but as observed leakage between milking as 1 (no), 2 (some), and 3 (obvious) leakage. Milking speed and leakage is currently weighted with 2.0% and 0.5%, respectively. Their heritability is 0.19 and 0.11, respectively as included in current breeding value estimation of NR cows (Interbull, 2019a).

1.3.3 Udder Health

Recording of health traits are integrated in the NDHRS, and each treatment have been recorded by veterinarians since 1975 (Ruane et al., 1997), which makes Norwegian health records a reliable source of information in the selection towards improved udder health. Selection for udder health in NR cows started in 1978 and were based on information on clinical mastitis (CM) measured as a binary trait as healthy or infected (0,1), where 1 indicated at least one treatment. in 2014, somatic cell count (SCC)was added to the udder health index. SCC was included because CM have a low heritability and frequency. In the genetic evaluation, CM is defined as 7 binary traits. Clinical mastitis in first to third parity is included, and each lactation is divided in shorter periods; three periods in first parity, two in each of second and third parity. In the udder health index, each parity is weighted by one third each (Interbull, 2019b). This means that CM in the 7 periods are considered a genetically correlated trait. Test day SCC is measured every second month in Norway. The trait used in genetic evaluation is lactation average somatic cell score (LSCS) of first to third parity cows. Udder health is currently weighted with 13.4% in the TMI of NR, and the relative weight of LSCS and CM is 69.4% and 30.6%, respectively (Interbull, 2019b). Udder health is an economically important trait necessary to consider in dairy cattle breeding. Increased milk yield has an antagonistic genetic correlation to udder health (Luttinen and Juga, 1997; Windig et al., 2006), therefore, genetic selection for improved udder health is important.

The number of CM treatments in Norway have decreased in recent years, from 0.2 per cow-year in 2008 to 0.138 per cow-year in 2018 (Tine, 2019). The reduced frequency of CM allows for including other aspects of udder health in the genetic evaluation. Therefore, to start looking into using other sources of information is beneficial for further genetic improvement of udder health.

In automatic milking systems, sensors are developed to help the visual inspection and quality control of the milk before it enters the milk tank. The standard equipment measures electrical conductivity. Other sensors like OCC measure the number of white blood cells in milk contributing with more direct information on udder health status. Electrical conductivity has been investigated for genetic purposes by others (Norberg et al., 2004a; b; Santos et al., 2018). Test-day SCC are used as indicator trait in the routine genetic evaluations (Heringstad et al., 2000), but repeated records on cell count from every milking are available from AMS (Sørensen et al., 2016). Compared to SCC registered routinely every month, data from AMS can contribute with a more detailed picture on the cow's udder health status, and in general AMS provides longitudinal data of repeated records for each cow.

2. AIMS AND OUTLINE

The main objective of the current PhD project was to investigate how objective and repeated measurements from AMS could be used to define new milkability, temperament, and udder health traits to be used in genetic evaluation. The first paper was based on registrations from NDHRS used in the current genetic evaluation for herds with different milking systems, whereas the two last papers used phenotypic data collected from AMS. Specific aims of this study were to estimate genetic parameters of new traits derived from AMS data and evaluate their potential for use in genetic evaluation and thereby selection for an efficient and healthy dairy cow.

The following objectives were investigated in three scientific articles:

1. Examine whether farmer-assessed temperament, milking speed, and leakage genetically are the same traits in AMS as in traditional milking systems.

2. Estimate genetic parameters of novel milkability and temperament traits from phenotypic data in AMS.

3. Identify new phenotypes from AMS, for an in-line measure of udder health traits and estimate genetic parameters for these traits and their genetic relationship with current udder health trait(s).

3. DATA MATERIAL

The data material included in the first paper derived from the NDHRS. Information were on workability traits routinely scored by the farmer and used in the genetic evaluations. AMS data used in the two last articles was downloaded manually from each of the 77 herds directly from the AMS software, DeLaval DelPro version 3.7, 4.5, or 5.2. Herds with AMS were chosen according to the distribution of dairy herds across Norway, and all counties were represented. The farmers gave oral permissions before data was downloaded from their AMS. The number of observations and animals with data used in the three scientific articles are given in Table 1. Statistical method and models used in genetic analyses are explained separately in each scientific article.

Table 1. Data sources for the traits included in genetic analyses in the scientific papers, the total number of observations, cows, parities, and years of data.

	PAPER 1	PAPER 2	PAPER 3
Data source	NDHRS	AMS	AMS
Number of observations	260,731	1,012,912	2,363,928
Numbers of cows	260,731	4,883	4,714
Years with observations	2009-2019	2015-2017	2015-2017

PAPER I

Wethal, K. B., Svendsen, M., and Heringstad, B. (2020)

Are farmer assessed temperament, milking speed, and leakage genetically the same traits in automatic milking system as in traditional milking systems?

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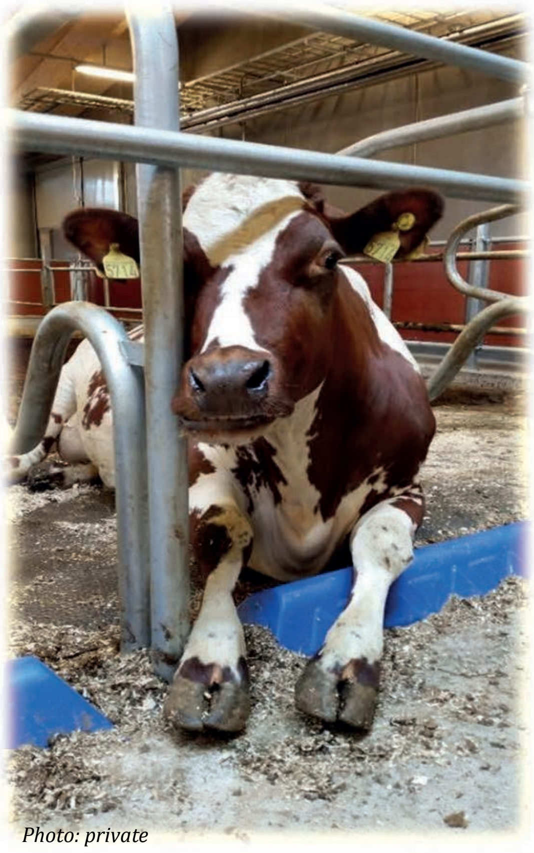

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Are farmer assessed temperament, milking speed, and leakage genetically the same traits in automatic milking system as in traditional milking systems?

K. B. Wethal,*[1] **M. Svendsen,**[2] **and B. Heringstad.**[1]

[1]Department of Animal and Aquacultural Sciences, Faculty of Biosciences, Norwegian University of Life Sciences, P.O. Box 5003, 1432 Ås, Norway

[2]GENO Breeding and A.I Association, 2326 Hamar, Norway

*Corresponding author: karoline.bakke@nmbu.no

ABSTRACT

The aim was to investigate whether subjectively scored milking speed, temperament, and leakage are genetically the same trait when measured in different milking systems. Data were provided by the Norwegian Dairy Herd Recording System and included a total of 260,731 first parity Norwegian Red cows calving between January 2009 and February 2019 and milked either in a traditional milking system (milking parlor or pipeline) or by an automatic milking systems (AMS). Genetic parameters were estimated and resulted in lower heritabilities and less genetic variation for the three traits when measured in AMS herds. The heritability of temperament, leakage, and milking speed were 0.05, 0.04, and 0.22 respectively, with data from AMS herds; and 0.09, 0.14, and 0.27 respectively, with data from cows milked in traditional milking systems. The genetic correlation between temperament and leakage of -0.19, between milking speed and leakage of -0.88, and between milking speed and temperament of 0.30 in AMS, was slightly stronger than between the corresponding traits assessed in other milking systems (-0.15, -0.82, and 0.16, respectively). The genetic correlations between traits across milking systems were strong; 0.98, 0.96, and 0.86 for milking speed, leakage, and temperament, respectively. Strong correlations indicate that the traits were almost genetically similar despite being scored in different milking systems. The rank-correlation among estimated sire breeding values were strong; 0.98 and 0.99 for milking speed and leakage, with little or no re-ranking of bulls performance across milking systems. Temperament had the lowest genetic correlation (0.86) and rank-correlation (0.91) across milking systems. These data suggest that AMS farmers evaluate temperament slightly differently from farmers using other milking systems or that different aspects of temperament are important for farmers with AMS.

Key words: Workability, genetic correlations, AMS, milking parlor.

INTRODUCTION

Dairy production in Norway is moving towards larger herds with more automatic milking systems (**AMS**). In 2018, 45% of the Norwegian dairy cows were milked by AMS (Tine, 2019) a proportion expected to increase further. The workability traits; temperament, milking speed, and leakage have been included in the selection program for Norwegian Red (**NR**) since the 1970s. Genetic evaluation of these traits are based on owner assessments of first parity cows on a 3-point scale, with 1 being favorable and 3 unfavorable. Workability in freestall systems is important, especially due to tightened time budgets in larger herd units.

Subjectively scored workability traits are reported to have heritabilities from 0.05 to 0.35 (Jakobsen et al., 2008). Leakage is not commonly included in routine genetic evaluations. Undesirable dripping of milk from the udder between milkings can transmit udder bacteria between individuals when milk is left in the stall, and is associated with a higher risk of mastitis (Persson Waller et al., 2003). Heritability of leakage has been estimated to 0.08 in first parity Holstein and Ayrshire cows (Luttinen and Juga, 1997), and 0.14 for NR cows (Bakke and Heringstad 2015). An unfavorable genetic correlation between milking speed and leakage of 0.65 have been estimated for Finnish dairy cattle (Luttinen and Juga, 1997), and an even stronger correlation of -0.84 was estimated for NR by Bakke and Heringstad (2015) where reversed scales for leakage and speed lead to a negative value. Heritability of farmer assessed milking speed range from 0.10 to 0.24 in literature (Luttinen and Juga, 1997, Rensing and Ruten, 2005, Wiggans et al., 2007, Sewalem et al., 2011), whereas larger heritability estimates were reported for milking speed measured more exactly e.g. as kg of milk per minute (Carlström et al., 2014, Wethal and Heringstad, 2019). Heritability of temperament, phenotypically scored from easy/calm to uneasy/nervous, range from 0.05 to 0.21 in various breeds and countries, according to the international genetic evaluations of workability traits reported by Jakobsen et al. (2008). Sewalem et al. (2011) estimated similar heritabilities of temperament ranging from 0.13 to 0.20. To this date, few studies investigating differences of farmer-assessed traits between milking systems has been done. There is an interesting question whether the subjectively scored workability traits are genetically the same trait in AMS as in traditional milking systems (pipeline or milking parlor). One approach to examine this is to define traits measured in different systems as different traits and estimate the correlation between them. A genetic correlation <1 would then indicate that farmers do not necessary measure the same genetic trait when they score workability traits. If so, a revision of the genetic evaluation of the trait may be recommended. A similar approach was used by Lassen and Mark (2008), who estimated a strong genetic correlation between tiestall and freestall for both temperament and milking speed (0.95 and 0.94). We aimed to compare AMS and other milking systems with the following hypotheses. (1) A lower frequency of cows are scored for leakage in AMS, (2) milking speed scored in AMS herds have better quality and variation because farmers have access to extra information on for example, flowrate; and (3) temperament of AMS cows is not the same trait genetically as temperament in other milking systems because other aspects are favored by the farmers. The specific aims of our study were thus to estimate heritability and genetic correlations among workability traits within the same type of milking system, and to estimate genetic correlations across milking systems to evaluate whether farmer-assessed temperament, milking speed, and leakage of NR cows are genetically the same traits for different milking systems.

MATERIALS AND METHODS

Data Material

The Norwegian dairy herd recording system (**NDHRS**) provided all necessary data to this study. First parity cows with calving dates from January 2009 to February 2019 were included for genetic analyses. The pedigree was traced back as far as possible, up to eight generations. All herds had information about barntype (tiestall or freestall) and milking system (pipeline, milking parlor, or AMS), that made it possible to compare traits recorded on cows in different systems.

Traits

The workability traits milking speed, leakage, and temperament were scored subjectively by the farmer on a scale from 1 to 3. Milking speed was scored as 1 (fast), 2 (intermediate), or 3 (slow). Temperament was scored as 1 (extra nice), 2 (ordinary), or 3 (bad-tempered/mean). Leakage of milk between milkings was scored with 1 (no), 2 (some), or 3 (obvious dripping of milk). The traits are routinely scored in first parity, and the guidelines suggests temperament to be scored during milking and all traits to be scored 30 days after calving. Each trait also had a fourth category of “unknown”, but this class did not enter the genetic analyses. We defined farmer-assessed workability traits in herds with AMS and in herds with “traditional” milking systems (milking parlor or pipeline) as different traits, which gave 6 traits in total.

Data Edits

To ensure only reasonable records being included in the genetic analyses, we applied the following restrictions to the dataset: Each cow had a known NR AI sire, scoring of each trait was performed between day 30 and 320 after first calving, and age at calving was between 21 and 32 months. Further, we restricted the dataset to include only herds with at least 15 cows evaluated for the traits over a 5-year period. The final dataset contained 260,731 cows in total, with an assessment of workability either in AMS or in other milking systems. Descriptive statistics and number of cows included in the analysis for each trait are given in Table 1.

Statistical Method and Models

The (co)variance components were estimated for the six workability traits; temperament, milking speed, and leakage in AMS, and correspondingly in other milking systems. The genetic correlations within and between milking systems were estimated. The DMUAI package, for average information restricted maximum likelihood method (AI-REML) in the DMU software by Madsen and Jensen (2013) was used. Fixed effects were included in the model if the effect was significant with $p < 0.01$ in analyses by GLM procedure in SAS (version 9.4; SAS Inst. Inc., Cary, NC).

Models. Bivariate models were used to estimate the (co) variance components, as follows:

$$\begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\end{bmatrix} = \begin{bmatrix}\mathbf{X}_1 & 0\\ 0 & \mathbf{X}_2\end{bmatrix}\begin{bmatrix}\mathbf{b}_1\\ \mathbf{b}_2\end{bmatrix} + \begin{bmatrix}\mathbf{Z}_1 & 0\\ 0 & \mathbf{Z}_2\end{bmatrix}\begin{bmatrix}\mathbf{a}_1\\ \mathbf{a}_2\end{bmatrix} + \begin{bmatrix}\mathbf{e}_1\\ \mathbf{e}_2\end{bmatrix}$$

where $\mathbf{y}_1$ and $\mathbf{y}_2$ were vectors of observations of 2 traits; milking speed, temperament, or leakage in either AMS or other milking systems. The incidence matrices $\mathbf{X}_1$ and $\mathbf{X}_2$ relates each observation to the fixed effects in $\mathbf{b}_1$ and $\mathbf{b}_2$. The $\mathbf{Z}_1$ and $\mathbf{Z}_2$ were incidence matrices relating the random additive genetic effects of animal in $\mathbf{a}_1$ and $\mathbf{a}_2$ to each observation, while $\mathbf{e}_1$ and $\mathbf{e}_2$ is the random residual effects for the 2 traits. For the additive genetic effect of animal ($\mathbf{a}$) the following assumptions were made:

$$\begin{bmatrix}\boldsymbol{a}_1\\ \boldsymbol{a}_2\end{bmatrix} \sim \mathrm{N}\left(\begin{pmatrix}0\\ 0\end{pmatrix}, \mathbf{A} \otimes \begin{pmatrix}\sigma^2_{a_1} & \sigma_{a_1 a_2}\\ \sigma_{a_1 a_2} & \sigma^2_{a_2}\end{pmatrix}\right),$$

where $\mathbf{a}_1$ and $\mathbf{a}_2$ were additive genetic effect of animal for the two traits, assumed to be normally distributed, with expectation 0. $\mathbf{A}$ was the additive relationship matrix containing 805,008 animals. The Kronecker product was denoted by $\otimes$. The components $\sigma^2_{a_1}$ and $\sigma^2_{a_2}$ denoted the additive genetic variances for the two traits and $\sigma_{a_1a_2}$ the additive genetic covariance between the traits. Following assumptions were made about the residual effects assigned two traits within milking systems:

$$\begin{bmatrix}\boldsymbol{e}_1\\ \boldsymbol{e}_2\end{bmatrix} \sim \mathrm{N}\left(\begin{pmatrix}0\\0\end{pmatrix}, \mathbf{I} \otimes \begin{pmatrix}\sigma_{e_1}^2 & \sigma_{e_1e_2}\\ \sigma_{e_1e_2} & \sigma_{e_2}^2\end{pmatrix}\right),$$

where $\mathbf{e}_1$ and $\mathbf{e}_2$ were normally distributed with expectation 0, **I** was an identity matrix, $\sigma_{e_1}^2$ and $\sigma_{e_2}^2$ were the residual variance for the two traits, and $\sigma_{e_1e_2}$ was the residual covariance between the traits. For estimating genetic correlations between the same workability trait across milking systems, the following assumptions were made about the residuals in the model:

$$\begin{bmatrix}\boldsymbol{e}_1\\ \boldsymbol{e}_2\end{bmatrix} \sim \mathrm{N}\left(\begin{pmatrix}0\\0\end{pmatrix}, \mathbf{I} \otimes \begin{pmatrix}\sigma_{e_1}^2 & 0\\ 0 & \sigma_{e_2}^2\end{pmatrix}\right),$$

where no covariance existed between the residuals and therefore $\sigma_{e_1e_2}$ was restricted to zero for traits assessed in different milking systems.

Fixed Effects. The following fixed effects were included in the models for milking speed, leakage, and temperament: Calving year and month, with 121 levels from January 2009 to February 2019; age at first calving, with 12 classes from 21 to 32 months; and days in milk grouped in 12 periods of ~ 25 days each. Finally, the fixed effect of herd by year grouped in 5-year periods due to small subclasses of animals, was included. The total number of levels for herd by 5-year were 1,548 and 6,326 in AMS and in other milking systems, respectively. Additionally, type of milking system was included as fixed effect in model when workability in other milking systems was analyzed, due to two possibilities (parlor or pipeline).

Heritability. Heritability (h^2) was calculated as:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

were σ_a^2 = is the additive animal genetic variance and σ_e^2 is the residual variance.

Genetic Correlations. Genetic correlations were estimated by:

$$r_g = \frac{\sigma_{\ a_1 a_2}}{\sqrt{\sigma_{a_1}^2 , \sigma_{a_2}^2}}$$

where $\sigma_{\ a_1 a_2}$ is the additive genetic covariance between the two traits, $\sigma_{a_1}^2$ and $\sigma_{a_2}^2$ is the additive genetic variance estimated for the respective traits.

Rank Correlations of Sire EBV. As a measure of re-ranking among bulls Spearman correlations between EBV of NR sires with at least 20 daughters in each milking system was estimated, by using proc Spearman procedure in SAS, version 9.4 (SAS Inst. Inc., Cary, NC).

RESULTS

Distributions within Traits

Proportion of cows scored for workability traits since 2009 are seen in Figure 1, and almost 50 % of the farmer-assessed first parity cows were by February 2019 milked in AMS. The percentage of first parity cows scored in each category of temperament, leakage, and milking speed in different milking systems are shown in Figures 2, 3, and 4, respectively. The distribution of cows over classes of temperament were similar in the 3 milking systems (Figure 2), although pipeline system tended to have higher proportions of cows in the extreme classes scored as extra nice or bad, and AMS showed largest proportion of cows scored as ordinary. All three milking systems had low proportion of unclassified animals (unknown).

For leakage, a much larger proportion (9 %) of cows in AMS were not scored compared to < 1 % in the other systems. AMS also showed the lowest proportion of cows scored with some and obvious leakage (Figure 3). For milking speed (Figure 4) the largest difference between AMS and other milking systems were for the categories intermediate and slow, AMS showed the largest proportion of cows with slow milking, and less cows scored with intermediate milking speed.

Heritability

Variance components for all traits measured in both AMS and other milking systems were significantly different from zero and had low standard errors on estimates (Table 2). The heritabilities varied from 0.04 to 0.27, and all traits had lower heritability in AMS. The largest difference showed in leakage, where the heritability was 0.04 in AMS and 0.14 in the other systems.

Genetic Correlations within Milking System. Estimated genetic correlations between milking speed, temperament, and leakage of cows within the same milking system are shown in Table 3, and were slightly higher in AMS for all combinations of traits. Estimates were larger than the standard errors. The genetic correlations showed absolute values ranging from 0.15 to 0.88. The strongest genetic correlation was found between leakage and milking speed in AMS- an unfavorable correlation of -0.88 resulting in increased leakage with higher milking speed. The correlations of temperament to milking speed and leakage were weak**.**

Distribution of Breeding Values for Bulls. Figure 5 show the distribution of EBV of NR sires for temperament in different milking systems. The frequency of bulls with EBV around population mean where larger for the traits when in AMS, except for milking speed that showed larger variation in EBV's for AMS. The range of EBV's for each trait in the different milking systems can be seen in Table 4.

Rank Correlations Between Bull EBV's. Rank correlation between bull EBV's in different milking systems are shown in Table 4. The strong spearman correlations implied low degree of re-ranking among bulls. Temperament showed some re-ranking among bulls despite strong correlations. Results showed that six out of ten bulls were among top 10 for both systems. For milking speed nine out of ten bulls where among top ten in both systems.

Genetic Correlations within Trait across Milking Systems. The genetic correlations between the same traits measured in the two groups of milking systems are in Table 4. All genetic correlations were strong and ranged from 0.86 to 0.98, indicating that the traits are the same genetically. The weakest genetic correlation was for temperament in AMS to other milking systems.

DISCUSSION

Genetic Parameters of Workability

The heritabilities estimated for traits assessed in AMS were lower than for corresponding traits in traditional milking systems. Estimates for temperament and leakage were much lower in AMS, while the difference was relatively small for milking speed. No other study has been found to compare genetic parameters of workability in AMS with other milking systems. However, heritability estimates from both milking systems were within the range of heritability reported in previous studies estimating genetic parameters of farmer-assessed milking speed and temperament (Cue et al., 1996, Wiggans et al., 2007, Jakobsen et al., 2008, Sewalem et al., 2011). Milking speed assessed by farmers were reported to have the largest heritability amongst the workability traits (0.10 to 0.24) (Luttinen and Juga, 1997, Rensing and Ruten, 2005, Wiggans et al., 2007, Sewalem et al., 2011). A larger heritability was reported when classifiers evaluated milking speed (Lassen and Mark, 2008). Heritability of farmer-assessed milking speed for Nordic Red Cattle are reported to be 0.25, similar to current results (Jakobsen et al., 2008). Heritability for average milk flow rate ranged from 0.27 to 0.38, accordingly for Swedish Red and Swedish Holstein when milked in parlor (Carlström et al., 2014). For milking speed measured in AMS heritability estimates were even higher ranging from 0.37 to 0.48 (Carlström et al., 2013, Wethal and Heringstad, 2019).

The heritability of leakage measured in traditional milking systems was larger (0.14) in this study than previous estimates. Luttinen and Juga (1997) studied leakage in Finnish Holstein and Ayrshire and estimated a heritability of 0.08 when measured as a binary trait (leakage/no leakage). The frequency of cows observed with leakage (9%) was lower in the study by Luttinen and Juga (1997) than currently observed. Our estimated heritability for leakage (0.04) in AMS was much lower than in traditional milking systems. In AMS a larger proportion of animals had unknown leakage (9%) thus fewer cows were scored.

Previous literature reported heritability estimates of temperament to range from 0.05 to 0.25 (Visscher and Goddard, 1995, Rensing and Ruten, 2005, Jakobsen et al., 2008, Lassen and Mark, 2008). The presented heritability estimate of temperament of NR in traditional milking systems was in agreement with 0.10 reported by Bakke and Heringstad (2015). A heritability of 0.128 estimated for Canadian Holstein (Sewalem et al., 2011) was also comparable to our results from traditional milking systems. The heritability estimate for temperament was lower in AMS than in other milking systems (0.05 vs. 0.09). Lassen and Mark (2008) compared tiestall and freestall systems and estimated lower genetic variation for temperament in the freestall systems, with heritability estimates of 0.17 and 0.22, respectively. They suggested errors in ID or pedigree as a reason for lower additive genetic variance in freestall systems, and that these farmers also had more difficulties of scoring animals correctly. In our study, each category of the scale for temperament and leakage were used to a lower extent in AMS than in other systems (Figure 2 and 3), causing lower phenotypic variance.

Genetic Correlations Between Milking Systems. The strong genetic correlations (≥ 0.86) between milking systems suggests milking speed, temperament, and leakage to be the same genetically trait in AMS as in traditional milking systems. As far as we know this study is unique as the first comparing farmer-assessed workability traits in AMS with other milking systems genetically. However, Lassen and Mark (2008) compared tiestall versus freestalls and estimated strong genetic correlations between the barn types for milking speed and temperament of 0.94 and 0.95, respectively. Our results showed even stronger correlations between milking speed than Lassen and Mark (2008). Although not directly comparable to our study, Mulder et al. (2004) reported strong genetic correlations (0.79-1) for yield and SCS between milking systems, with lower heritabilities for all traits in AMS. After AMS was installed, the residual variances were reported to increase for yield and SCS (Mulder et al., 2004). In the current study a large proportion of farms did not change milking system. An alternative approach to provide a picture of how assessments changes after introduction of AMS, could be to compare workability traits on the same farms before and after AMS were installed.

Relationship between Workability Traits. We found slightly stronger genetic correlation estimates among traits assessed in AMS. The strongest genetic correlation was, as expected from previous studies, between milking speed and leakage. The genetic relationship between these two workability traits are sparsely investigated, but our result were in line with Luttinen and Juga (1997). The strong unfavorable genetic correlation implies that selection for faster milking speed without considering milk leakage would genetically increase the frequency of cows with leakage in the population. In this study the genetic correlation between milking speed and temperament was doubled in AMS compared to other systems (0.30 vs. 0.16). The correlation was favorable indicating faster milking speed is correlated with preferable temperament. Similar results were found by Sewalem et al. (2011) and Bakke and Heringstad (2015). Even though the genetic correlation between temperament and milking speed was found to be relatively low, it suggests selecting for cows with better temperament will increase cows milking speed, and vice versa. The unfavorable correlation between leakage and temperament was weak with large standard error, especially in AMS.

Interpretation and Practical use of the Results

Reasons for decreased heritability when workability was assessed in AMS may include larger herds and less direct contact with the individual cow. AMS herds in Norway are on average larger than average herd size, and this gives lower time budgets per animal and might make it challenging to asses individual characteristics. Individuals may appear anonymous to farmers and therefore scored as average. One of our hypotheses was that other aspects of temperament are favored by farmers in AMS. We found a strong genetic correlation suggesting that very similar aspects of temperament are important for all milking systems. However, a correlation of 0.86 suggests some different demands regarding cows' behavior in AMS. Such demands might be related to being milked without human contact and that cows must be self-motivated for visiting the AMS. Cows scored with better temperament in AMS may be favored for being more active, but at the same time calm when they are milked. In tiestalls cows are judged based on behavior during milking.

For milking speed, differences were smaller between milking systems. We hypothesized more precise recording of milking speed in AMS herds, but this was not reflected in the heritability estimate. An explanation for more successful subjectively scoring of milking speed in AMS, compared to leakage, is the possibility to use registrations about average flowrate (kg / min) as additional information.

Another hypothesis was that leakage is more difficult to detect in AMS herds. This was partly confirmed. A lower frequency of leakage was observed, and a higher proportion of cows were scored as unknown in AMS herds, but a strong genetic correlation across systems indicates that farmers are observing the same traits genetically. Despite this, leakage recorded in AMS herds is suffering from the lower proportion of cows scored, low prevalence and thereby lower heritability. Considering that larger milk pressure in the milk alveoli gives larger likelihood of milk leakage, so the best time for registering leakage is probably just before milking. In AMS herds, it becomes challenging to observe each cow before they are milked. Also, frequent milkings in the robot with an average milking frequency around 2.45 to 2.63 milkings per day for Red cattle (Carlström et al., 2013, Wethal and Heringstad, 2019), are likely to reduce amount of leakage between milkings, due to less milk pressure in the udder. We found that few cows were recorded with obvious dripping of milk, 2% in AMS and 4% in other systems. This is in contrast to Persson Waller et al. (2003) who observed a larger proportion of cows with leakage in AMS than in parlor. It will be important to consider alternative ways of recording leakage in AMS herds in the future. An objective alternative way is currently lacking, whereas for temperament there are alternative phenotypes that can be utilized for genetic evaluations.

Objective recording in AMS can substitute farmer-assessed temperament, and a few studies have confirmed genetic variability of such traits. Automatically recorded kick offs, connection time and number of teat cup attachments in AMS are examples of objective records describing temperament, and generally they have larger heritability than traditionally subjectively scored temperament (Carlström et al., 2016, Stephansen et al., 2018, Wethal and Heringstad, 2019). Stephansen et al. (2018) also analyzed average connection time and number of attachments per teat in AMS as measurement of cows milking temperament. The estimated heritability was 0.36

for connection time and 0.26 for number of attachments, and the correlation with farmer-assessed temperament was -0.29 and -0.37, respectively, indicating calmer temperament are connected to shorter connection time and fewer attachments.

In the future, data from AMS may serve us with alternative sources of information for genetic evaluations of NR dairy cattle. A functional cow suited for automatically milking becomes more important in the future as the herd size continue to increase, and workability traits is an important contribution to the perfect “robot cow”. Even though leakage in AMS had relatively low heritability, the large correlation to other milking systems is providing genetic information for genetic evaluation. It should be possible to develop new ways of measuring leakage of cows held in freestalls, even though this might be costly. Further investigation of objective ways of recording temperament is recommended. Phenotypic records on subjectively assessed milking speed have alternatives already available, such as flow rate in AMS. The genetic correlations estimated for similar workability traits measured in different milking systems were large in current study. This indicates that redefinition of today’s traits is not necessary and that there is no genotype by environment interaction between milking systems. Despite strong genetic correlations across milking systems, a multitrait model might be beneficial for temperament due to heterogeneous variances for different milking systems. Our results do not suggest that we need a new breeding goal for workability traits of AMS cows.

CONCLUSIONS

Heritability estimates were lower when milking speed, temperament, and leakage were assessed in AMS herds. Strong and unfavorable genetic correlation between milking speed and leakage were estimated, and the genetic correlations between the three workability traits were stronger when assessed in AMS than for other systems. The genetic correlations between the same trait measured in different milking systems were strong (> 0.85), and the rank correlations between EBV of bulls with daughters in both systems were even stronger (> 0.90). This confirms that workability traits are genetically similar in AMS and in traditional milking systems. Lower heritability for leakage and temperament in AMS is one aspect to consider in future genetic evaluation of workability traits, when the majority of Norwegian dairy farms will have AMS.

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Table 1. Descriptive statistics of first parity cows with subjective scores for temperament, leakage, and milking speed in AMS and other milking systems.

	Trait[1]	No. cows	Mean	SD	No. cows unknown
AMS[2]	Temperament	72,683	1.90	0.46	48
	Milking speed	72,487	1.96	0.64	244
	Leakage	66,743	1.16	0.42	5,988
Other[3]	Temperament	187,979	1.90	0.53	21
	Milking speed	187,897	1.91	0.56	103
	Leakage	187,511	1.24	0.51	489

[1] Trait: Temperament as 1="Extra nice", 2="Ordinary", or 3="Bad"; Milking speed as 1="Fast", 2="Intermediate", or 3="Slow"; Leakage as 1="No", 2="Some", or 3="Obvious".

[2] AMS = Automatic milking systems.

[3] Other = Milking parlor or pipeline milking systems.

Table 2. Estimated additive genetic variance (σ_a^2), residual variance (σ_e^2), and heritability (h^2) with standard errors (SE) of subjectively assessed traits in AMS and other milking systems.

	Variance component	Milking Speed	Leakage	Temperament
AMS[1]	σ_a^2	0.09 (0.005)	0.005 (0.001)	0.01 (0.001)
	σ_e^2	0.31 (0.004)	0.13 (0.001)	0.18 (0.001)
	h^2	0.22 (0.01)	0.04 (0.004)	0.05 (0.006)
Other[2]	σ_a^2	0.08 (0.002)	0.03 (0.001)	0.02 (0.001)
	σ_e^2	0.22 (0.002)	0.19 (0.001)	0.21 (0.001)
	h^2	0.27 (0.007)	0.14 (0.006)	0.09 (0.006)

[1] AMS = Automatic milking systems.

[2] Other = Milking parlor and pipeline milking systems.

Table 3. Estimated genetic correlations with standard error (SE) between milking speed, temperament, and leakage within milking system.

Traits	AMS[1]	Other[2]
Milking speed – Temperament	0.30 (0.06)	0.16 (0.03)
Milking speed – Leakage	-0.88 (0.03)	-0.82 (0.01)
Temperament – Leakage	-0.19 (0.11)	-0.15 (0.04)

[1] AMS = Automatic milking systems.

[2] Other = Milking parlor and pipeline milking systems.

Table 4. Estimated genetic correlations (SE) between milking speed, temperament, and leakage in AMS and other milking systems. Spearman correlation among bull EBV (SD) and range of EBV for 704 Norwegian Red A.I bulls with ≥ 20 assessed daughters in each system.

	Milking speed	Leakage	Temperament
Genetic correlation	0.98 (0.01)	0.96 (0.02)	0.86 (0.03)
Rank correlation bull EBV[1]	0.99 (< 0.01)	0.98 (< 0.01)	0.91 (< 0.01)
EBV[1] range for AMS[2]	-0.71 - 0.92	-0.14 - 0.22	-0.23 - 0.16
EBV[1] range for Other[3]	-0.62 - 0.86	-0.35 - 0.56	-0.40 - 0.26

[1] EBV = Estimated breeding values.

[2] AMS = Automatic milking systems.

[3] Other = Milking parlor and pipeline milking systems.

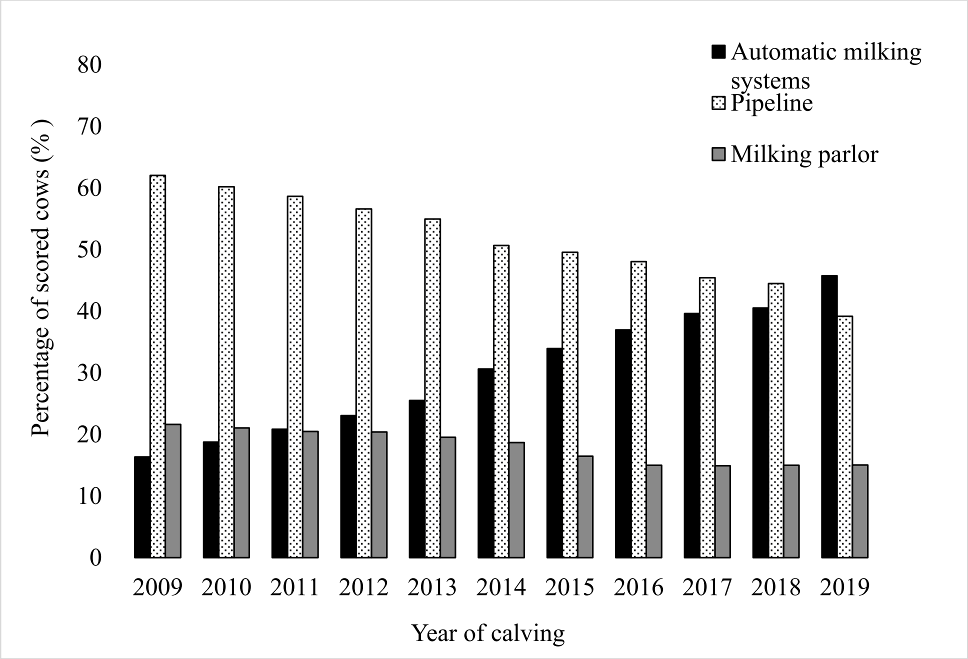

Figure 1. Percentage of Norwegian Red first parity cows assessed by farmers for workability (milking speed, temperament, and leakage) in different types of milking systems, from January 2009 to February 2019.

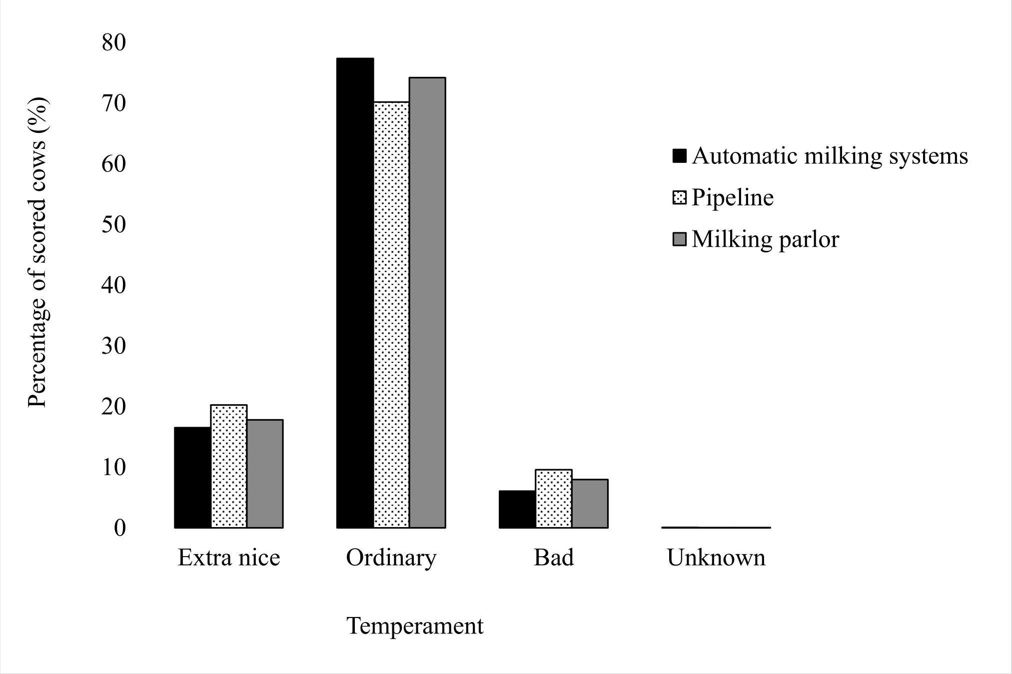

Figure 2. Farmer-scored temperament of first parity Norwegian Red cows.

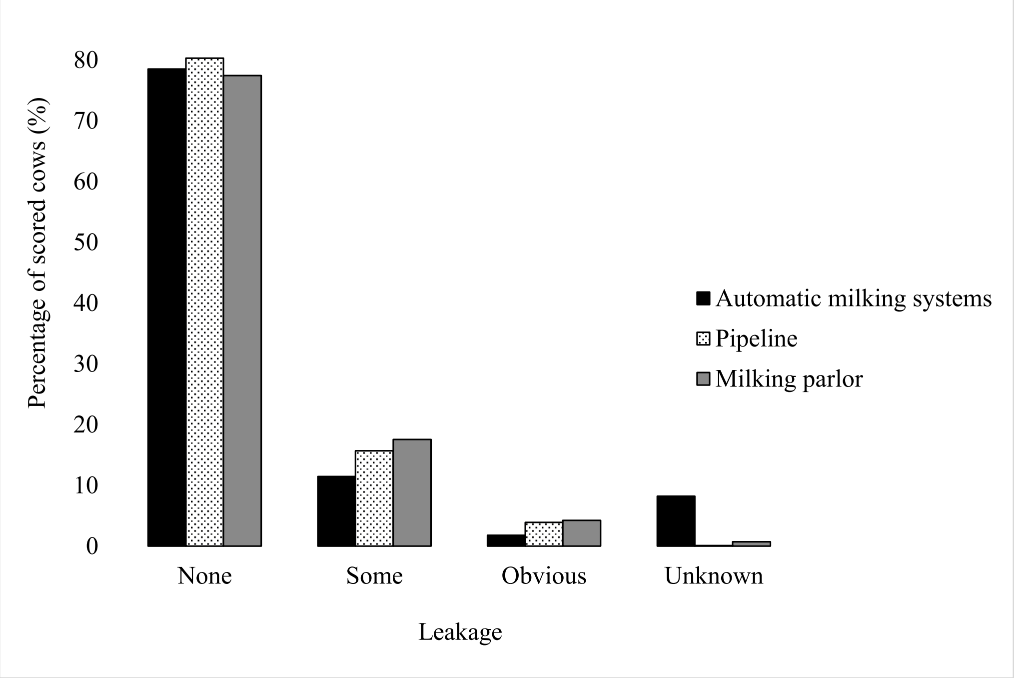

Figure 3. Farmer-scored milk leakage of first lactation Norwegian Red cows in different milking systems.

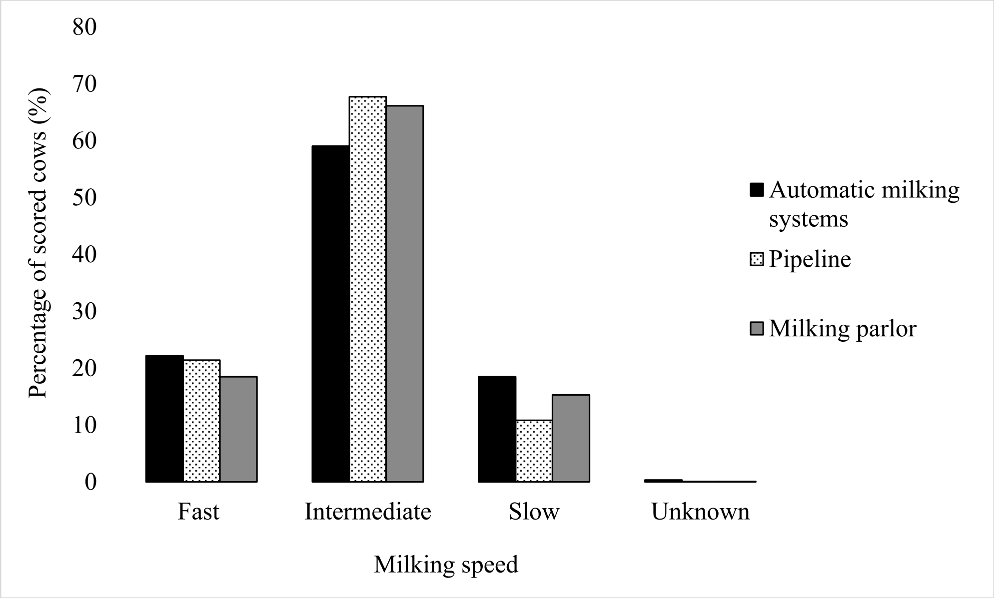

Figure 4. Farmer-scored milking speed of first parity Norwegian Red cows milked in different milking systems.

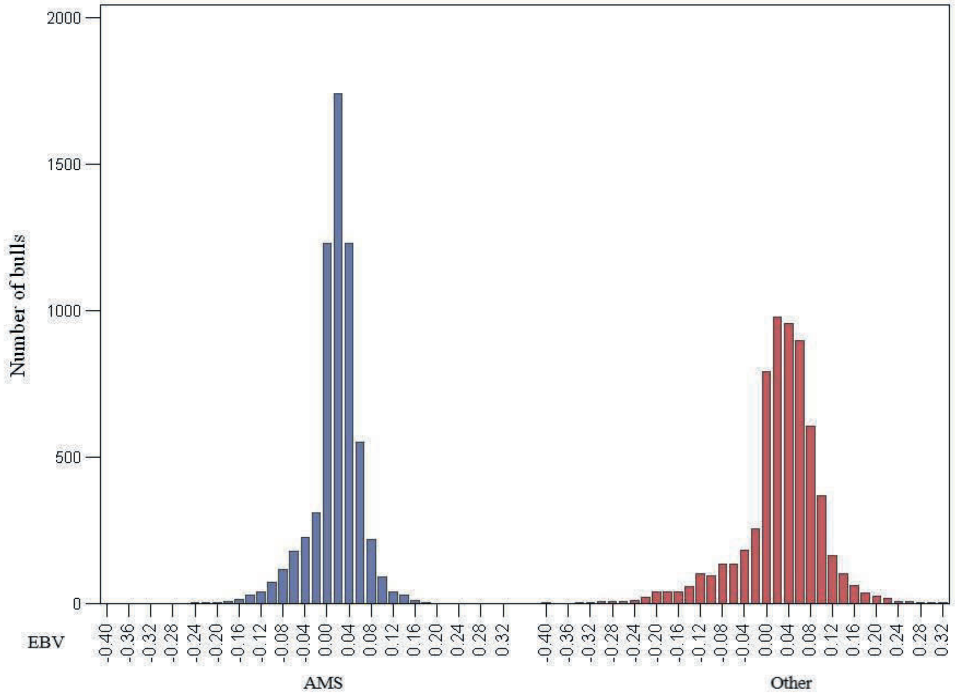

Figure 5. Distribution of estimated breeding values (EBV) of Norwegian Red A.I bulls for temperament in AMS and other systems (parlor and pipeline).

PAPER II

Wethal, K. B., and Heringstad, B. (2019)

Genetic analyses of novel temperament and milkability traits in Norwegian Red cattle, based on data from automatic milking systems

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Genetic analyses of novel temperament and milkability traits in Norwegian Red cattle based on data from automatic milking systems

K. B. Wethal* **and B. Heringstad**
Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, PO Box 5003, 1432 Ås, Norway

ABSTRACT

The number of dairy cows milked in automatic milking systems (AMS) is steadily increasing in Norway. Capacity and efficiency of AMS are highly dependent on the individual cow's milking efficiency, such as milking speed and occupation time in the milking robot. Cows meet new challenges in herds utilizing AMS. Consequently, new or revised traits may be needed for genetic evaluation of dairy cattle. The AMS records relevant information on an individual cow basis. The aims of this study were to estimate genetic parameters of new automatically recorded milkability and temperament traits. Data from 77 commercial herds with Norwegian Red dairy cattle were analyzed by mixed linear animal models. The final data set contained 1,012,912 daily records from 4,883 cows in first to ninth lactation. For variance component estimation, univariate and bivariate models were used. Daily records of box time (BT), average flow rate (FR), kilograms of milk per minute of box time (MEF), handling time (HT), log-transformed HT, milking frequency, and milking interval were analyzed with repeatability models. Among these traits, FR, BT, and MEF showed the highest heritabilities of 0.48, 0.27, and 0.22, respectively, whereas heritability of log-transformed HT, HT, milking frequency, and milking interval was low (0.02–0.07). Unsuccessful milkings expressed as rejected milkings, incomplete milkings (IM), milkings with kick-offs (KO), and teat not found also showed low heritabilities (0.002–0.06). Due to low frequency, KO, rejected milkings, IM, and teat not found were also analyzed as proportions per lactation, which resulted in slightly higher heritability estimates. Genetic correlations were favorable and intermediate to strong between BT, HT, MEF, and FR with absolute values above 0.50. Intermediate and favorable correlations were found for IM and KO with BT, HT, MEF, and FR. Cow milkability in AMS can be improved by selection for reduced number of unsuccessful milkings, faster FR, increased MEF, and shorter BT and HT. Our results confirm that automatically recorded data on milkability and temperament can be valuable sources of information for routine genetic evaluations and that milking efficiency in AMS can be genetically improved.

Key words: milking efficiency, temperament, automatic milking system, genetic parameter

INTRODUCTION

The number of dairy farms with milking robots or automatic milking systems (**AMS**) has increased in Norway since the first farm installed an AMS in 2000. The Norwegian dairy association Tine reported that 44% of milk produced in 2017 came from cows in AMS herds, and by 2018 the proportion was predicted to be more than 50% (Tine, 2017). Automatic milking systems are believed to be common in Norway due to small average herd size (~26 cows; Tine, 2017) and relatively high labor costs. The proportion of dairy farms with AMS is expected to further increase as the government bans the use of tiestalls beginning in 2034.

Dairy cows meet new challenges in AMS that may necessitate new traits or revise existing traits in the breeding program. Automatic milking systems generate vast amounts of data with potentially novel phenotypes, and records on, for example, milkability or unsuccessful milkings may be useful for assessing the efficiency of individual cows. The objective information being collected from the AMS shows high repeatability between milkings, ranging from 0.73 to 0.89 for milkability (Gäde et al., 2006; Carlström et al., 2013). Several traits are important for cow efficiency and functionality in AMS, including ability to stay calm during preparation and attachment of milking equipment as well as high yield and milking speed. Uneasy cows that kick off the milking equipment prolong preparation and attachment times. In addition, the cows might have longer occupation time due to kick-offs (**KO**). There-

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*Corresponding author: karoline.bakke@nmbu.no

fore, short occupation time and ability to quickly leave the AMS after the last teat cup is removed are desirable traits. All of these traits are important for utilizing AMS efficiently. Thus far, relatively few genetic studies have analyzed different milkability, temperament, and behavioral traits in AMS.

The majority of studies using data from AMS focus on genetic parameters of production traits, milkability, flow rate (**FR**), and milk quality traits (Gäde et al., 2006; König et al., 2006; Nixon et al., 2009; Byskov et al., 2012; Carlström et al., 2013, 2014). Objective registration of milking traits and time used is accurate and shows genetic variation. In a study by Carlström et al. (2013), average FR (kg of milk/min) and occupation time (box time, **BT**; min) were estimated to have heritabilities from 0.37 to 0.48 and 0.38 to 0.44, respectively, in first- to third-parity Swedish Red cows. Vosman et al. (2018) and Bakke and Heringstad (2015) estimated heritabilities for milkability (measured as kg of milk/min of BT) to be around 0.30.

Some studies investigated the use of AMS records as objective measurements of behavioral traits (Rinell et al., 2014; Carlström et al., 2016; Stephansen et al., 2018). Teat cup KO in AMS were found to be genetically related to cows' milking temperament. Rinell et al. (2014) analyzed 2 differently defined KO traits in Swedish Holstein cows; daily number of milkings with KO and proportion of KO during lactation showed heritability of 0.06 and 0.31, respectively. Carlström et al. (2016) investigated traits related to cow temperament in AMS for Swedish Red dairy cattle. Information about unsuccessful milkings, such as incomplete milking (**IM**) and teat cup attachment failures (or KO), showed low to medium heritabilities of 0.06 and 0.21, respectively. In the same study, genetic parameters of handling time (**HT**; defined as time in AMS before and after milking) in minutes were investigated. The estimated heritability for handling time was 0.15 for Swedish Reds and 0.05 for Swedish Holsteins; a strong genetic association between subjectively scored temperament and teat cup KO in AMS was also found (Carlström et al., 2016). Temperament in Swedish Reds scored subjectively on a 9-point scale showed a genetic correlation of −0.71 with KO traits. Hence, the current subjectively scored temperament describes, to a large degree, the same genetic variation as KO in AMS. Similarly, Bakke and Heringstad (2015) estimated a favorable genetic correlation of 0.54 between temperament scored subjectively on a 3-point scale and proportion of KO in AMS for Norwegian Red cows. Even though studies have shown a considerable potential of AMS data for genetic evaluation (Carlström et al., 2013, 2014, 2016), studies have yet to define new temperament and milkability traits in AMS for Norwegian Red cows. The aim of this study was to estimate genetic parameters for traits important for cow milking efficiency in AMS.

MATERIALS AND METHODS

Description of Data Set

The data used in the current study were from 77 commercial Norwegian dairy herds with AMS first installed between 2000 and 2015. All farms had a DeLaval (Tumba, Sweden) Voluntary Milking System and were randomly chosen such that they were representative of the robot density in each Norwegian county. DeLaval Norway provided remote access to on-farm computers, and an external connection was set up after permission from each farmer. Data were downloaded between January and July 2017, and the farms had DeLaval DelPro version 3.7, 4.5, or 5.2 software installed. The raw data contained information about each milking and rejected milking (**RM**) for each cow. Due to local memory limitations, the systems deleted records older than 1 yr on a daily basis. Therefore, only 365 d with data could be obtained from each herd. The reports contained information on milk yield and milking speed in each udder quarter; date, time, and length of each visit; and problems with the milking session, such as KO and IM.

Definition of Traits

Milkability. Box time is the time from when a cow enters the AMS to when it exits the milking unit when milking is finished. Milk yield per time unit (**MEF**) was defined as the ratio of milk yield (kg) and BT (min), measuring the milking efficiency in AMS. Handling time is the difference between BT and milking time and sums the time before the milk starts flowing and the time from when the last teat cup was removed to the time the cow leaves the AMS (same definition as Carlström et al., 2016). Milking time was calculated from records on FR by dividing milk yield (kg) in each udder quarter by the average FR for the respective udder quarter. We used the value from the udder quarter with the longest milking time for calculation of HT. Milking time was not further analyzed. Information on FR (measured as average kg of milk/min of milking time) was available in the milking report. Values on FR in each udder quarter added up to 1 FR record at each milking. Therefore, cows with fewer than 4 milked udder quarters had a lower FR. In addition, milking interval (**MI**; the time between milking sessions) and milking frequency (**MF**; the number of milkings per day) were analyzed. Information on visits to the milking unit that were unapproved due to short time since the previous milking was also analyzed. This trait (RM) is the daily number of visits for cows in AMS without being milked. The time until a cow again obtains milking permission usually depends on lactation stage and expected milk yield. Restrictions on MI can also be set individually. It is preferred that the animals have few or no RM because RM reduces the milking capacity of the AMS and is therefore described as an undesirable behavior.

Unsuccessful Milkings. The trait called KO is the daily number of milkings with at least 1 teat cup kicked off. This occurs if the teat cup falls out of the gripper or loosens from the teat during attachment or udder milking. The trait was defined as binary (0 or 1) per milking and summarized across all milkings per day. A cow with 1 or more KO in each milking session and with 3 daily milkings would thus be registered as KO = 3. The AMS records a teat as not found if the robot arm is unable to detect the teat, resulting in 0 kg of milk for the specific udder quarter. Teat not found (**TNF**) was defined as the number of daily milkings in which the milking robot was unable to find at least 1 of the teats for milking. Incomplete milkings was defined as number of daily milkings with a minimum of 1 teat registered as incompletely milked. The expected milk yield for a milking session depends on previous milkings. If the yield was less than 60% of expectation for a teat, the milking session would be recorded as having an incompletely milked teat.

Traits with Daily Observations. Traits that describe cows' daily milkability and temperament were defined as daily averages of BT, MEF, HT, FR, and MI. The MF and RM were daily sums. To obtain a closer to normal distribution of HT, a constant (1.5) was added before the natural logarithm was calculated and analyzed as an alternative definition of HT (**lnHT**).

Traits Summarized over Lactations. Due to the low frequency of recorded unsuccessful milkings when defined as a daily record, a second definition of KO, IM, TNF, and RM was analyzed in which they were summarized to 1 observation per lactation. The proportion (**p**) of milkings with KO, TNF, and IM was calculated with the following formula:

$$\text{pKO, pTNF, pIM} = \text{No. of milkings with KO, TNF, or IM/Total milkings per lactation.}$$

The following formula was used to calculate pRM:

$$\text{pRM} = \text{No. of rejected milkings/Total visits per lactation.}$$

Data Edits

The data set included a total of 4,907,751 observations, and only Norwegian Red cows were included in the analysis. A record consisted of either a milking or a rejected milking. Additional information such as calving dates and pedigree for all animals was collected from the Norwegian Dairy Herd Recording System. Records from each visit were summarized to 1 record per day for each cow and further edited. Each cow should have a minimum of 10 successive DIM between d 5 and 305 of a parity. For each test day and cow, the number of milkings and rejected milkings was restricted to a maximum of 11 and 30, respectively. Milk yield had to be ≤ 50 kg in total per milking and ≤ 13 kg per udder quarter per milking. Average FR and peak FR had a respective maximum of 3 and 4 kg of milk/min and udder quarter per milking. The time interval between milkings should not be shorter than 5 min, and time variables had to be positive and logical. The BT was restricted to be between 1 and 20 min. The minimum and maximum length of HT was 0.3 and 15 min, respectively. The final data set had a total of 1,012,912 daily observations dated from December 2015 to July 2017 on 4,883 cows and 6,493 lactations in 77 herds.

Summary statistics are given in Table 1. The total number of daily observations varied among traits from 977,522 to 1,012,912. The mean BT per visit was 7.46 min. Both BT and HT showed large variation. Average MI was 9.91 h; however, a few observations had a large interval from one milking to the next. The maximum MI value of 1,207.8 h was likely caused by an udder health or milk quality problem resulting in a longer period without recorded milkings in AMS. Average FR was 3.25 kg of milk/min, whereas milk per minute of BT, MEF, was on average 1.48 kg/min. Average MF was 2.63. Average number of daily milkings with KO, IM, and TNF ranged from 0.11 to 0.17. Traits summarized per lactation (pKO, pTNF, pIM, and pRM) had in total 6,706 observations, and proportion ranged from 0 to 1 (Table 2). The mean proportions were generally low, ranging from 0.05 to 0.11.

For BT, HT, MEF, and FR, the daily average varied over DIM within parity and between parities. The largest difference between first and later lactations was found for MEF, with a difference of 0.3 kg/min in the first part of the lactation (Figure 1). Cows in first lactation showed peak MEF around 140 DIM, whereas the peak occurred earlier for older cows in our data. First-lactation cows showed lower average FR compared with later parities, with a flatter curve through the parity (Figure 2). The pattern of HT through lactation was relatively similar across parities. There was longer HT

Table 1. Summary statistics for traits with 1 daily record in automatic milking systems

Trait	n	Mean	SD	Minimum	Maximum
Box time (min)	1,012,534	7.46	1.96	1	20
Milking efficiency (kg/min)	1,012,588	1.48	0.44	0	4
Handling time (min)	1,007,179	3.14	1.13	0.3	15
Log-transformed handling time (ln)	1,007,179	1.51	0.21	0.59	2.8
Flow rate (kg/min)	977,522	3.25	0.93	0	8.8
Milking frequency (no.)	1,012,912	2.63	0.80	0	11
Milking interval (h)	1,012,092	9.91	5.61	0.91	1,207.8
Rejected milkings (no.)	1,012,912	0.5	1.55	0	30
Milkings with kick-off (no.)	1,012,601	0.17	0.52	0	7
Incomplete milkings (no.)	1,012,601	0.12	0.45	0	7
Milkings with teat not found (no.)	1,012,601	0.11	0.43	0	7

early and late in the lactations, except for first parity, which showed a pattern of lower HT toward the end of the lactation (Figure 3).

Statistical Method and Models

Mixed linear animal models were used for analyzing the traits. Univariate models were used for variance components and heritability estimation of all the traits, and bivariate models were used for estimating genetic correlations. All variance and covariance components were estimated with the DMUAI package in DMU (Madsen and Jensen, 2012) based on the average information restricted maximum likelihood method. Which fixed effects to include in the model were determined using the GLM procedure in SAS version 9.4 (SAS Institute Inc., Cary, NC). Only fixed effects that had a significant effect were included in the final model for genetic analysis.

Model for Traits with Daily Records. Animal models with repeated measurements within lactations were used for traits with daily records. The univariate model was as follows:

$$y_{\mathrm{ijklmn}} = \mathrm{CYM_i} + \mathrm{PCAge_j} + \mathrm{DIM_k} + \mathrm{HTD_l} + \mathrm{pe_m} + \mathrm{a_m} + \mathrm{e_{ijklmn}},$$

where y_{ijklmn} is a daily record of BT (min), HT (min), lnHT, MEF (kg/min of BT), FR (kg/min), MI (h), or MF (number of milkings) for cow m; $\mathrm{CYM_i}$ is the fixed effect of calving year and month i; $\mathrm{PCAge_j}$ is the fixed effect of calving age in months within parity j; $\mathrm{DIM_k}$ is the fixed effect of DIM k; and $\mathrm{HTD_l}$ is the fixed effect of herd-test day l. The random effects included were permanent environment ($\mathrm{pe_m}$) of cow m due to repeated observations, $\mathrm{pe} \sim N\left(0, \mathbf{I}\sigma^2_{\mathrm{pe}}\right)$, where **I** is the identity matrix, σ^2_{pe} is the permanent environmental variance, and additive genetic effect ($\mathrm{a_m}$) of animal m, $\mathrm{a} \sim N\left(0, \mathbf{A}\sigma^2_{\mathrm{a}}\right)$, where σ^2_{a} is the additive genetic variance and **A** is the relationship matrix containing pedigree information 8 generations back for 43,224 animals. The random effect of residual ($\mathrm{e_{ijklmn}}$) of observation n was assumed to have the following distribution: $\mathrm{e} \sim N\left(0, \mathbf{I}\sigma^2_{\mathrm{e}}\right)$, where σ^2_{e} is the residual variance.

The following model was used for daily number of milkings with KO, IM, TNF, and daily number of RM:

$$y_{\mathrm{ijklmno}} = \mathrm{CYM_i} + \mathrm{PCAge_j} + \mathrm{DIMperiod_k} + \mathrm{HY_l} + \mathrm{htd_m} + \mathrm{pe_n} + \mathrm{a_n} + \mathrm{e_{ijklmno}},$$

where y_{ijklmno} is a daily observation of KO, IM, TNF, or RM for cow n with fixed effect of CYM i and PCAge j. For these traits, DIM was grouped in periods of 30 d (k = 1–10), and herd by year ($\mathrm{HY_l}$) was included as a fixed effect. The effect of herd-test day ($\mathrm{htd_m}$) was included as random due to low frequency in the subclasses and had the following distribution: $\mathrm{htd} \sim N\left(0, \mathbf{I}\sigma^2_{\mathrm{htd}}\right)$, where **I** is the identity matrix and σ^2_{htd} is the herd-test day variance. Other random effects included were as defined in the model for daily records. Some classes of fixed effects were merged to ensure enough observations in each class. For example, CYM (21 classes) were recorded from April 2015 to June 2017, and the size of classes in the tails was small; CYM from April to August 2015 were merged into 1 class, as were CYM from April to June 2017. Animals

Table 2. Summary statistics for proportion of traits (1 observation/lactation) of first- to ninth-parity cows in automatic milking systems (n = 6,706)

Trait[1]	Mean	SD	Minimum	Maximum
pKO	0.07	0.14	0	1
pIM	0.05	0.09	0	1
pTNF	0.05	0.10	0	1
pRM	0.11	0.18	0	0.88

[1] pKO = proportion of milkings with kick-off; pIM = proportion of incomplete milkings; pTNF = proportion of milkings with teat not found; pRM = proportion of rejected milkings.

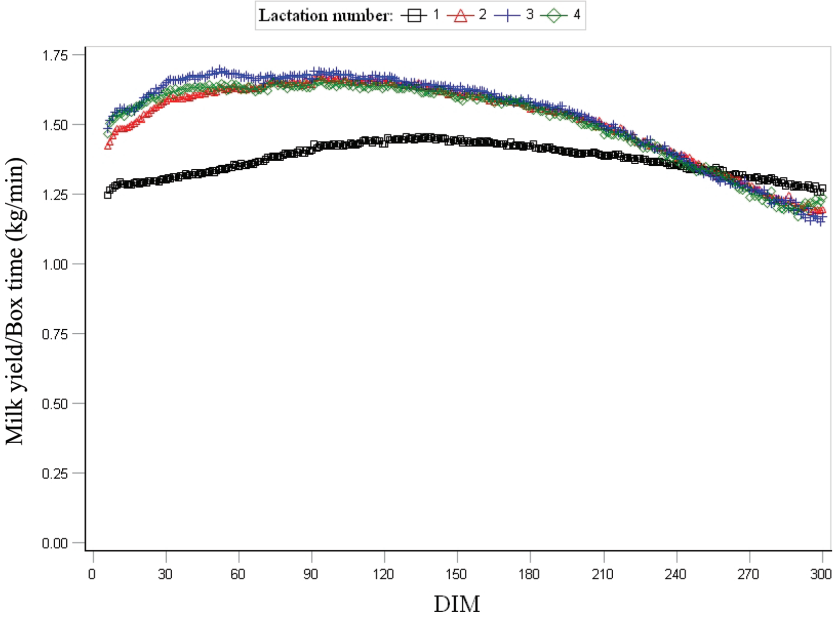

Figure 1. Milking efficiency measured as kilograms of milk per minute of box time in automatic milking systems for dairy cows in first, second, third, and fourth or greater parity.

in first and second lactation were fitted with an effect of parity by calving age (PCAge), whereas cows in later parities only had the effect of lactation number. The effect of parity 5 or later was in 1 class. In first parity, the calving ages ≤20 mo were merged and ages >32 mo were merged. In second parity, calving ages <33 were in one group and ages >43 mo were in another. The total number of classes of PCAge was 30, and there were 27,655 levels of htd and 149 classes of HY.

Model for Traits Summarized over Lactations. For pKO, pIM, pTNF, and pRM, variance components were estimated using the following repeatability model:

$$\mathrm{y_{ijklm}} = \mathrm{CYM_i} + \mathrm{PCAge_j} + \mathrm{hy_k} + \mathrm{pe_l} + \mathrm{a_l} + \mathrm{e_{ijklm}},$$

where $\mathrm{y_{ijklm}}$ is an observation of pKO, pIM, pTNF, or pRM on cow l. For pRM and pKO, the models included fixed effects of CYM i and PCAge j. For pIM and pRM, no fixed effects were included in the models. Due to small subclasses, herd-year (hy) was included as a random effect in the models, with hy ~ $N\left(0, \mathbf{I}\sigma^2_{\mathrm{hy}}\right)$, where **I** is the identity matrix. Permanent environmental effect (pe) was included due to repeated observations over parities. Other effects were as defined above.

Repeatability and Heritability. Heritability (h^2) for the traits was defined as

$$\mathrm{h}^2 = \frac{\sigma^2_{\mathrm{a}}}{\sigma^2_{\mathrm{a}} + \sigma^2_{\mathrm{pe}} + \sigma^2_{\mathrm{e}}},$$

where σ^2_{a} is the additive animal genetic variance, σ^2_{pe} is the permanent environment variance, and σ^2_{e} is the residual variance.

Repeatability (R) of a trait is the proportion of the total variance explained by the animal, both their additive genetic and permanent environmental effects. The following formula was used to calculate repeatability:

$$\mathrm{R} = \frac{\sigma^2_{\mathrm{a}} + \sigma^2_{\mathrm{pe}}}{\sigma^2_{\mathrm{a}} + \sigma^2_{\mathrm{pe}} + \sigma^2_{\mathrm{e}}}.$$

Genetic Correlations

A set of bivariate models was used for estimating the genetic correlations among traits. Genetic correlations were estimated only within the groups of traits defined as daily or as a proportion. The following assumptions were made for distribution of random effects:

$$\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} \sim N\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{A} \otimes \begin{pmatrix} \sigma^2_{a_1} & \sigma_{a_1a_2} \\ \sigma_{a_1a_2} & \sigma^2_{a_2} \end{pmatrix}\right],$$

$$\begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} \sim N\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{I} \otimes \begin{pmatrix} \sigma^2_{pe_1} & \sigma_{pe_1pe_2} \\ \sigma_{pe_1pe_2} & \sigma^2_{pe_2} \end{pmatrix}\right],$$

$$\begin{bmatrix} htd_1 \\ htd_2 \end{bmatrix} \sim N\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{I} \otimes \begin{pmatrix} \sigma^2_{htd_1} & \sigma_{htd_1htd_2} \\ \sigma_{htd_1htd_2} & \sigma^2_{htd_2} \end{pmatrix}\right],$$

and

$$\begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \sim N\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{I} \otimes \begin{pmatrix} \sigma^2_{e_1} & \sigma_{e_1e_2} \\ \sigma_{e_1e_2} & \sigma^2_{e_2} \end{pmatrix}\right],$$

where $\sigma^2_{a_1}$ and $\sigma^2_{a_2}$ are the additive genetic variance for the 2 traits, $\sigma_{a_1a_2}$ is the additive genetic covariance between the 2 traits, $\sigma^2_{pe_1}$ and $\sigma^2_{pe_2}$ is the permanent environmental variance for repeated observations within lactation and between parities for daily and proportion traits, $\sigma_{pe_1pe_2}$ is the permanent environmental covariance, $\sigma^2_{htd_1}$ and $\sigma^2_{htd_2}$ is herd-test day variance, and $\sigma_{htd_1htd_2}$ is the herd-test day covariance between the 2 traits. The residual variance for the 2 traits is $\sigma^2_{e_1}$ and $\sigma^2_{e_2}$, whereas $\sigma_{e_1e_2}$ is the residual covariance.

RESULTS

Estimates of variance components, heritabilities, and repeatabilities for traits with daily records are given in Table 3. The highest heritability was found for FR (0.48), together with BT and MEF (0.27 and 0.22). All traits except TNF had a genetic component significantly different from 0, and TNF was the only trait not heritable when defined as daily records. Heritability was very low (0.01–0.02) for IM, RM, and MI, whereas HT, MF, and KO had slightly higher heritability (0.05–0.06). Repeatabilities varied from 0.13 to 0.86, and estimates for milkability traits ranged from 0.66 to 0.86. For traits related to temperament or behavior,

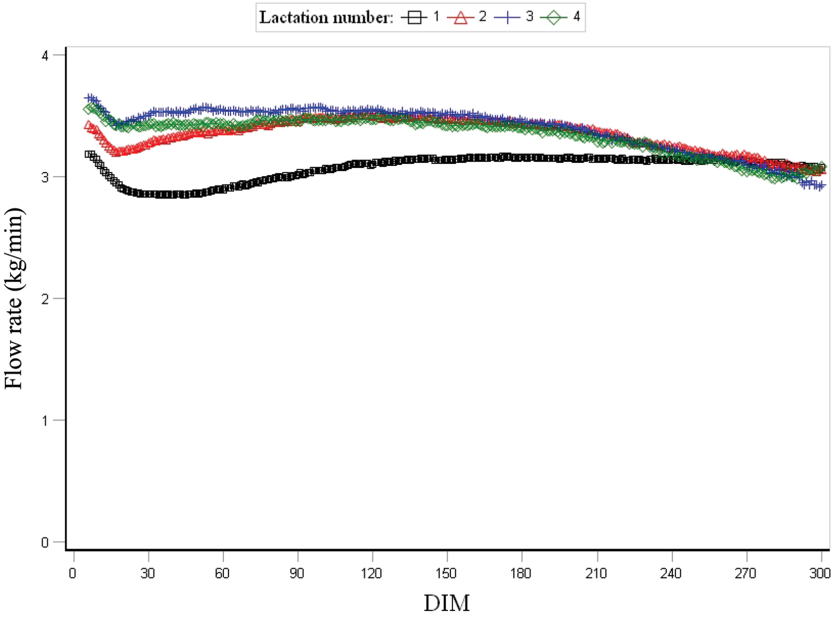

Figure 2. Daily average flow rate (kg of milk/min of milking time) in automatic milking systems for dairy cows in first, second, third, and fourth or greater parity.

Table 3. Variance components, repeatability, and heritability (SE in parentheses) for traits with daily records in automatic milking systems

	Variance component[2]						
Trait[1]	σ^2_{a}	σ^2_{pe}	σ^2_{htd}	σ^2_{e}	σ^2_{p}	R	h^2
HT (min)	0.06 (0.02)	0.51 (0.02)	NI[3]	0.61 (<0.001)	1.18	0.48	0.05 (0.01)
lnHT	0.002 (<0.001)	0.02 (<0.01)	NI	0.02 (<0.001)	0.04	0.50	0.07 (0.02)
BT (min)	0.96 (0.11)	1.47 (0.09)	NI	1.16 (<0.01)	3.59	0.68	0.27 (0.03)
MEF (kg/min of BT)	0.04 (<0.01)	0.07 (<0.01)	NI	0.06 (<0.001)	0.17	0.66	0.22 (0.03)
FR (kg/min)	0.40 (0.04)	0.33 (0.03)	NI	0.12 (<0.001)	0.84	0.86	0.48 (0.04)
MF (no.)	0.03 (<0.01)	0.12 (<0.01)	NI	0.38 (<0.001)	0.52	0.28	0.05 (0.01)
MI (h)	0.46 (0.12)	3.09 (0.12)	NI	24.6 (0.04)	28.1	0.13	0.02 (<0.01)
RM (no.)	0.02 (0.01)	0.50 (0.01)	0.30 (0.03)	0.81 (0.001)	1.33	0.39	0.02 (<0.01)
KO (no.)	0.02 (0.004)	0.11 (<0.01)	0.001 (<0.001)	0.17 (<0.001)	0.30	0.43	0.06 (0.01)
IM (no.)	0.002 (0.001)	0.05 (0.001)	0.002 (<0.001)	0.16 (0.002)	0.21	0.25	0.01 (0.005)
TNF (no.)	0.0005 (0.001)	0.06 (0.002)	0.002 (<0.001)	0.13 (0.002)	0.20	0.32	0.002 (0.004)

[1] HT = handling time; lnHT = log-transformed HT; BT = box time; MEF = milking efficiency; FR = flow rate; MF = milking frequency; MI = milking interval; RM = rejected milkings; KO = kick-offs; IM = incomplete milkings; TNF = teat not found.

[2] σ^2_{a} = additive genetic variance; σ^2_{pe} = permanent environmental variance; σ^2_{htd} = herd-test day variance; σ^2_{e} = residual variance; σ^2_{p} = phenotypic variance $\left(\sigma^2_{\mathrm{a}} + \sigma^2_{\mathrm{pe}} + \sigma^2_{\mathrm{e}}\right)$; R = repeatability, h^2 = heritability.

[3] Not included in the model.

HT and KO had the highest repeatability (0.48 and 0.43), together with RM (0.39). Low repeatability and heritability were estimated for MI.

Results on pKO, pIM, pTNF, and pRM analyzed as proportion of occurrence within lactations are given in Table 4. Variance component estimates were significantly different from 0 for all traits, with heritabilities varying from 0.05 to 0.14. Heritability was lowest for pRM and highest for pIM. Proportion of milkings with KO (pKO) showed the highest repeatability (0.72),

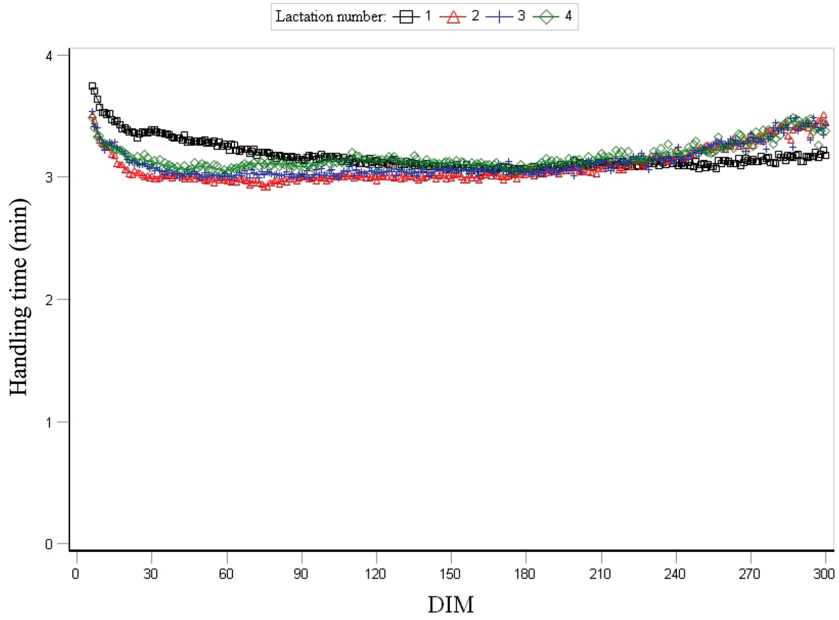

Figure 3. Daily average handling time (min) measured in automatic milking systems for dairy cows in first, second, third, and fourth or greater parity.

whereas the other traits had relatively low repeatabilities ranging from 0.29 to 0.36.

Estimated genetic correlations between temperament and milkability traits with daily records are given in Table 5. The correlations were intermediate to strong and favorable among the continuous traits MEF, HT, FR, and BT. They were lower than −0.50 and larger than 0.53. The strong correlation between FR and MEF (0.98) confirmed that these are genetically the same traits. A negative and strong correlation of −0.92 between FR and BT means that selection for higher FR results in shorter BT. The negative moderate correlation HT showed with MEF and FR (−0.58 and −0.50, respectively) was favorable because shorter HT is genetically associated with higher MEF and FR.

Both MF and MI showed a weak or nonexistent genetic relationship with the continuous traits (BT, HT, MEF, and FR) but were strongly interrelated (−0.99). The genetic correlation of 0.98 between KO and IM means that they are the same trait genetically, and their genetic correlations with other traits are also in the same range. Among traits associated with unsuccessful milkings, IM and KO had the strongest genetic correlations with milkability traits. These correlations were moderate and in expected directions. The stronger genetic correlation between KO and IM when measured as daily observations compared with pKO and pIM may be related to the definition of the traits. When defined as proportions, total number of milkings are accounted for, resulting in larger variation between the traits and a more continuous scale. Positive correlations ranging from 0.31 to 0.53 for KO and IM with BT and HT means that increased number of milkings with KO and incompletely milked teats will increase occupation time and HT in the AMS. The negative genetic correlation between KO and IM with MEF and FR suggests that increased KO and IM will reduce yield per minute. The strong and negative genetic correlation between IM and MI (−0.7) suggests reduced milk yield in each session with shorter MI; this leads to IM according to the definition. For TNF, no significant genetic correlations with other traits when defined as daily number of milkings were found, as standard errors were larger than estimated correlations or analysis did not converge.

Five out of six of the genetic correlations estimated among pIM, pTNF, pKO, and pRM were significantly different from zero (Table 6). The strongest genetic correlation was found between pIM and pTNF (0.99 ± 0.02). This indicates that the 2 traits are genetically the same. Moderate genetic correlations were estimated between pIM and pKO (0.30) and between pIM and pRM (0.36). Further, a moderate genetic correlation between pTNF and pRM was estimated to be 0.46 but with a relatively large standard error (0.2).

DISCUSSION

Heritability and Repeatability

Several of the novel phenotypes investigated associated with milkability, milking temperament, and efficiency in AMS showed genetic variation. The low heritability of MF (0.05) was in line with estimates (0.02–0.07) found for Swedish cows (Carlström et al., 2013). Nixon et al. (2009) estimated heritabilities for 24-h milking frequency ranging from 0.02 to 0.08 for primiparous Holstein cows. König et al. (2006) reported slightly higher heritability for MF at 3 different test days (0.16, 0.19, 0.22) when a linear regression of milking frequency on milk yield was included in the model. Heritability for MI of 0.02 is very low compared with the results of Carlström et al. (2013) in the range of 0.09 to 0.26. This may be due to less restrictive data edits than those applied by Carlström et al. (2013). The relevance of MF for breeding is related to robot capacity. Both too few and too many daily milkings are

Table 4. Variance components, repeatability, and heritability for proportion traits (1 observation/lactation; SE in parentheses) in automatic milking systems

	Variance component[2]						
Trait[1]	σ^2_a	σ^2_{pe}	σ^2_{hy}	σ^2_e	σ^2_p	R	h^2
pKO	0.002 (<0.001)	0.01 (<0.01)	0.0004 (0.0001)	0.005 (<0.001)	0.02	0.72	0.13 (0.03)
pIM	0.001 (<0.001)	0.002 (<0.001)	0.0006 (0.0001)	0.005 (<0.001)	0.008	0.36	0.14 (0.03)
pTNF	0.001 (<0.001)	0.002 (<0.001)	0.0007 (0.0001)	0.007 (<0.001)	0.01	0.29	0.12 (0.03)
pRM	0.0003 (0.0001)	0.001 (<0.001)	0.03 (<0.01)	0.004 (<0.001)	0.006	0.31	0.05 (0.02)

[1] pKO = proportion of milkings with kick-off; pIM = proportion of incomplete milkings; pTNF = proportion of milkings with teat not found; pRM = proportion of rejected milkings.

[2] σ^2_a = additive genetic variance; σ^2_{pe} = permanent environmental variance; σ^2_{hy} = herd-year variance; σ^2_e = residual variance; σ^2_p = phenotypic variance $\left(\sigma^2_a + \sigma^2_{pe} + \sigma^2_e\right)$; R = repeatability, h^2 = heritability.

Table 5. Genetic correlations (SE in parentheses) between milkability and temperament traits in automatic milking systems, measured as daily observations[1]

Trait	BT	MEF	HT	FR	MF	MI	RM	KO	IM	TNF
MEF (kg/min of BT)	−0.87 (0.03)									
HT (min)	0.53 (0.1)	−0.58 (0.1)								
FR (kg/min)	−0.92 (0.02)	0.98 (0.01)	−0.50 (0.11)							
MF (no.)	−0.14 (0.1)	0.08 (0.12)	0.14 (0.17)	0.14 (0.1)						
MI (h)	−0.01 (0.13)	0.12 (0.13)	−0.21 (0.19)	0.014 (0.12)	−0.99 (<0.01)					
RM (no.)	−0.12 (0.18)	0.06 (0.2)	0.25 (0.25)	0.17 (0.17)	0.69 (0.17)	−0.67 (0.18)				
KO (no.)	0.36 (0.12)	−0.47 (0.12)	0.50 (0.15)	−0.40 (0.11)	0.16 (0.15)	−0.23 (0.17)	−0.14 (0.25)			
IM (no.)	0.31 (0.12)	−0.45 (0.12)	0.53 (0.15)	−0.40 (0.11)	0.23 (0.15)	−0.70 (0.21)	NC[2]	0.98 (<0.01)		
TNF (no.)	−0.25 (0.43)	0.02 (0.41)	0.64 (0.45)	0.08 (0.41)	0.68 (0.61)	NC	NC	NC	NC	
lnHT	0.64 (0.08)	−0.68 (0.08)	0.99 (0.01)	−0.59 (0.09)	0.16 (0.15)	−0.22 (0.18)	0.24 (0.23)	0.54 (0.14)	0.63 (0.11)	NC

[1] BT = box time; MEF = milking efficiency; HT = handling time; FR = flow rate; MF = milking frequency; MI = milking interval; RM = rejected milkings; KO = kick-offs; IM = incomplete milkings; TNF = teat not found; lnHT = log-transformed HT.

[2] Not converged.

undesirable: low MF increases labor related to fetching cows, whereas MF that is too large reduces available milking capacity for each cow.

Moderate to high heritability for BT (0.27) was in the same range as the only comparable results reported by Carlström et al. (2013). This trait relates directly to robot capacity because short BT improves animal flow. Also, MEF relates to milking capacity and showed a heritability of 0.22. This trait has been sparsely investigated, but Bakke and Heringstad (2015) found a heritability of 0.29 in a study based on data from 46 commercial herds with Norwegian Red cows. Vosman et al. (2018) estimated the heritability of kilograms of milk per minute of BT to be 0.33 and 0.29, respectively, for 2 definitions of milking efficiency (EFF1, EFF2). In the work by Vosman et al. (2018), the EFF1 definition corresponds to MEF, but EFF2 is kilograms of milk divided by BT and includes values from previous IM. Løvendahl et al. (2014) found higher heritabilities for milking efficiency at different stages of first lactation (0.4–0.5). They defined milking efficiency as a ratio of total daily BT to energy corrected yield, almost identical to MEF in the current study. Løvendahl et al. (2014) also defined residual milking BT as BT adjusted for ECM yield at every visit. This definition showed lower heritability compared with milking efficiency in kilograms per minute. They used average values of 10 stages through first lactation only, and this may be a reason for their relatively higher heritability estimates.

The highest heritability in the current study was estimated for FR (0.48), and the repeatability of 0.86 confirmed that milking robots measure milking speed highly accurately. Carlström et al. (2013) estimated heritability of average FR in Swedish Red cows to be 0.37 in first parity and 0.48 in second and third parity. Both heritability and repeatability of FR in the Swedish study were comparable with the current study, where FR was analyzed across all parities. A heritability of FR close to 0.50 was reported for Holsteins by Pretto et al. (2014). Gäde et al. (2006) found that heritabilities of average and maximum FR were 0.55 when based on daily records. They also found milking time to have a

Table 6. Genetic correlations between proportion traits in automatic milking systems (1 observation/lactation; SE in parentheses)[1]

Trait	pKO	pTNF	pRM
pTNF	0.20 (0.17)		
pRM	−0.20 (0.22)	0.46 (0.2)	
pIM	0.30 (0.14)	0.99 (0.02)	0.36 (0.19)

[1] pKO = proportion of milkings with kick-offs; pTNF = proportion of milkings with teat not found; pRM = proportion of rejected milkings; pIM = proportion of incomplete milkings.

high heritability (0.39) and estimated strong correlations between these traits, ranging from −0.89 to 0.98.

Milking speed of first-lactation Norwegian Red cows has been scored subjectively on a 3-point scale by farmers and is currently used in the genetic evaluation of temperament. Heritability estimates of milking speed scored subjectively by either farmers or classifiers were in the range of 0.16 to 0.25 for different breeds (Luttinen and Juga, 1997; Rupp and Boichard, 1999; Ilahi and Kadarmideen, 2004). Average FR based on objective measurements by milk meters have higher heritabilities, from 0.27 to 0.54 (Ilahi and Kadarmideen, 2004; Gray et al., 2011). Carlström et al. (2014) showed that heritability decreased when fewer days of data were included, but estimates were still relatively large for milking speed measured as average FR. This implies that few days with data from AMS may still be feasible as information for genetic evaluation of milkability. Pretto et al. (2014) reported a strong and positive genetic correlation (0.92) between average FR in AMS and FR in milking parlors. Carlström et al. (2014) found even higher correlations between FR in AMS and FR registered in milking parlors for Swedish Red and Holstein cows (0.98 and 0.97, respectively). Strong genetic correlations between FR in AMS across parities (>0.9) were also found by Carlström et al. (2014).

Transformation of HT to lnHT reduced skewness and increased heritability from 0.05 to 0.07. The trait is a relevant source of information on cow temperament and time usage before attachment of milking equipment and after teat cups are removed. Carlström et al. (2013) used a similar definition of HT and found similar estimates of heritability of 0.05 and 0.15 for first- to third-lactation Holstein and Swedish Red cows, respectively. Negative HT values were deleted in the data edit. They may arise from measurement errors in FR, leading to calculated milking time being longer than actual BT. Time from start of milking until milk flow stops when the last teat cup is removed may be a better measurement of milking time to prevent illogical HT. Almost the same definition of milking time was used by Carlström et al. (2013), but they added a constant of 30 s to the attachment time of each fore udder quarter before keeping the record with the largest milking time.

In a recent study, Stephansen et al. (2018) estimated heritability of connection time of attachment of teat cups and number of attachments per udder quarter as a measure of milking temperament in AMS. They found relatively high heritabilities (0.36 and 0.26, respectively). They also reported significant favorable correlations between farmer-assessed temperament and connection time of teat cups in minutes and number of attachments of −0.29 and −0.37, respectively. In the current study, KO was investigated as an indicator of milking temperament in AMS. Kick-offs defined as teat cup attachment failures (**AtF**) in AMS were studied for Swedish Holstein cows by Rinell et al. (2014). They found heritability estimates of 0.31 and 0.06 for proportion and number of AtF, respectively. The KO in the present study showed heritability similar to AtF, whereas it was lower for pKO. This may be due to larger means for proportion of AtF (30%) than for pKO (7%) in this study. Carlström et al. (2016) investigated proportion of AtF in first-parity Swedish Red cattle and found mean percentage of AtF to be 22.6% and a heritability of 0.21. The current study included later lactations as well, and animals with poor milking temperament were probably culled during first lactation. This may explain the lower percentage of KO when later parities are included. For pIM, heritability was larger than that found in Carlström et al. (2016), whereas the mean was almost equal. Bakke and Heringstad (2015) also found a smaller heritability for pIM (0.08).

The trait TNF had a heritability of 0.12 when defined as pTNF, but with no significant genetic variation as daily observations. Rejected milking was the only trait describing behavior between milkings in AMS, and this study appears to be the first attempt to estimate genetic parameters of such a trait. This makes RM an interesting trait considering behavior unrelated to milking. The heritability of RM was, however, low for both definitions; instead, there were considerable nongenetic animal effects and herd × year differences. As far as the authors know, there are no other studies with which to compare the results for TNF and RM.

Genetic Correlations

Among the traits recorded on a continuous scale (BT, MEF, HT, FR), genetic correlations were relatively strong as expected, partly because these traits overlap each other by definition. To describe AMS-efficient cows, MEF was analyzed because it is a ratio trait considering both yield and occupation time. The strong correlation of 0.98 between FR and MEF indicates that yield per minute of milking time and per minute of BT are genetically the same trait. With its higher heritability and repeatability, FR has the best potential for utilization in genetic evaluation and can substitute for today's subjective scoring of milking speed.

The strong negative and favorable correlation of −0.92 between FR and BT means that faster FR gives shorter occupation time in the AMS and is in agreement with Carlström et al. (2014). They concluded that BT is an interesting trait explaining efficiency in AMS and has a larger effect on milking capacity of the robot compared with average FR and milking time

(Carlström et al., 2014, 2016). Occupation time is less important than FR in nonrobotic milking systems because milkers can influence individual occupation time in the milking unit, and milking efficiency is mostly dependent on cows' genetic ability to milk fast. Genetic correlations between FR and both lnHT and HT (−0.50 and −0.59, respectively) are desirable in terms of less preparation time before and after milking if selection is for increased FR. Another desirable relationship that makes FR interesting for breeding was the correlation suggesting that fewer KO and IM are associated with larger FR (−0.4).

A favorable and intermediate genetic correlation between milkability measured as MEF and KO in the current study was in agreement with Bakke and Heringstad (2015), who estimated the genetic correlation between pKO and milking speed scored subjectively by farmers to be 0.27. Contradictory to our results, they found a positive correlation because of inverse scale for the subjective evaluated milking speed. Genetic correlations from both studies therefore suggest that a slow-milking cow also has a tendency for more KO. Bakke and Heringstad (2015) also found a genetic correlation of −0.22 between farmer-assessed temperament and MEF, again a favorable correlation because bad temperament is scored with a larger number. Genetic correlations between farmer-assessed temperament and KO in AMS were estimated to be −0.44 and −0.71 for Holsteins and Swedish Reds, respectively, in a study by Carlström et al. (2016). An intermediate and favorable correlation of 0.54 was also found in Bakke and Heringstad (2015), with a positive correlation due to opposite temperament scale.

The study by Carlström et al. (2016) showed the correlations between HT and farmer-assessed temperament in Swedish Reds and Holsteins (−0.20 and −0.29, respectively) to be lower than the correlation between temperament and KO. The correlation with farmer-assessed temperament is valuable for confirming the feasibility of the new traits as a measure of temperament already included in today's breeding program.

Data and Statistical Model

The current study was a first attempt to estimate genetic parameters of traits that can be defined from phenotypes that can be routinely uploaded from AMS and used for genetic evaluations of temperament and milkability of Norwegian Red dairy cattle. Despite a relatively small data set of around 4,000 cows, estimates were accurate and demonstrate the value of AMS records. The mixed linear animal model with repeated measures per cow was chosen for being a robust model. In addition, this model uses day-to-day information captured by AMS. More advanced models, such as random regression models, could have been used. However, Carlström et al. (2014) showed that the advantages of random regression models were small for FR, BT, and milking time in AMS. For the traits with daily records, HTD was included as a fixed effect because number of daily observations was larger than 40 and the traits were continuous with sufficient variation within each contemporary group. For the categorical traits with daily observations (KO, IM, TNF, and RM), we defined herd-test day as a random effect due to low frequency of the traits in each subclass. The repeated observations for 1 cow could be both within and across lactations. It is arguably a simplification to assume constant variance within and over different lactations, and an alternative would be to treat parities as different traits with larger data material.

Interpretation of Results

Milkability. It is possible to combine several milkability and temperament traits in a future genetic evaluation of Norwegian Reds because both categories of traits are important in automatic milking. Previous studies show that BT, FR, HT, and pKO are correlated with subjectively scored milkability and temperament in traditional milking systems. The most promising milkability traits are FR and BT. A heritable alternative explaining milking efficiency in AMS is MEF, which is a ratio trait. This create uncertainty about responses in numerator and denominator. Following Zetouni et al. (2017), a multitrait selection index was proposed as more effective than selecting for a ratio trait. Therefore, selection of yield and BT separately may be a better solution. Initial analysis revealed a weak correlation between MEF and daily milk yield (0.15 ± 0.12) but a stronger correlation between BT and MEF (−0.87). As a result of the negative genetic correlation, selecting for high MEF will reduce BT at each milking.

Restrictions set by the milking system or manually by the farmer decide how often the cow can be milked, and environmental factors such as social rank and cows per robot have a significant effect on MI and MF. Feeding strategies will also affect the milking frequency in each herd (König et al., 2006). Average MF was 2.63 milkings per day in agreement with Nixon et al. (2009) and Carlström et al. (2013) but lower than 2.7 to 3.05 found by König et al. (2006).We found low heritabilities and weak correlations with other traits for MI and MF, but they were strongly correlated with each other, being 2 definitions of the same feature. However, MF and MI may express characteristics that are important for milking efficiency.

Temperament Traits in AMS. This study supports pKO as the most promising automatically recorded measure of milking temperament in AMS (Rinell et al., 2014; Bakke and Heringstad, 2015; Carlström et al., 2016). In addition, HT covers other aspects of milking behavior in AMS. Long HT may be caused by a challenging temper or udder conformation. Genetic correlations with pKO and pIM were not estimated, but strong correlations of 0.56 to 0.89 were found by Carlström et al. (2016). They also found a correlation of −0.29 to subjectively scored temperament for Swedish Reds.

Cows with unfavorable udder conformation are likely to also show a large pKO, pIM, and pTNF because teat cups may be improperly attached, fall off, or not be attached at all. Genetic correlation to udder conformation would therefore call for further studies. Important udder conformation traits may also be based on teat coordinate data from AMS (Byskov et al., 2012; Carlström et al., 2016; Poppe et al., 2019). Heritabilities of pKO, pIM, and pTNF (0.12–0.14) are sufficient to obtain genetic progress if properly weighted in a selection scheme, and the genetic correlation shows that pIM and pTNF must be regarded as identical traits. Possible reasons for low heritability of pRM can be restrictions on daily number of visits (forced traffic). This information was not available, so herds practicing both free and forced traffic entered the analysis.

Correlated Traits

Short BT and HT and fast FR are desirable for efficient and fast milking in AMS. On the other hand, it may not be desirable with premature letdown of milk. Milking speed and FR are optimum traits where milking speeds that are both too fast and too slow correlate with poorer udder health. Unfavorable genetic correlations have been reported between increased SCC, leakage, and milking speed (Luttinen and Juga, 1997), and this relationship should be considered when selecting for a milking-efficient dairy cow.

CONCLUSIONS

The current study revealed promising genetic parameters for new traits describing milking efficiency and milking temperament in AMS. High heritabilities and genetic variation makes many of the milkability and temperament traits investigated useful for routine genetic evaluation. High repeatability for the continuous traits shows that only few observations are needed during the lactation to get substantial information for breeding purposes. Many traits will be beneficial in other milking systems as well. Our results showed BT, FR, pKO, and HT to be the most promising traits for describing and improving milkability and temperament in AMS systems.

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PAPER III

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A genetic study of new udder health indicator traits with data from automatic milking systems

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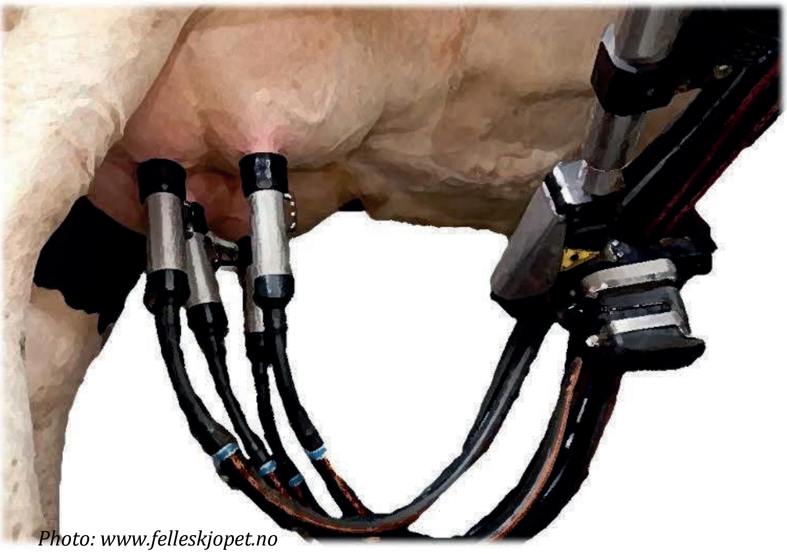

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A genetic study of new udder health indicator traits with data from automatic milking systems

K. B. Wethal,*[1] **M. Svendsen,**[2] **and B. Heringstad,**[1]

[1]Department of Animal and Aquacultural Sciences, Faculty of Biosciences, Norwegian University of Life Sciences, P.O. Box 5003, 1432 Ås, Norway

[2]GENO Breeding and AI Association, 2326 Hamar, Norway

*Corresponding author: karoline.bakke@nmbu.no

ABSTRACT

Automatic milking systems (AMS) record udder health indicator traits on individual cows at every milking. The current study investigated new udder health traits based on data from AMS for use in routine genetic evaluations. Data were from 77 commercial herds and included a total of 4,714 Norwegian Red (NR) dairy cows and 2,363,928 milkings. Out of these, 24 herds provided records from online cell count (OCC) whereas electrical conductivity (EC) could be downloaded from all herds. EC were available on quarter level for each milking, whereas OCC was measured per milking. The AMS traits analyzed were; log-transformed online cell count (lnOCC), maximum conductivity (ECmax), mean conductivity (ECmean), elevated mastitis risk (EMR), and log-transformed EMR (lnEMR). EMR express the probability of a cow having mastitis and was calculated from records of lnOCC by applying a procedure of double exponential smoothing. This adjusted each lnOCC measurement according to individual trend and level of the curve, reducing the variation over time caused by random factors such as machine drift and measurements errors. The traits were analyzed as repeated milkings from 30-320 DIM. In addition, were both ECmax and lnOCC analyzed as multiple traits by splitting the lactation in five periods. (Co)variance components were estimated from bivariate mixed linear animal models. All traits showed genetic variation, with heritability being significantly different from zero. Estimated heritabilities of ECmean, ECmax, and lnEMR were 0.35, 0.23, 0.12, respectively; whereas EMR and lnOCC both showed heritabilities of 0.09. Heritability varied between periods of lactation, from 0.04 to 0.13 for lnOCC, and from 0.12 to 0.27 for ECmax, but these estimates had large standard errors and were not significantly different for lnOCC. Genetic correlations among the AMS traits ranged from 0 to 0.99. The genetic correlation between ECmax and ECmean was close to one, but there was no genetic correlation between these EC traits and other udder health traits from AMS. For comparison we estimated genetic correlations between new udder health indicators from AMS and lactation mean somatic cell score (LSCS) from test-day records, a trait currently used in genetic evaluations. Genetic correlations to LSCS were all favorable and ranged from 0.37 to 0.80 (± 0.11 - 0.22), strongest with lnEMR and lnOCC of 0.80 (± 0.13) and 0.79 (± 0.11), respectively. The results showed that EC traits were heritable but lack genetic correlation to OCC-based traits. The value of ECmax and ECmean from AMS as indicators of udder health in genetic evaluation is therefore questionable. This study demonstrates a potential of using AMS data as additional information on udder health, but further investigation of especially EMR and its correlation to clinical mastitis is recommended before use in routine genetic evaluations.

Key words: mastitis indicator, online cell count, electrical conductivity, elevated mastitis risk, AMS.

INTRODUCTION

Automatic milking systems (**AMS**) provide frequent and objective measures with potential as indicators of udder health, which is of great importance due to both economical and animal welfare reasons. The opportunity of longitudinal recording of udder health arise with sensors in AMS, and this is especially relevant because mastitis is a complex trait. The disease vary from acute with clinical signs, such as warm and swollen udder and loss of milk production (Lohuis et al., 1990), to mild cases with few or subclinical mastitis without any visible signs for the infected cow (Oliveira et al., 2013). Veterinary treated clinical mastitis (**CM**), together with somatic cell count in milk (**SCC**), are the two main traits used in genetic evaluation of udder health (Heringstad et al., 2000). Udder health have been part of the breeding program of Norwegian Red (**NR**) since 1978. The prevalence of CM reported to the Norwegian Dairy Herd Recording System (**NDHRS**) declined from 0.22 cases per cow-year in 2002 to 0.138 in 2018 and the trend is still decreasing (Tine, 2018), suggesting a need for additional information about intramammary infections for routine genetic evaluation of udder health. Treating CM as a binary trait analyzed by linear model, leads to heritability estimates being generally low, varying from 0.01 to 0.035 (Luttinen and Juga, 1997; Heringstad et al., 1999; Rupp and Boichard, 1999; Ødegård et al., 2004a). The indicator trait SCC is moderately correlated to CM, with an average genetic correlation of 0.6 reported in the Nordic countries (Heringstad et al., 2000). Measurements of SCC are mainly based on monthly test-day records, thus there may be time for an animal to get infected and recover from a mastitis case between test-days, leading to undiscovered udder infections if information is based on test-day SCC. In AMS repeated and objective records per milking, are available and can be used for genetic evaluation purposes (Carlström et al., 2013; Wethal and Heringstad, 2019). In-line recording of online cell count (**OCC**, DeLaval,Tumba,Sweden) and electrical conductivity (**EC**) offers alternative phenotypes for continuous monitoring of udder health in AMS. EC is standard equipment and measured for each quarter per milking, as an average or maximum value. OCC is additional equipment and not yet available from every AMS herd. Heritability estimates of EC vary from 0.12 to 0.36, and moderate genetic correlations to mastitis have been found as reviewed by Norberg, (2005).

Udder infections might be difficult to discover if clear clinical signs are lacking. Further, AMS herds may have a reduced time budget per cow, making it more challenging to discover intramammary infections. Therefore, sensor systems have been developed to detect mastitis, and alert the farmer if the mastitis indicator reach a certain level. The indicator may be based on changes in e.g. EC, milk yield, and milking speed. Based on OCC data, Sørensen et al., (2016), suggested elevated mastitis risk (**EMR**) on a 0 to 1 scale as an alternative measure of intramammary infection in AMS. An EMR closer to 1 indicate a larger probability for a cow to have mastitis, and the sensitivity for detecting true cases of CM have been reported to vary from 38 - 89 % depending on specificity levels (Sørensen et al., 2016; Dalen et al., 2019). The ability of the EMR algorithm to detect subclinical mastitis caused by two groups of pathogens were reported with sensitivities from 12 - 69 % for specificities of 80 to 90 % (Dalen et al., 2019). Heritability of log-transformed EMR (**lnEMR**) ranging from 0.06 to 0.15 was estimated by Sørensen and Løvendahl (2014). They reported that lnEMR performed better than traditionally recorded clinical mastitis due to higher heritability. Comparing data on OCC, EC, and EMR from AMS with test-day SCC and records of CM from the NDHRS offers an opportunity to evaluate new phenotypes as additional information in the routine genetic evaluation of udder health. The aim of this study was to estimate heritability of udder health indicator traits defined from OCC and EC data from AMS. We also aimed at estimating genetic correlations among udder health indicators from AMS, and their genetic correlations to the lactation mean somatic cell score (**LSCS**) currently used in genetic evaluation of udder health.

MATERIALS AND METHODS

Data Material

Information included in the current study came from 77 Norwegian herds equipped with AMS from DeLaval (Tumba, Sweden). The data was gathered between year 2016 to 2017 using remote desktop connections to the same herds as used in Wethal and Heringstad (2019). Due to memory limits records per milking were only available one year back in time as data get deleted daily from the AMS. Information about single milkings with known time and date were retained, together with information about EC, milk yield, and OCC. Records of EC were available per udder quarter at each milking in AMS, whereas OCC equipment was optional and available on 24 farms. For each milking OCC were available per cow. For all animals, additional information was extracted from the NDHRS, including birth date, calving dates, test-day SCC, and pedigree information. Records from parity 1 to 9 within 30 to 320 DIM for cows with minimum 9 days of milking in AMS within a parity, were included in the genetic analyses. Further, milk yield had to be > 0 kg, whereas EC ≤ 0.5 mS and OCC less than 500 cells / mL milk were set to missing. Only cows with known NR A.I. sire were included in the genetic analyses. After editing, data contained information on EC from a total of 2,363,928 milkings for 4,714 cows, of which 1,490 cows had records on both EC and OCC from the AMS (Table 1). Pedigree were traced back eight generations if possible, resulting in a total of 39,523 animals in the pedigree file.

Traits

During each milking EC of each udder quarter is measured in milli Siemens (**mS**). Change in EC is used as an indicator of udder health, where an increase may indicate an ongoing udder infection (Norberg et al., 2004a). Two traits were analyzed: Maximum EC (**ECmax**) was the highest value among the udder quarters at each milking and; **ECmean** was the average value of all milked udder quarters at a given milking. Data on OCC were potentially available at each milking, but because the OCC-unit can be switched off manually and farmers decide how often it should be used, the numbers of milkings and cows with OCC records were lower. Before further analyses, the OCC values were log-transformed (**lnOCC**) to obtain a more normal distributed trait. Further, lnOCC was used to estimate EMR, that express the probability of a cow having mastitis at a specific time in the lactation. Calculation of EMR followed Sørensen et al., (2016), adjusting lnOCC for machine induced drift, before a double exponential Holt-Winter smoothing was applied to correct the trait for cow level effects. EMR is expressed on a continuous scale from 0 to 1, with 0 indicating a healthy udder whereas 1 indicate infection. Both EMR and lnEMR were included for genetic analyses. Traits provided by AMS had one observation per milking. For milkings lacking OCC records, predicted OCC values were derived from previous OCC measurements weighted together with values from a standard lactation curve using the Wilmink function (Wilmink, 1987). Predicted values were used in the EMR calculations. Further, LSCS per parity up to third parity based on test-day records from NDHRS was available. Among the 4,714 cows with AMS records, 4,516 had data on LSCS, whereas 1,490 cows had records on lnOCC and (ln)EMR (Table 1). All traits based on AMS were analyzed as repeated records from 30 to 320 DIM, and in addition ECmax and lnOCC were defined as multiple traits within lactation, by dividing the lactation in five periods.

Descriptive Statistics. Number of observations for the udder health indicator traits from AMS varied from 451,949 to 2,363,928 for records of OCC and EC, respectively. Descriptive statistics of lnOCC, ECmax, ECmean, EMR, and lnEMR measured in AMS are given in Table 2. An example of individual OCC and EC curves from continuous measurements in AMS are depicted in Figure 1.

Traits with Repeated Milkings from 30-320 DIM. Udder health indicators: LnOCC, ECmax, ECmean, EMR, and lnEMR were first defined as consistent traits across lactation and analyzed by repeatability models. Repeated milkings from 30 to 320 days in milk were used. The traits were also assumed to be consistent across parities, including all parities for (co)variance components estimation.

Multiple Traits within Lactation. ECmax and lnOCC were also defined as different traits in periods of the lactation. Five periods: 30-90, 90-150, 150-210, 210-270, and 270-320 DIM were defined, and traits were assumed to be the same within a DIM-period across lactations. Genetic parameters were estimated to check for consistency across periods.

Calculation of EMR. The main purpose of EMR is to characterize cows as healthy or sick on a continuous scale giving the probability of udder infection at each milking. EMR was calculated based on lnOCC following Sørensen et al., (2016). First, observations within herd was adjusted based on the milking unit's deviation from an expected mean lnOCC value. Values in a time-series might vary considerably from one timepoint to the next, therefore single exponential smoothing as described by Hyndman et al., (2008) was applied. A weighted mean of past observations together with today's value was calculated, with larger weight put on newer records. An observation was only used if the deviation from expected forecasted value was less than 2 ln-units (more details in supplementary material in Sørensen et al., (2016)). Secondly, a double exponential (Holt-Winter) smoothing was applied, mainly to adjust records according to the individual cows OCC level and trend over time, resulting in a smoothed OCC curve for each cow. Missing OCC values were predicted using previous known value, weighted together with expected values using the Wilmink function, in accordance with Sørensen et al., (2016). Factor analysis in SAS 9.4, (SAS Inst. Inc., Cary, NC) was used to find weights of the individual OCC-level and trend, before latent variable of the k^{th} milking entered the formula for calculating EMR (see supplementary material, Sørensen et al., (2016)). Distribution of EMR was skewed towards larger frequency of animals with 0, thus a log- transformation of EMR (lnEMR) was also carried out to ensure a more normal distribution.

Statistical Methods

For each analysis the GLM procedure in SAS 9.4, (SAS Inst. Inc., Cary, NC) was used to test for which fixed effects to include in the model. The DMUAI-package of the DMU-software (Madsen and Jensen, 2013) was used to estimate variance components. Bivariate linear mixed animal repeatability models were used for estimating heritabilities and genetic correlations between traits.

Models for Udder Health in AMS. For all traits measured in AMS the following linear animal repeatability model was used:

$$y_{ghijklmn}= CYM_g+ CAP_h+ Mno_i+ DIM_j+ HY_k + htd_l+ pe_m+ a_m+ e_{ghijklmn}$$

where $y_{ghijklmn}$ is the nth observation of either lnOCC, ECmean, ECmax, EMR, or lnEMR for cow *m.* The fixed effects were: Calving year and month *g,* from March 2015 to June 2017 ($CYM_{g,}$ 24-26 classes); calving age by parity number *h* (CAP_h, 37 classes); milking number *i* within a day (Mno_i, 5 classes); days in milk *j* (DIM_j, 291 or 50/60 classes); and herd by year *k* (HY_k, 47-151 classes). Random effects were: Herd by test-day (htd_l, 7,898-27,983 levels); permanent environmental effect of animal *m* due to repeated milkings (pe_m, 1,490-4,714 levels); additive genetic animal effect (a_m,); and residual of each observation ($e_{ghijklmn}$). Some fixed effect levels had few observations and were therefore merged. Age at calving in parity four or later were defined as one CAP-class.

Model for LSCS. The following model was used for repeated LSCS observations:

$$y_{ijklmn}= CYM_i+ CAP_j+ DO_k+ hy_l+ pe_m+ a_m+ e_{ijklmn}$$

where: y_{ijklmn} is the LSCS observation for cow *m* in parity *n*. Fixed effects were: CYM_i (310 levels); CAP_j (58 levels); and Days $Open_k$ within parity defined as days from calving to conception grouped in 10 day periods (42 levels: 20-160 DIM). Random effects were: Herd-year (hy_l; 757 levels); pe_m is the permanent environment effect of cow due to repeated records over parities; and the effects a_m and e_{ijklmn} were defined as earlier. For LSCS, CYM was from November 2005 to July 2019, and ages at calving ranged from 19 to 63 months (parity 1-3).

Assumptions for Bivariate Models. Bivariate models were used for estimating genetic covariances and the following variance structure was assumed:

$$V\begin{bmatrix}\mathbf{htd_1}\\ \mathbf{htd_2}\\ \mathbf{a_1}\\ \mathbf{a_2}\\ \mathbf{pe_1}\\ \mathbf{pe_2}\\ \mathbf{e_1}\\ \mathbf{e_2}\end{bmatrix}=\begin{bmatrix}\mathbf{I}\sigma^2_{\mathrm{htd}_1} & \mathbf{I}\sigma_{\mathrm{htd}_{12}} & 0 & 0 & 0 & 0 & 0 & 0\\ & \mathbf{I}\sigma^2_{\mathrm{htd}_2} & 0 & 0 & 0 & 0 & 0 & 0\\ & & \mathbf{A}\sigma^2_{\mathrm{a}_1} & \mathbf{A}\sigma_{\mathrm{a}_{12}} & 0 & 0 & 0 & 0\\ & & & \mathbf{A}\sigma^2_{\mathrm{a}_2} & 0 & 0 & 0 & 0\\ & & & & \mathbf{I}\sigma^2_{\mathrm{pe}_1} & \mathbf{I}\sigma_{\mathrm{pe}_{12}} & 0 & 0\\ & & \text{symm.} & & & \mathbf{I}\sigma^2_{\mathrm{pe}_2} & 0 & 0\\ & & & & & & \mathbf{I}\sigma^2_{\mathrm{e}_1} & \mathbf{I}\sigma_{\mathrm{e}_{12}}\\ & & & & & & & \mathbf{I}\sigma^2_{\mathrm{e}_2}\end{bmatrix},$$

where $\sigma^2_{htd\,i}$, $\sigma^2_{a\,i}$, $\sigma^2_{pe\,i}$, and $\sigma^2_{e\,i}$ are the herd test-day, animal, permanent environmental, and residual variances, respectively, for the two traits (*i=1,2*), and $\sigma_{htd_{12}}$, $\sigma_{a_{12}}$, $\sigma_{pe_{12}}$, and $\sigma_{e_{12}}$ are the corresponding covariances between traits. All effects were assumed to be ~ N (0, σ). **I** is the identity matrix relating the observations to the random effect of $\mathbf{htd}_i$, $\mathbf{pe}_i$, or $\mathbf{e}_i$, for trait *i,* and **A** is the additive relationship matrix.

When estimating covariances between periods of the lactation for ECmax and lnOCC, the following assumptions were made for the residuals in the model:

$$\begin{bmatrix}\boldsymbol{e}_1\\ \boldsymbol{e}_2\end{bmatrix} \sim \mathrm{N}\left(\begin{pmatrix}0\\0\end{pmatrix},\mathbf{I}\otimes\begin{pmatrix}\sigma^2_{e_1} & 0\\ 0 & \sigma^2_{e_2}\end{pmatrix}\right),$$

where $\mathbf{e}_1$ and $\mathbf{e}_2$ is ~ $N(0, \sigma_e^2)$. $\mathbf{e}_1$ is residual variance of either lnOCC or ECmax for DIM-period i, whereas $\mathbf{e}_2$ is residual variance for DIM-period j for the same trait. DIM periods for the same cow occur at different time points, consequently the residual covariance between such traits were restricted to zero.

In bivariate models between AMS traits and LSCS, similar (co)variance structures were assumed for animal and permanent environmental effects, while the residual covariances were restricted to zero.

Heritability. Heritability (h^2) of the traits were calculated using:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

Genetic Correlations. Genetic correlations were calculated as:

$$r_g = \frac{\sigma_{\,a_1 a_2}}{\sqrt{\sigma_{a_1}^2, \sigma_{a_2}^2}}$$

where $\sigma_{a_1 a_2}$ is genetic covariance between traits, $\sigma_{a_1}^2$ and $\sigma_{a_2}^2$ is the additive genetic variance for trait 1 and 2, respectively.

RESULTS

Udder Health Traits from AMS

Estimated variance components for udder health indicator traits in AMS based on repeated milkings from DIM 30 to 320 are given in Table 3. All heritabilities were significantly different from zero. LnOCC and EMR had lowest heritabilities of 0.09, and ECmean the largest heritability of 0.35. When log-transforming EMR heritability increased to 0.12. Repeatability varied from 0.47 to 0.90, where lnOCC showed the lowest value. LnEMR showed as expected the highest value, due to inclusion of smoothed OCC values corrected for effects not caused by animal factors.

LnOCC showed large residual variance, almost 53 % of the total phenotypic variance; whereas for lnEMR only 10 % of the variation were unexplained by the model.

Estimated genetic correlations between udder health indicator traits based on repeated milkings from DIM 30-320, varied from not significant different from zero to close to one (Table 4). The strongest correlation was estimated between ECmean and ECmax (0.99). However, there were no genetic correlations between these two EC traits and lnOCC, EMR, or lnEMR. Genetic correlations to LSCS were significantly different from 0 for all traits, ranging from 0.34 to 0.80; with lnOCC and lnEMR showing the strongest correlations of 0.79 and 0.80, respectively.

DIM Periods of ECmax and lnOCC. LnOCC and ECmax were also defined as different traits for five 60-day periods of the lactation. Heritabilities (Figure 2) ranged from 0.04 to 0.13 for lnOCC, and from 0.12 to 0.27 for ECmax. For the last two DIM periods the heritability for lnOCC increased, but for ECmax heritability was reduced from 0.27 in DIM 210-270, to 0.12 in DIM 270-320. For lnOCC the largest heritability was at the last period of the lactation, but estimates had large standard error due to reduced number of animals.

Genetic correlations among the five periods were strong both for lnOCC (Table 5) and ECmax (Table 6). Genetic correlations between DIM periods varied from 0.60 to 0.99 for lnOCC. For ECmax the genetic correlations among the periods were stronger, ranging from 0.81 to 1. Adjacent periods had in general stronger correlations, both for lnOCC and ECmax. Splitting the lactation in shorter periods was a first approach to investigate the variation in EC and OCC over time. ECmax had strong genetic correlation > 0.92 among all periods except for 30-90 and 270-320 in DIM, suggesting this trait to be the same genetically throughout lactation and defining the trait for different stages of lactation is not necessary. Genetic correlations of lnOCC were strong (≥ 0.90) with low standard errors (0.08-0.12) when adjacent periods were compared. Lowest correlation of 0.60 as found between start lactation to mid-lactation (150-210 DIM), showing cell count in these periods to be most distinct.

DISCUSSION

Genetic Variances and Repeatability

This study successfully estimated heritabilities for all udder health indicator traits measured in-line during milking in AMS, and also found significant genetic correlations to LSCS. As previous studies mostly were focusing on the use of sensor data in AMS for herd-management purposes results to compare with are scarce. Only Sørensen and Løvendahl, (2014) have analyzed OCC and EMR genetically. They divided first parity into periods of 30 days and estimated heritabilities of lnOCC from 0.06 to 0.14. This is in good agreement with the heritability estimates of 0.04 to 0.13 for lnOCC in five different DIM periods found in our study. While there so far have been few genetic studies of OCC in AMS, the genetic nature of test-day SCC and LSCS have been widely investigated (e.g. Emanuelson et al., 1988; Ødegård et al., 2003; Ødegård et al., 2004b; Heringstad et al., 2008). In general, the heritability of SCC when defined as a mean value over the lactation range from 0.11 to 0.26 (Luttinen and Juga, 1997; Ødegård et al., 2004b; Kirsanova et al., 2019). These estimates were mostly larger than what we found for lnOCC. It is generally known that averaging records of a trait over a longer period increase heritability, thus larger estimates would be expected if OCC where summarized over a longer period.

The heritability estimates of ECmax (0.23) and ECmean (0.35) were in line with results reported by Norberg et al., (2004c) who found heritability of 0.28 for EC measured as a daily mean in first parity Holstein. Further, they reported heritabilities ranging from 0.26 to 0.36 using random regression models with Legendre polynomials. Heritability of ECmean and ECmax were also in agreement with estimate of 0.23 for log-transformed EC measured as maximum values from each milking (Povinelli et al., 2005). Santos et al., (2018) found even larger heritability of 0.53 for EC measured at cow level and 0.37 to 0.46 for udder quarters in a study based on data from three herds over period of 30 days. When EC was measured as inter-quarter ratio between the individual teats with highest and lowest EC values, heritabilities were relatively low, ranging from 0.05 to 0.12 in Norberg et al., (2004b). They found this definition of EC to work better for detecting clinical mastitis. Preliminary results of the current study did not find any significant additive genetic variance of inter-quarter ratio (results not shown). This may be related to small differences in EC between udder quarters in our data. Another difference is that our data contained one record of ECmean and ECmax per udder quarter per milking, whereas in Norberg et al., (2004b), EC were measured every 2 seconds.

The heritability estimates of of EMR (0.09) and lnEMR (0.12) were in the same range as reported by Sørensen and Løvendahl, (2014) who estimated heritabilities from 0.06 to 0.15 for lnEMR, and 0.02 to 0.09 for EMR in first parity Holstein at different periods of DIM. In their study, EMR did not show genetic variance significant different from 0 for some of the investigated periods of lactation, thus they argue that lnEMR may be a better definition than EMR. EMR in shorter periods of DIM were not investigated in the current study, but it would be relevant to check whether the trait differ genetically throughout the lactation. When calculating EMR, OCC measurements from 6 days after calving were included in the algorithm. The reason for this was to ensure fast stabilization of the smoothed OCC-values before genetic components were estimated. The genetic analyses included only records after day 30 in milk to avoid the period of elevated SCC-level right after calving.

Figure 2 showed a slightly u-shaped curve of heritability estimates for lnOCC, with higher heritability toward the end of lactation. Similar pattern was reported for heritability of test-day SCC analyzed by random regression models (Norberg et al., 2004b). In the study by Sørensen and Løvendahl, (2014), heritability of lnOCC increased steadily and peaked around 200 DIM. The pattern was opposite for the heritability of ECmax, where heritability dropped drastically after 200 DIM. Larger genetic variation in first period of lactation were also found for CM (Lund et al., 1999; Heringstad et al., 2003b) and for both test-day SCS and EC(IQR) analyzed by random regression models (Norberg et al., 2004b). Larger genetic variation for EC in first part of the lactation may be due to increased frequency of infection in this period. Larger genetic variation and frequency of CM in early lactation are reported earlier (Heringstad et al., 2003a). Repeatability of lnOCC was low (0.47) compared to the high repeatability observed for EMR and lnEMR (0.90). This was in line with the study by Sørensen and Løvendahl, (2014), and likely caused by the smoothing process used for EMR. Therefore, EMR observations showed less variation over time, and was to a larger degree explained by effects of the animal itself i.e. permanent non-genetic and genetic effects.

Genetic Correlations

Genetic correlations of zero between lnOCC and the two EC traits were not expected and are not comparable with other studies at this point. The genetic correlation of 0.86 between test-day SCC and EC defined as IQR in the first month of lactation reported by Norberg et al., (2004b), suggest that there is a genetic relationship. However, when EC and in-line measurements of SCC from the same milkings were compared, a phenotypic correlation less than 0.4 was reported by Hovinen et al., (2006) for commercial AMS farms. These authors also reported that measurements of EC alone were very poor at detecting SCC level in milk. Others do report a low phenotypic correlation between SCS from herd test-day records and EC (Nielen et al., 1992; Hovinen et al., 2006; Boas et al., 2017). Considering the larger number of animals from different herds in the current study we consider the results to be reliable, even though they are contradictory to earlier findings.

Strong and favorable genetic correlations from LSCS to lnOCC and lnEMR (0.79 and 0.80, respectively) in AMS confirms that in-line records of cell count in milk provides accurate measurements related to that already included in the NDHRS. However, a correlation less than unity indicate that OCC may also contribute with some complementary genetic information. CM is also included in the udder health index for NR. However, the genetic relationship to EMR could not be investigated in the current study due to limited number of animals and very low frequency of CM in the material (~ 4 %). Sørensen and Løvendahl, (2014) could not estimate the relationship between EMR and clinical mastitis for the same reason. Many studies have estimated the relationship between traditionally measured SCC and CM, yielding genetic correlations ranging from 0.37 to 0.97 (Lund et al., 1994; Pösö and Mäntysaari, 1996; Koeck et al., 2010). Results based on a large dataset of first parity NR cows show a genetic correlation between CM and LSCS of 0.53 (Ødegård et al., 2004b). Estimating the genetic correlation between CM and EMR should be done in order to evaluate how well it is capturing the cases of CM. Even though the number of herds and observations were large in our study, the time period with detailed data possible to extract from each farm was relatively short, mainly caused by memory limitations in the AMS software.

In the current study, traits were defined the same across parities because of a limited number of cows. This assumption should be checked with more cows in the dataset for OCC traits. However, many studies have estimated strong genetic correlations between CM across parities ranging from 0.70 to 1.0 (Pösö and Mäntysaari, 1996; Nielsen et al., 1997; Carlén et al., 2004;

Urioste et al., 2012). Also, SCC and LSCS are genetically correlated across lactations (Pösö and Mäntysaari, 1996; Samoré et al., 2008; Urioste et al., 2012). Genetic correlation between log-SCC measured early and late in lactation have been reported in the range from 0.14 to 0.55 for first to third parity Holsteins, whereas adjacent periods in the same lactation were highly correlated and reported to be almost unity (Haile-Mariam et al., 2001). If the genetic correlation of test-day SCC or OCC in different lactation periods and/or parities is < 1, alternative models such as multitrait model or random regression model should be considered to take the time aspect into account and utilize the information from the different periods.

Implications and Further Recommendations

This is the first genetic study of large-scale udder health indicator traits from OCC recorded during milking in AMS. Studies investigating OCC have so far been based on data from one (research farm) up to eight commercial farms (Sørensen and Løvendahl, 2014; Sørensen et al., 2016; Dalen et al., 2019), but these studies were not genetic studies. However, more data are still needed to estimate genetic correlations to CM and to investigate alternative trait definitions.

Average OCC in the current study was slightly higher (88,000 cells / ml) than average test-day SCC in the NDHRS (75,000 cells / mL). Herds investing in OCC equipment may have elevated SCC level in milk and thereby be more motivated for monitoring. The frequency of cows reported with CM in these herds were slightly higher (~ 6 %,) compared to the average for the AMS-herds without the OCC equipment (~ 3 %). Another aspect may be that these herds were relatively large which made it more challenging to monitor individual cows.

A high level of OCC in milk over time may indicate an ongoing subclinical infection, with bacteria’s that might be transmitted, hence this is a trait relevant in selection for improved udder health. Further studies are needed to clarify the usefulness of EC as indicator of udder health, including genetic correlations to CM to understand how well udder health is measured.

When OCC measured in AMS were compared with test-day SCC from milk recordings the correlation between them were strong (Sørensen et al., 2016; Nørstebø et al., 2019). The current study did confirm a strong genetic agreement between OCC to LSCS which supports in-line measured cell count as an indicator of udder health. Health indicators from AMS do provide more precise information due to repeated records from every milking. Continuous data present opportunities for new udder health traits, e.g. individual cows' susceptibility to udder infections and their ability to recover after being infected. EMR could cover other aspect of susceptibility to mastitis such as number of days from calving to first EMR value above some fixed threshold. Other alternative traits could be days (or hours) from infection to recovery, or whether the animal recovers without treatment. Results from the current study show that data from AMS can contribute with additional udder health traits for use in genetic evaluation.

CONCLUSIONS

Udder health indicator traits based on EC and OCC data recorded in commercial AMS herds were heritable and might contribute with genetic information on longitudinal udder health. All traits were genetically correlated to LSCS, a trait included in the routine genetic evaluations of udder health today. The strongest genetic correlation with LSCS was estimated for lnOCC and lnEMR, and the lowest with the EC traits. No genetic correlation was found between OCC based traits and the two EC traits. Despite a large heritability, their importance as indicator traits for improved udder health is unclear, while traits based on OCC from AMS are promising.

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Table 1. Number of observations per trait combination of udder health traits from automatic milking systems (AMS)[1] and lactation average somatic cell score (LSCS) from the Norwegian dairy herd recording system (NDHRS). Number of cows in parenthesis.

Data source	Trait[1]	lnOCC	ECmean	ECmax	EMR	lnEMR
AMS	ECmean	451,216				
		(1,490)				
	ECmax	451,216	2,363,928			
		(1,490)	(4,714)			
	EMR	451,949	769,309	769,309		
		(1,490)	(1,490)	(1,490)		
	lnEMR	451,949	769,309	769,309	770,919	
		(1,490)	(1,490)	(1,490)	(1,490)	
NDHRS	LSCS	11,020	11,020	11,020	11,020	11,020
		(1,490)	(4,516)	(4,516)	(1,490)	(1,490)

[1] lnOCC = log-transformed online cell-count; ECmean = mean electrical conductivity; ECmax = maximum conductivity; EMR = Elevated mastitis risk; lnEMR = log-transformed EMR.

Table 2. Descriptive statistics for repeated measures of log-transformed online cell count (lnOCC), maximum electrical conductivity (ECmax), average electrical conductivity (ECmean), elevated mastitis risk (EMR) and log-transformed EMR (lnEMR) in automatic milking systems; and lactation average somatic cell score (LSCS) from the first three parities (based on SCC testday-records).

Trait	N	Mean	Sd	Min	Max	No. animals
lnOCC (log cells / mL)[1]	451,949	4.48	1.15	0.69	9.12	1,490
ECmax (mS)[1]	2,363,928	4.82	0.55	0.80	16.95	4,714
ECmean (mS)[1]	2,363,928	4.71	0.48	0.80	11.80	4,714
EMR[1]	770,919	0.11	0.20	$0.39*10^{-6}$	1	1,490
lnEMR[1]	770,919	-3.62	1.85	-14.76	0	1,490
LSCS (log cells / mL)[2]	11,020	4.32	0.89	2.02	8.67	4,516

[1] Based on repeated milkings in AMS from 30-320 DIM.

[2] Repeated over parities.

Table 3. Estimated variance components[1], repeatability[2] (R) and heritability[2] (h^2) with standard error in parenthesis for log-transformed online cell count (lnOCC), electrical conductivity (EC) measured as maximum (ECmax) and mean (ECmean), elevated mastitis risk (EMR), and log-transformed EMR (lnEMR) from 30 to 320 days in milk.

	Variance Components					
	σ^2_a	σ^2_{pe}	σ^2_{htd}	σ^2_e	R	h^2
lnOCC	0.12	0.48	0.04	0.67	0.47	0.09
	(0.04)	(0.04)	(<0.001)	(0.001)	(0.01)	(0.03)
ECmax	0.049	0.061	0.009	0.105	0.51	0.23
	(0.006)	(0.004)	(<0.001)	(<0.001)	(0.006)	(0.02)
ECmean	0.053	0.036	0.008	0.062	0.59	0.35
	(0.005)	(0.003)	(<0.001)	(<0.001)	(0.006)	(0.03)
EMR	0.004	0.037	0.0002	0.006	0.87	0.09
	(0.002)	(0.002)	(<0.0001)	(<0.0001)	(0.004)	(0.04)
lnEMR	0.43	2.77	0.033	0.37	0.90	0.12
	(0.17)	(0.18)	(<0.001)	(<0.001)	(0.004)	(0.04)

[1] σ^2_a = additive genetic variance, σ^2_{pe} = permanent environment variance, σ^2_{htd} = herd-testday variance, σ^2_e = residual variance, σ^2_p = total phenotypic variance ($\sigma^2_a + \sigma^2_{pe} + \sigma^2_e$).

[2] R = repeatability ($\sigma^2_a + \sigma^2_{pe}$) /$\sigma^2_p$, h^2 = heritability (σ^2_a/σ^2_p).

Table 4. Genetic correlations, with standard error in parenthesis, between udder health indicator traits from automatic milking systems (AMS)[1] and lactation average somatic cell score (LSCS) from test-day records from NDHRS[2]. Traits recorded in AMS with one record per milking and cow from 30 to 320 days in milk, and LSCS as repeated records from first to third parity

	Trait[1]				
	lnOCC	ECmax	ECmean	EMR	lnEMR
ECmax	-0.0004 (0.17)				
ECmean	0.04 (0.16)	0.99 (0.002)			
EMR	0.50 (0.22)	-0.05 (0.22)	-0.03 (0.21)		
lnEMR	0.91 (0.08)	-0.05 (0.22)	-0.008 (0.20)	0.76 (0.15)	
LSCS	0.79 (0.11)	0.34 (0.11)	0.37 (0.10)	0.58 (0.22)	0.80 (0.13)

[1] lnOCC = log-transformed online cell count in milk; ECmax = Maximum electrical conductivity; ECmean = mean electrical Conductivity; EMR = Elevated mastitis risk; lnEMR = log-transformed EMR.

[2] NDHRS = Norwegian dairy herd recording system.

Table 5. Heritability on the diagonal and genetic correlations below the diagonal between log-transformed online cell count (lnOCC) from automatic milking systems at different days in milk (DIM) periods. Corresponding standard errors in parenthesis.

DIM period	30-90	90-150	150-210	210-270	270-320
30-90	0.09 (0.04)				
90-150	0.92 (0.09)	0.07 (0.03)			
150-210	0.60 (0.24)	0.90 (0.11)	0.04 (0.03)		
210-270	0.75 (0.21)	0.78 (0.22)	0.99 (0.12)	0.09 (0.04)	
270-320	0.83 (0.21)	0.79 (0.23)	0.92 (0.23)	0.99 (0.08)	0.13 (0.06)

Table 6. Heritability on the diagonal and genetic correlations below the diagonal between maximum electrical conductivity (ECmax) measured by automatic milking systems at different days in milk periods (DIM). Corresponding standard errors in parenthesis (SE).

DIM period	30-90	90-150	150-210	210-270	270-320
30-90	0.26 (0.03)				
90-150	0.98 (0.01)	0.27 (0.03)			
150-210	0.93 (0.03)	0.98 (0.01)	0.27 (0.04)		
210-270	0.92 (0.04)	0.99 (0.02)	1.00 (0.01)	0.16 (0.03)	
270-320	0.81 (0.08)	0.92 (0.06)	0.94 (0.05)	0.98 (0.02)	0.12 (0.04)

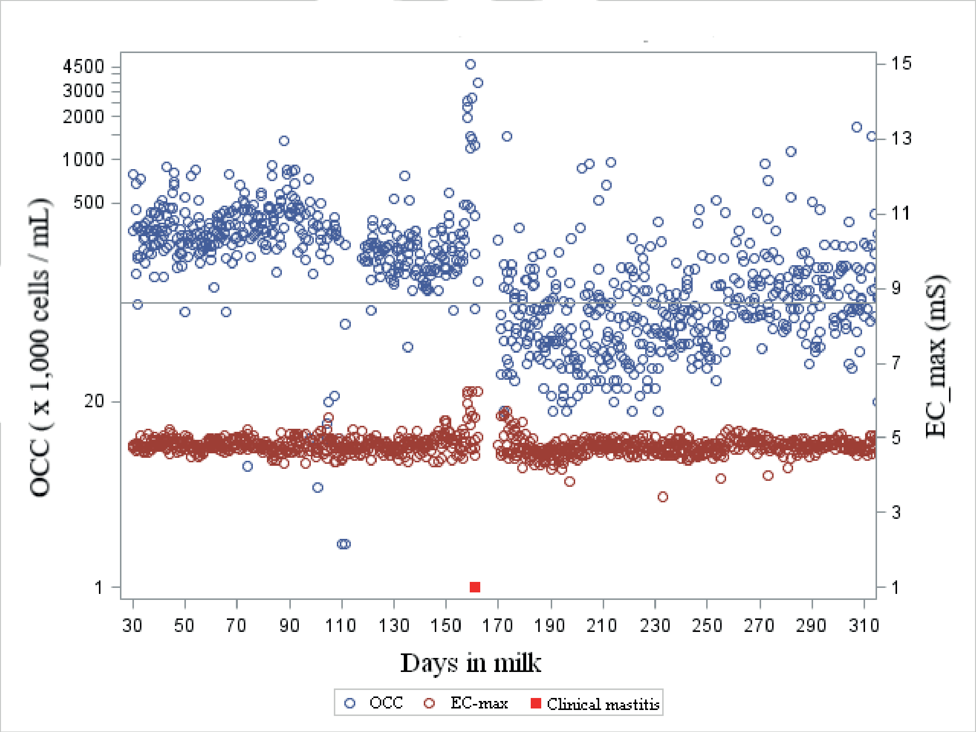

Figure 1. Plot of records for one cow with data from online cell count (OCC) measured as thousand cells / mL of milk, and electrical conductivity in milli Siemens (mS) measured as maximum (EC-max). At around 160 days in milk an incident of mastitis occurred (red square indicate veterinary treatment of clinical mastitis at day 160), causing increased OCC and EC-max. The solid line indicates a SCC level of 100,000 cells / mL milk.

Figure 1.

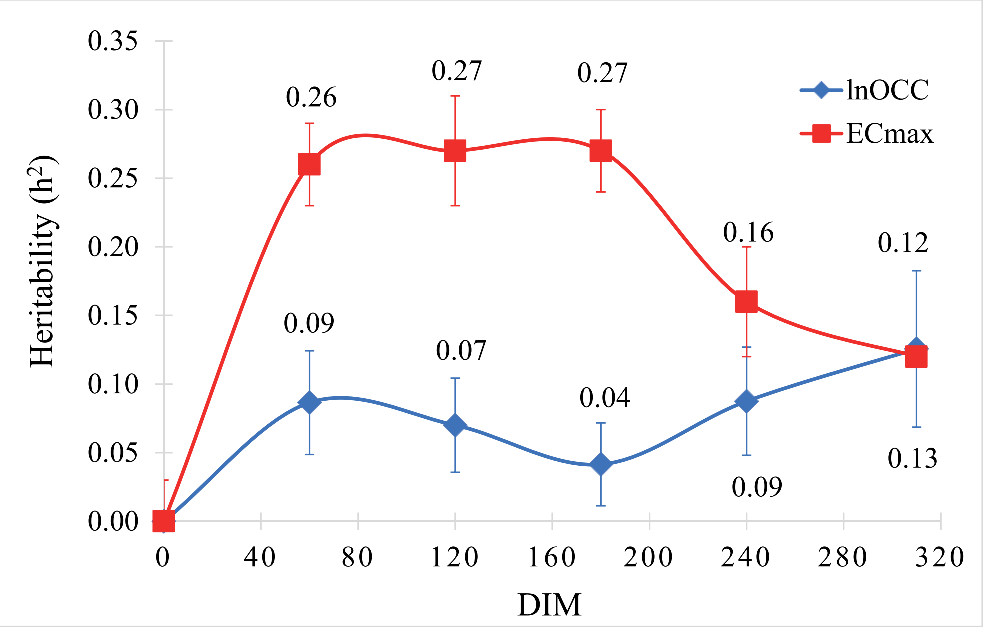

Figure 2. Heritability of log-transformed online cellcount (lnOCC) and maximum electrical conductivity (ECmax) measured in automatic milking systems, for five different periods of the lactation; 30-90, 90-150, 150-210, 210-270, and 270-320 days in milk (DIM). Whiskers indicate standard error of the heritability estimate.

Figure 2.

4. GENERAL DISCUSSION

This study aimed at using records from AMS to investigate novel phenotypes related to milkability, temperament, and udder health in NR cows. In addition, the first paper compared workability traits in different milking systems. Less genetic variation in AMS-herds was found for subjectively scored milkability and temperament traits, suggesting additional information might be needed for these traits in the future. These results added value to the aim of using new records from AMS in genetic analyses of new phenotypes interesting for genetic selection.

It was shown that data from AMS are feasible to use in genetic evaluations, and that genetic variation exists for the majority of the analyzed traits. The results from the second paper supports previous studies showing milkability and temperament traits from AMS to be heritable (Carlström et al., 2013, 2016a). In the third paper genetic variation of new udder health indicators in AMS were investigated. The results were similar with previously reported results for udder health traits in AMS (Norberg et al., 2004b, c; Sørensen and Løvendahl, 2014).

4.1 Workability in Different Milking Systems

Results from the first paper revealed strong genetic correlations across milking systems for workability traits. Approximately 50% of the Norwegian cows are milked in AMS, and the rest in traditional milking systems, such as milking parlors or pipeline systems. These systems differ in milking routines in addition to the larger average herd-size for AMS. These differences made it important to compare how farmers are scoring their cows in different milking systems. Similar studies investigating traits across systems were scarce, but Lassen and Mark, (2008) report strong genetic correlations of workability and conformation traits between freestall and tiestall systems. In addition, their study also reported lower heritabilities for milking speed and temperament in freestalls. The current thesis found lower heritability for workability in AMS while genetic correlations between systems were strong. Low genetic correlations might indicate a reranking among the EBV of bulls in the different systems. No reranking was observed for milking speed and leakage, but temperament had the lowest rank-correlation and genetic correlation between milking systems. This means that some of the bulls among the top ten were reranked when temperament was measured on daughters in AMS. The correlation was large enough to consider the trait to be the same across milking systems. However, one option to account for milking system by including it as a fixed effect in the models. Lower estimates of variance components in AMS might be handled as heterogeneous variances. Defining traits in the two milking systems as different using a multitrait model would be more relevant if the genetic correlation differs considerably from unity.

The genetic correlation between milking speed and leakage found in this thesis was stronger for AMS cows than for other systems (-0.88 vs -0.82), and the estimates were larger than those found for Finnish

Ayrshire, but similar to the correlation reported for Holstein (Luttinen and Juga, 1997). Selection for increased milking speed may therefore result in elevated problems with milk leakage. Because a larger proportion of cows in AMS are scored with "unknown" it might become challenging to collect enough phenotypic information on this trait in the future. Alternative ways to monitor milk leakage might be explored; this is important in breeding programs with large emphasis on milking speed. On the other hand, greater MF in AMS might reduce the problem. Even though Norwegian farmers to a large extend are scoring workability traits, a reduction in phenotypic and genetic variance can be challenging for the genetic evaluations in the future if solely based on cows from AMS.

4.2 New Phenotypes in AMS

The value of in-line measured data from AMS as new phenotypes in breeding programs is a relatively sparsely investigated field. Previous studies have mainly been focusing on milkability traits (Gäde et al., 2006; König et al., 2006; Nixon et al., 2009; Carlström et al., 2013, 2014), in addition to a few studies investigating genetic parameters of novel temperament traits (Carlström et al., 2016b; Santos et al., 2018). Genetic background of udder health measured as EC in AMS are previously analyzed but to a smaller extend than the other traits (Norberg, 2005; Santos et al., 2018), and a single study has investigated genetic parameters of in-line measured OCC (Sørensen and Løvendahl, 2014).

Before new phenotypic traits can be implemented, the genetic variation of the trait should be addressed in terms of heritability. In addition, its genetic correlation to other important traits should be clarified. If the new trait has an antagonistic relationship to traits already included in the breeding goal, this will affect expected total genetic gain. Traditionally, phenotypes have been available at low cost whereas in the future this might change (Egger-Danner et al., 2015). Therefore, the cost of including additional phenotypic information, relative to the increased genetic and economic gain should also be considered. Phenotypic records of traits investigated in current study were easily accessible in AMS, although not yet included in routine data collection to the NDHRS. All traits investigated in this thesis were heritable and possible to use in a genetic selection of milkability, temperament, and udder health.

4.2.1 Milkability and Temperament. Milkability traits with detailed information on a continuous scale were found to have largest heritabilities among traits analyzed. FR, BT, and MEF had highest heritability of 0.48, 0.27, and 0.22, respectively. For FR, the results agreed with corresponding research based on data from commercial and research farms (Gäde et al., 2006; Carlström et al., 2013). For BT, the results were in agreement with literature on Holstein, whereas a slightly lower heritability was found than reported for Swedish Red cows (Carlström et al., 2013). For MEF, measured as kg milk / min of BT, heritability was in accordance with earlier findings in NR cows, and also in Holstein (Bakke and Heringstad, 2015; Vosman et al., 2016, 2018). These results supports that FR from AMS is a more accurate measure than subjectively scored milking speed with heritabilities ranging from 0.10 to 0.24 (Luttinen and Juga, 1997; Rensing and Ruten, 2005; Wiggans et al., 2007; Sewalem et al., 2011). Heritability of farmer-assessed milking speed as currently shown in Paper I, were 0.21 and 0.27 for AMS and other systems respectively, which is lower than estimates for FR. This is a reason to use AMS data in the routine genetic evaluation of milking speed. Larger heritability of the traits of interest will improve the accuracies of estimated breeding values. This again will increase our chances of selecting the candidates with the best genetic potential of the trait.

Milking frequency, MF, measured in AMS had low heritability (0.05) and agreed with Carlström et al., (2013). The value of using daily MF or MI may therefore be questionable when based on current definitions. Milking routines, capacity of the AMS and herd size might affect individual MF to a large degree, thus partly explain the large environmental effect. When MF was measured in different periods of the lactation, the heritability is reported to be larger than found in current thesis (König et al., 2006). The cows' production level is likely to influence MF, since higher milk production increases pressure on the udder. This motivates the cow to be milked, and larger milking frequency are associated with increased daily milk production (Melin et al., 2005; Jacobs and Siegford, 2012; Tse et al., 2018).

Daily records of phenotypes expressing milking temperament in AMS (KO, IM, TNF, RM) had heritabilities lower than farmer-assessed temperament (0-0.06). This is mainly due to low frequency when expressed as categorical traits. Defining them on a continuous scale increased heritability slightly (0.05-0.14). The heritabilities of traits expressing temperament in AMS, were comparable with the study by Carlström et al., (2016b), who also investigated pKO (named AtF in their study), HT, and pIM in AMS. Our heritability estimate of pKO was lower than their results of 0.21 and 0.31. For HT, they reported heritabilities of 0.05 for Holstein, while 0.15 for Swedish Red which was larger than the estimate of NR (0.05). Heritability of pIM was higher (0.14) than their results (0.02 and 0.06). The low heritability of HT suggests other definitions to be an option. It is suggested that this is an important trait because it describes time-usage in AMS before and after the actual milking process. A low HT is desirable, and it may have effect on cows milking efficiency.

Data from AMS provide measures of cow behavior and temperament that could supplement the current definition of temperament, or possible replace some of the measurements in the future. Other studies have reported a genetic correlation with pKO and pIM to farmer-scored temperament with absolute values from 0.27 to 0.72 (Rinell, 2014; Bakke and Heringstad, 2015; Carlström et al., 2016b). Lower genetic variation in farmer-assessed temperament in AMS herds supports the relevance of supplementing this trait with phenotypic information from sensors in the future.

The strong and favorable genetic correlation between higher FR and shorter BT (-0.92) indicate they are strongly related, which is logical. Selection for higher FR will reduce BT due to a negative correlation (or vice versa). BT might provide some additional information related to other aspects of milking efficiency in AMS such behavior or udder characteristics that affect occupation time. FR mainly contributes genetic information about the cows' actual milk flow. Including both FR and BT when selecting an AMS-efficient cow might be beneficial. MEF was investigated with the purpose of explaining robot efficiency and showed a strong correlation of almost unity with FR (0.98). This indicates that MEF does not contribute with additional genetic information compared with FR.

Before milkability traits from AMS can be used in genetic evaluation, their relationship with traits currently included in the TMI should be investigated. A previous study on NR estimated the genetic correlation between MEF in AMS with farmer-assessed milking speed to be -0.88 (Bakke and Heringstad, 2015). If the correlation between farmer-assessed milkability and FR in AMS is one, milking speed measured subjectively is no longer needed. If AMS data becomes available on routine basis, FR should therefore be included in the routine genetic evaluations.

There are additional benefits of replacing subjective measurements with objective registrations from AMS. The subjective assessments may cause biases, e.g. if a sire is known to produce slow-milking daughters, the results achieved from farmers assessment of daughters might change and become more extreme when this bull becomes a known A.I bull. The farmer's own opinion might influence the phenotypic measurements. Objective measures will remove such biases and may improve accuracy of selection. Slightly higher heritabilities were estimated for new traits expressing temperament in AMS, compared with farmer-assessments. In addition, information from AMS are recorded over a longer time period and it is possible to achieve data on more traits. This means that AMS provides more information regarding the traits which might improve accuracies. Adding relevant information in a multi-trait model with various temperament traits is an opportunity in future genetic evaluations.

4.2.2 Udder Health. Udder health traits based on measures of EC and OCC in milk are heritable. Heritability of ECmean (0.35) and ECmax (0.23) corresponds with previous studies reporting EC to be a highly heritable trait (Norberg et al., 2004c, 2006; Povinelli et al., 2005; Santos et al., 2018). Norberg et al., (2004a, 2006) has suggested EC in milk as possible to use as an indicator trait to selection for reduced mastitis, but few have investigated the genetic correlation between EC and CM. The genetic correlation between EC traits and CM was not possible to estimate with the dataset analyzed in this project. Defining the EC-level as lactation mean might have been an alternative definition, and this definition had a genetic correlation of 0.75 to CM according to Norberg et al., (2006). The strong correlation in their study might be related to a relative high prevalence of CM, with 32.2% of the cows being treated at least once. In the current dataset the overall frequency of CM was 4% and only 180 of the cows included in the genetic analyses were treated for severe or mild CM. More animals may be included in the future so that genetic correlations between EC and CM in the NR population can be estimated.

The mean EC-level of the investigated herds were in accordance with literature values ranging from 4.68 - 4.96 mS (Norberg et al., 2004a; Boas et al., 2017; Santos et al., 2018), while Norberg et al., (2004a) report higher values (5.37) for Holstein cows with subclinical mastitis. In addition, they found mean EC level for cows classified as healthy to be 4.87 mS, which is larger than the average for both ECmean and ECmax in the current study. This, in addition to few CM treatments and low levels of LSCS and OCC, indicate that the NR cows in our dataset were healthy. The genetic correlations among ECmean and ECmax with LSCS were intermediate (0.34, 0.37).

The genetic correlations between EC traits and OCC were 0, but because there are few previous studies of udder health traits from AMS these results were not possible to compare at present day. An overall good udder health status of animals in the current study may be one reason for these non-exiting correlations. When phenotypic records of OCC is compared to testday SCC from the NDHRS, higher levels also showed a better resemblance between the measurements (Nørstebø et al., 2019), although not directly comparable to results in current thesis. They suggested lower levels of SCC and OCC to have a weaker phenotypic correlation, than higher ln-levels. No relationship between OCC and EC can possible be explained by low levels and relatively healthy cows. Other studies did find a relatively weak phenotypic relationship between test-day SCS and EC (Nielen et al., 1992; Hovinen et al., 2006; Boas et al., 2017).

A weak genetic relationship between EC traits and LSCS was in contrary to the only comparable estimate for genetic correlation of 0.90 between EC and test day-SCC (Norberg et al., 2004b). This could be due to breed-differences and higher levels of SCC in their data. In addition to this, their study was based on one research herd meaning that the effect of animal and herd might be confounded. The frequency of cows reported to have CM are in general low in Norway, with 13% of the cows per year are recorded with veterinary treatments (Tine, 2019). Additional health indicators are needed in the future and sensor data from AMS offer alternatives. New definitions of subclinical mastitis are possible by using OCC-based traits from AMS. One of the challenges with subclinical mastitis is that the pathogens might be transmitted without being discovered. A longitudinal measure of OCC might help to discover these problems at an earlier stage. Kirsanova et al., (2019) suggested defining subclinical mastitis based on different threshold levels of SCC, and new definitions of subclinical mastitis can be included in the udder health index.

Elevated mastitis risk, EMR, as an indicator of udder health in AMS seems promising as current thesis identified lower residual variation, and larger repeatability and heritability than for lnOCC. EMR was corrected for random variation in OCC such as drift in sensors and a large deviation from the cows expected level and trend in OCC-level. With OCC data available it is possible to express number of days before reaching a certain threshold level, as one trait describing resilience to udder infections. Also, resilience or ability to recover without treatments are alternative udder health traits of interest (Welderufael et al., 2017).

4.3 Data Quality from AMS

Editing and quality control of the data was a large part of the work. As sensors might deliver measurement errors from time to time, a large number of observations can be lost in the editing process. Carlström et al., (2013) reported 57% loss of observations from the process of matching ID, restricting the dataset on DIM, incomplete milkings, and "inconsistent" records. The current study did not put restrictions on incomplete milkings. Values that were not logical were set to missing. For example, a milking with normal milk yield but with unreasonable large FR, the record was retained while setting the FR value to missing. The raw data consisted of more than 5 million AMS-visits, but when summarized as one daily record per cow (Paper II), this was reduced to 1 million. Whereas in Paper III the number of observations were ~ 2 million because all milkings per cow and day were retained.

Currently, AMS data are not available from a central database on routine basis in Norway, except for certain traits such as milk yield that are collected routinely through the Nordic cattle data exchange, NCDX (Tine, 2018). There were some challenges related to matching

ID-numbers of animals in the AMS data with the correct animal in NDHRS, especially for animals that were bought, and origin ear tag number did not match. In addition, farmers may use a different ID-number in the AMS than the national number. This makes it challenging to match all the individuals to NDHRS. Another challenge was related to the joint-farming system in Norway were several farmers run one big herd together, and the herd consists of cows originating from different producers. This means some AMS had individuals with different origin markings. In addition, national ID numbers can be reused after ten years. To ensure correct individuals to match in NDHRS, calving dates were checked against date of AMS records.

Because AMS data were deleted daily from the software on farm, it is possible to lose historical information. Therefore, only 1.5 year of data was available from herds in this study. In the future it is important that data are collected and stored long term, especially if the data will be used for breeding purposes. Another issue before AMS data can be included in routine genetic evaluations, is related to combining data from different data sources, e.g. different brands of AMS. The agreements between similar traits in different AMS-systems should be clarified in future studies.

4.4 Statistical Analysis of AMS-traits

Linear animal models were chosen in these first analyses of AMS data, because linear models are used in routine genetic evaluations of production, workability, and udder health traits today. In addition, solutions from these models are easy to interpret, with results given in the same unit as the phenotypic measure on the trait analyzed. Furthermore, linear models are feasible for implementation in a breeding program. An assumption made for the AMS traits was that traits were the same across parities. This was done because we had limited amount of data. Milkability from AMS analyzed by Carlström et al., (2014) had strong genetic correlations between parities (0.93-0.99) and this indicates that milkability can be treated as the same traits across parities.

A major benefit of data provided by AMS are the vast amounts of repeated measurements. To take the time aspect into account alternative models for estimating genetic components such as longitudinal models can handle this (Schaeffer, 2004). The trajectory of genetic variance over time can be estimated by e.g. random regression models. Carlström et al (2014) applied a random regression model and estimated heritability to be lower in the beginning and the end of the lactation for average FR, BT, and milking time in AMS (Carlström et al., 2014). In the current study genetic variation for several AMS traits was presented with results based on similar models, while genetic studies of new traits, other definitions or models are possible to investigate further in the future.

4.5 Traits important for AMS cows

Challenges related to milking and feeding routines differs in AMS compared to traditional milking systems. Cows are milked individually whereas in milking parlors several cows are milked at the same time. The perfect AMS cow should visit the milking robot regularly and voluntary to reduce farmers workload. At the same time, the interval since previous visit should not be too short. The AMS from DeLaval has two different cow traffic systems, one system of “free cow traffic” and “forced traffic” where animals have access to the milking area only if time interval since previous milking is acceptable. Acceptable time values might be controlled by farmers, but the system will automatically use a milking interval that corresponds to individual yield and lactation stage. In a free cow traffic system cows can frequently visit the AMS between milkings, and availability for some of the individuals with permission for milking might be lower. Forced traffic are reported to increase the average milking frequency in AMS (Ketelaar-de Lauwere et al., 1998).

Large MF are reported to increase the individual milk yield (Erdman and Varner, 1995). Selection for increased MF is possible, but as this study confirmed the heritability is low. Cows should have short occupation time in the AMS, without affecting milk production negatively. A large number of visits without permission in AMS is undesirable but might indicate that cows are highly motivated to visit the AMS. One can for example weigh the number of visits in early start lactation as desirable and use this as a measure of how fast heifers are adapting the milking routines.

It is important with a calm temperament. Feared animals might have reduced production and poorer welfare (Hemsworth, 2003). These are reasons to breed for improved temperament and thereby improving the dynamic between animals and humans. Therefore, it may be important to consider animals temperament and attitude towards humans in different situations, not only during milking in AMS. It is still highly relevant to consider the farmers own perception of the individual cows' behavior when they are handled by humans. The benefit with sensors is that information is collected on all animals, also when farmers are not present to observe.

Another important trait is udder conformation. Certain characteristics such teat placement can challenge teat cup attachment in AMS and might lead to unsuccessful attachments. Therefore, udder conformation influences both animal welfare and efficiency in AMS. Teat coordinates used for attaching milking equipment are heritable, and genetically correlated to subjective evaluated udder exterior (Byskov et al., 2012; Carlström et al., 2016; Poppe et al., 2019). Therefore, this might be used to score udder conformation objectively in the future. In addition, robust feet and legs, and a good claw health are important traits for dairy cows. Fertility and health, and clear physical signs of heat is of great importance in AMS and traditional milking systems. Sensors in AMS offers objective and repeated information on milkability, temperament, and udder health as confirmed in this thesis.

4.6 Further Recommendations

Based on the current results, using data from AMS in genetic evaluation of several traits for NR is possible. Novel traits expressing milkability, temperament, and udder health as repeated measurements are heritable. Because some of the investigated traits had higher heritability than corresponding traits currently selected for, phenotypic measurements from AMS might improve the accuracies of the breeding values. As traits relevant for expressing milkability in AMS, both BT and FR seems very promising both due to high heritabilities, and that they exhibit favorable correlations with the other milkability-, and temperament traits investigated. Traits expressing unsuccessful milkings where cows are not properly milked (pIM, pTNF, pKO) had larger heritability than farmer-assessed temperament. Temperament traits in AMS can probably contribute with additional information in future genetic evaluations. Udder health indicators routinely measured in AMS, both OCC and EC, were heritable. Still, results indicate that OCC-based trait are more promising and can be included in the genetic evaluation for improved udder health. Before this, their correlations to CM should be revealed. For considering milking efficiency in AMS in addition to animal welfare, the investigated phenotypes are important. AMS has the opportunity to combine sources of data from each milking, a potential that should be investigated in the future. There is a potential for using several of these AMS-traits in a breeding program, but their genetic relationship with other traits already included in the breeding goal should be identified before implementation. Lastly, a system for routinely collecting data from AMS should be established, in order to fully utilize the potential of these new traits in the genetic evaluations of NR cows.

5. GENERAL CONCLUSIONS

- Milking speed, temperament, and leakage scored by farmers had lower genetic variation in AMS-herds than in other systems. Strong genetic correlations between traits in AMS and other milking systems (≥ 0.86) suggest traits to be genetically the same in different systems.

- Milkability and temperament traits measured in AMS were heritable, with favorable and strong genetic correlations between many of the investigated traits.

- Traits expressing milking speed and temperament in AMS, had larger heritabilities than the subjective measurements currently used in the genetic evaluations of NR.

- For the milkability traits in AMS, highest heritability was estimated for FR, BT, and MEF. Traits expressing milking temperament in AMS had higher heritability when summarized within lactations.

- Udder health indicators based on in-line recorded EC and OCC in AMS were heritable and genetically correlated with LSCS, a trait currently used in routine genetic evaluations of udder health.

- No genetic correlation between EC and OCC-based traits were found. The importance of EC as indicator trait for udder health might therefore be questionable.

- This thesis successfully showed that in-line measured sensor data from AMS can be utilized to express milkability, temperament, and udder health. Data from AMS is possible to use in routine genetic evaluations of NR cows.

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Norwegian University
of Life Sciences

Postboks 5003
NO-1432 Ås, Norway
+47 67 23 00 00
www.nmbu.no

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