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## **Phenotypic and genetic variation in milk flow for dairy cattle in automatic milking systems**

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### **Abstract**

Increased dairy herd sizes have led to installment of automatic milking systems in many herds. Such systems put new demands on the cows as regards ease of milking. They also enable in-line recording of a number of traits. The aim of this study was to estimate the phenotypic and genetic variation in milk flow rate for dairy cattle in automatic milking systems. The first step was to investigate how data directly extracted from automatic milking systems should be edited in order to be usable for genetic analyses. Data on average milk flow rate (kg/min) and peak flow rate (kg/min) per udder quarter from 19 Swedish dairy herds with automatic milking systems were used. In total data from three million milkings of 4700 cows of the two breeds Swedish Holstein and Swedish Red from the years 2004-2008 were used. After an extensive editing process 64% of the milkings were considered suitable and used for a first analysis. Both milk flow traits were normally distributed and showed large variation among cows. For the Swedish Holstein the total means were 3.86 kg/min (SD=1.20) for the average milk flow rate and 5.58 kg/min (SD=1.52) for the peak flow rate. For the Swedish Red the total means were 3.03 kg/min (SD=1.17) for the average milk flow rate and 4.53 kg/min (SD=1.58) for the peak flow rate. Genetic parameters were estimated with a linear animal model. Estimates of the heritabilities ranged between 0.23 to 0.32 across lactations and traits for Swedish Holstein and between 0.34 to 0.60 for Swedish Red. As a following step genetic correlations for milk flow traits and udder and teat conformation will be estimated.

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### **Introduction**

Automatic milking systems (AMS) were introduced in Sweden in 1998 and have since then grown to comprise nearly 20 % of the 300 000 dairy cows in the national milk-recording scheme. About 10 % of the 5000 dairy herds enrolled in the national milk-recording scheme are currently using AMS. An advantage with this kind of systems is that high-yielding cows are milked more than two times per day and less pressure is put on the udder, which otherwise may cause some leaking. The question is if and to what extent AMS puts new requirements on the cows to fit in such systems.

Milk flow rate (milkability) is a very important trait for efficient use of AMS. It is a functional trait, together with health, fertility, calving ease and feed efficiency, which increase the productivity by reducing the costs (Groen et al., 1997). Both yield and milk flow rate has a large impact on robot milking capacity in kg of milk produced per day (Koning et al., 2000).

Milkability measured in different ways has been reported to have an enough high heritability to be useful in selection of cows (Aydin et.al., 2008; Boettcher et al., 1998; Gäde et.al., 2007; Luttinen & Juga, 1997). In Sweden, the genetic evaluation of milkability is currently based on subjective scoring first lactation cows by the herd manager. Average herd size is increasing in the Nordic countries as well as in many other countries, which makes it harder for the herd managers to subjectively score the animals in an accurate way. The possibility to use in-line registrations does not only mean that the observations are objectively measured but also that it is possible to get more than one observation per animal. Gäde et al. (2006) concludes from the variation in milkability from day to day that the performance test for milkability should include more than one observation. With the AMS we get a lot of in-line registrations for a number of traits from each milking which would make a very useful basis for genetic evaluation. Currently we don't have enough knowledge on how to extract and use this information correctly for genetic analysis purposes.

The aims of this study are to investigate how to use milk flow data directly extracted from AMS for genetic analysis and to study the genetic variation in milk flow traits of the two main dairy breeds in Sweden, Swedish Holstein and Swedish Red.

## **Material and Methods**

Data come from 19 commercial dairy herds using AMS from DeLaval. All herds have contributed with a copy of the backup file created in the AMS computer. Information from spring 2004 (alternatively since the AMS was installed) to autumn 2008 were used. In total there were observations from 4900 cows; 47% Swedish Holstein and 53% Swedish Red.

The data from the herds consisted of ID-information, milk yield, milking interval, average flow rates per quarter and peak flow rates per quarter. Complementary information about pedigree, calvings and lactation numbers come from the national milk-recording scheme.

The following edits were made:

1. Average flow rate per quarter must be in between 0.1 and 4 kg/min. (16% of the observations were lost.)
2. Milking interval must be in between 5 and 20 hours. (Another 2% of the observations were lost.)
3. The length of the visit in the AMS must be in between 1 and 20 minutes and the cow should not have kicked off the equipment from any quarter. (Another 17% of the observations were lost.)

4. The AMS has not classified this milking or the previous milking from the same animal as incomplete. (Another 1% of the observations were lost.)

After this editing process 64 % of the total number of observations were left, see fig. 1.

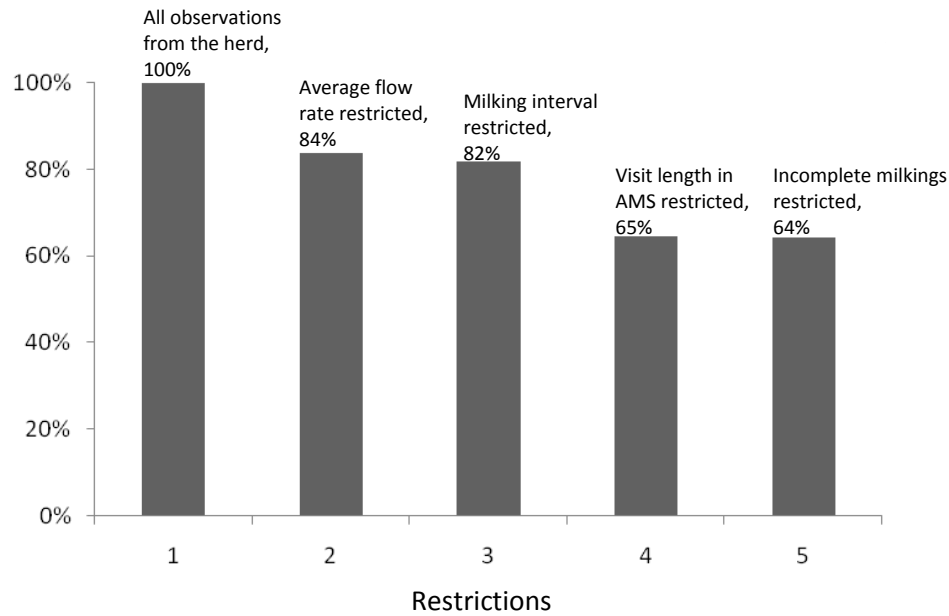


Figure 1. About 64% of the total number of observations is left after the restrictions in the editing process.

After the editing process the remaining observations were merged with data from the national milk-recording system to get the pedigree information. Since the AMS does not force the herd managers to use the same ID for the animal in the AMS computer as the national recording ID a number of animals disappeared and about 60 % of the original animals were left for the genetic analysis, see table 1.

Table 1. Number of observations and distribution of cows and sires in the genetic analysis by lactation number.

|                         |                    | No. of obs.   | No. of cows | No. of sires |
|-------------------------|--------------------|---------------|-------------|--------------|
| <b>Swedish Holstein</b> | Lactation 1        | 409733        | 962         | 233          |
|                         | Lactation 2        | 236111        | 569         | 183          |
|                         | Lactation $\geq 3$ | 112091        | 279         | 109          |
|                         | <b>Total</b>       | <b>757935</b> | <b>1299</b> | <b>305</b>   |
| <b>Swedish Red</b>      | Lactation 1        | 400046        | 783         | 191          |
|                         | Lactation 2        | 283109        | 530         | 149          |
|                         | Lactation $\geq 3$ | 153853        | 300         | 105          |
|                         | <b>Total</b>       | <b>837008</b> | <b>1035</b> | <b>245</b>   |

Pedigree information contained the ancestors for three generations. In total, 4632 animals were in the Swedish Holstein pedigree file and 3667 animals were in the Swedish Red pedigree file.

Variance components were estimated for average flow rate (AFR) and peak flow rate (PFR) for 1<sup>st</sup>, 2<sup>nd</sup> and  $\geq 3^{\text{rd}}$  lactations for Swedish Holstein and Swedish Red separately. The genetic parameters were estimated using restricted maximum likelihood (Madsen and Jensen, 2000). The model was as follows:

$$y_{ijklmn} = \mu + \text{HYS}_i + \text{MY}_j + \text{LW}_k + a_l + \text{pe}_m + e_{ijklmn}$$

where:

|                |                                                                                         |
|----------------|-----------------------------------------------------------------------------------------|
| $y_{ijklmn}$   | = observation for a particular cow in particular milking                                |
| $\text{HYS}_i$ | = fixed effect of herd*year*season                                                      |
| $\text{MY}_j$  | = fixed effect of milk yield                                                            |
| $\text{LW}_k$  | = fixed effect of lactation week within parity                                          |
| $a_l$          | = random additive genetic animal effect                                                 |
| $\text{pe}_m$  | = random permanent environmental effect to account for repeated measurements within cow |
| $e_{ijklmn}$   | = random error                                                                          |

## Results and discussion

### *Descriptive statistics*

In total there were information from 757935 milkings for Swedish Holstein and 837008 milkings for Swedish Red cows (see table 1). The phenotypic means and standard deviations for milk yield, AFR and PFR are given in Table 2. For Holstein the mean over all lactations for AFR was 3.86 and 5.58 for PFR. For Swedish Red the mean over all lactations for AFR was 3.03 and for PFR 4.53. The flow rates increased with 14% in Swedish Holstein and 6% in Swedish Red from first to second lactation while there were small changes between second and later lactations. When tested for normality the milkability traits followed a normal distribution but showed a large phenotypic variation (see fig. 2).

Table 2. Descriptive statistics of the data.

|                  |       | 1 <sup>st</sup> lactation |      | 2 <sup>nd</sup> lactation |      | $\geq 3^{\text{rd}}$ lactations |      |
|------------------|-------|---------------------------|------|---------------------------|------|---------------------------------|------|
|                  |       | mean                      | SD   | mean                      | SD   | mean                            | SD   |
| Swedish Holstein | Yield | <b>11.57</b>              | 3.14 | <b>13.77</b>              | 4.22 | <b>14.96</b>                    | 4.64 |
|                  | AFR   | <b>3.60</b>               | 1.12 | <b>4.11</b>               | 1.20 | <b>4.30</b>                     | 1.28 |
|                  | PFR   | <b>5.24</b>               | 1.40 | <b>5.90</b>               | 1.53 | <b>6.14</b>                     | 1.61 |
| Swedish Red      | Yield | <b>10.44</b>              | 3.05 | <b>11.69</b>              | 3.86 | <b>12.41</b>                    | 4.15 |
|                  | AFR   | <b>2.96</b>               | 1.11 | <b>3.13</b>               | 1.18 | <b>3.04</b>                     | 1.28 |
|                  | PFR   | <b>4.42</b>               | 1.49 | <b>4.66</b>               | 1.60 | <b>4.54</b>                     | 1.75 |

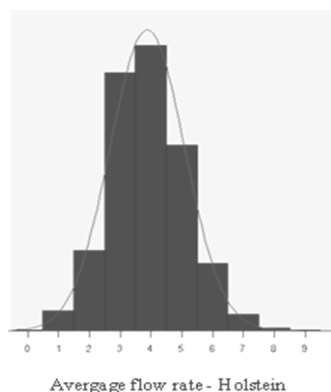


Figure 2. AFR is well fitted to a normality curve.

### Genetic analysis

Lactational heritability estimates for AFR for Swedish Holstein were moderate (0.25-0.32) and rather high for the Swedish Red cows 0.34-0.55 (see table 3). Lactational heritability estimates for PFR were very similar to the AFR, ranging between 0.23-0.32 for Swedish Holstein and between 0.36-0.60 for the Swedish Red cows (see table 3). The estimated heritabilities in this study are similar or a little higher than those found in the literature, which supports the inclusion of milk flow rates into the breeding schemes as also has been concluded in other studies (Aydin et.al., 2008; Gäde et.al., 2007). Most published heritability estimates of milkability traits come from singularly recorded milkability information and often from a subjectively scoring while these figures results from serial AMS objective information. Gäde et.al (2006) reported heritabilities for automatically recorded milk flow of 0.49 and 0.55 for AFR and PFR respectively for Holstein-Friesian. Our lower results for Holstein could partly be explained by the fact that in the present study the data come from commercial herds while in the former study the data was from one research farm with more standardized environment.

There seems to be a difference between the breeds in the size of additive genetic variance in the milk flow traits where it's about 50% larger in Swedish Red than in Swedish Holstein in first lactation, while there are only marginal differences in later lactations

Table 3. Additive genetic variances ( $\sigma_a^2$ ) and heritabilities of milkability traits per lactation and breed.

|                         |     | 1 <sup>st</sup> lactation |             | 2 <sup>nd</sup> lactation |             | ≥ 3 <sup>rd</sup> lactations |             |
|-------------------------|-----|---------------------------|-------------|---------------------------|-------------|------------------------------|-------------|
|                         |     | $\sigma_a^2$              | $h^2$       | $\sigma_a^2$              | $h^2$       | $\sigma_a^2$                 | $h^2$       |
| <b>Swedish Holstein</b> | AFR | 0.32                      | <b>0.32</b> | 0.31                      | <b>0.25</b> | 0.44                         | <b>0.30</b> |
|                         | PFR | 0.48                      | <b>0.32</b> | 0.45                      | <b>0.23</b> | 0.72                         | <b>0.31</b> |
| <b>Swedish Red</b>      | AFR | 0.47                      | <b>0.59</b> | 0.34                      | <b>0.34</b> | 0.51                         | <b>0.55</b> |
|                         | PFR | 0.75                      | <b>0.60</b> | 0.36                      | <b>0.36</b> | 0.79                         | <b>0.53</b> |

Even if it seems possible, according to the high heritability estimates, to use serial milk flow data from AMS for genetic analysis, other aspects are important to consider before including it into a selection index. Milk flow is suggested to be an optimal trait, where the highest milk flow rates

(Boettcher et al., 1998; Rupp & Boichard, 1998; Luttinen & Juga, 1997) as well as the lowest milk flow rates (Luttinen & Juga, 1997; Lund et al., 1994; Lawstuen et al., 1998) may lead to a decline in udder health. Therefore the relationship between milkability and udder health, mainly clinical mastitis, needs to be clarified before including objective measures of milkability in a selection index.

In order to fit into AMS the udder shape and teat shapes and placements must be relatively standardized. Relationships between udder and teat conformation and milkability traits have been reported (Boettcher et al., 1998; Rensing & Ruten, 2005). From AMS it is possible to get information about teat placement from the robot coordinates which will lead to a better precision than was previously possible. Correlations between such data and milk flow will be investigated to be able to define the type of udder and teats and their placement for best fit to automatic milking systems.

## **Conclusion**

- Serial milk flow data from AMS can be used for genetic analysis. Currently the data demand a lot of editing before being ready for genetic analysis. The most critical limitation is the differences in the way the ID of the animal is set in the AMS and in the national milk-recording scheme.
- The heritabilities for AFR and PFR are moderate (Swedish Holstein) to high (Swedish Red) which indicates that inclusion in breeding schemes may be advantageous.
- The genetic variation seems to stay at a high level also in later lactations which indicates that very little selection, if any, takes place after first lactation.
- Before including milk flow rates in a selection index further knowledge is needed about correlations to other important traits such as udder health, udder conformation and size and placements of teats.

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