

# Possibilities of implementing measures from Automatic Milking Systems in routine evaluations of Udder Conformation and Milking Speed

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## Abstract

Genetic parameters for nine udder conformation traits were estimated in first parity Danish Holstein cows by means of bi-variate linear animal models. The traits were either based on measures of teat coordinates from milking robots or linearly scored by professional classifiers. The heritabilities for the objectively measured AMS traits were higher than for the corresponding subjectively scored traits. All genetic correlations between two corresponding traits were high ( $r_g \geq 0.90$ ). In addition, genetic parameters for fat and protein flow measured in milking robots, fat and protein flow measured by means of TruTest milk meters and milking speed scored by dairy farmers were estimated in first parity Danish Holstein cows using a tri-variate linear animal model. The heritability for flow measured in milking robots was the highest among the three estimates and the heritability for milking speed was the lowest. The genetic correlations between the three traits were 0.91 or higher. According to these preliminary results it is possible to use information on teat co-ordinates and fat and protein flow from milking robots in the joint Nordic genetic evaluation of udder conformation and milking speed, respectively.

**Key words:** Automatic milking system, genetic parameter, udder conformation, milking speed

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## Introduction

In Denmark, conformation traits and milk production traits have been recorded for many years. Unlike milk production traits, conformation traits have usually only been scored once. Thus, it has not been possible to follow potential changes within lactation (e.g. because the udder swells up as a consequence of mastitis) or across lactations (e.g. because of a weak suspensory ligament). This situation has changed because it is now possible to transfer data from milking robots to the national database. One of the advantages of data from milking robots is that the phenotypes are measured at each milking. This provides the opportunity complying with the wish of some dairy farmers for a genetic evaluation of udder conformation in later parities.

So far, primarily first parity cows sired by young bulls are linearly scored whereas older cows are not scored on a routine basis. This procedure was chosen by the breeding company in order to hold down costs. In addition, bulls would be relatively old before they were evaluated for traits in later parities. However, when a reference population is made, genomic

selection can remove this obstacle. Thus, young animals can be genomically evaluated for traits realised in later lactations with similar reliabilities as for traits realised in first lactation.

Data from milking robots provide scope for replacing some subjective assessments by objective measurements. This applies to both udder conformation and milking speed that are scored by professional classifiers and dairy farmers, respectively. Milking speed belongs to the trait group workability and it is already included in the Nordic total merit index. In Denmark, milking speed is either measured by means of TruTest milk meters in connection with milk recording or scored subjectively. Today, owners of AMS herds have to score milking speed because data from milking robots are not yet included in the genetic evaluation.

The purpose of this preliminary study was to estimate heritabilities for udder conformation traits and milking speed measured in milking robots. In addition, we wanted to estimate genetic correlations between these new observa-

tions and observations that are applied in the genetic evaluation today.

## Materials and methods

### *Data collection from milking robots*

Initially, a group of AMS herds were selected to generate a test data set. In these test herds, data from milking robots were collected by four technicians in connection with milk recording. The technicians transferred both milking data and AMS data to the national database. The first time the technician visited the AMS herd he collected data from several years. Thus, the test data set contains AMS data that are older than the date of the first data collection. Subsequently, the technician collected data from the last milk recording to this milk recording.

Today, this arrangement is extended to more technicians and it is intended to comprise all Danish AMS herds. At this stage, the technicians collect AMS data from one milk recording to the next on a routine basis. It is our intention also to collect the stored data from the milking robots within a relatively short time frame.

For the time being, it is only possible to collect data from Lely's milking robots. However, 27% of the Danish milk recorded cows are milked in milking robots (23% of the Danish dairy herds) and about half of the robots are produced by Lely. Danish Cattle Federation collaborates with Lely in transferring data in real time but this is a long-term strategy.

The analyses of udder conformation and milking speed are based on two different data sets that are obtained on a routine basis and during the test period, respectively. Thus, the conformation data set comprises data for about 14 000 cows in 62 AMS herds and the registrations are performed from February 2011 to May 2012. The milking speed data set contains about 11 million observations and comprises data for about 16 000 cows in 76 AMS herds. These observations are recorded from May 2005 to February 2011.

### *Data description of udder conformation*

For each teat, the robot measures one set of X-, Y-, and Z-coordinates per milking. The coordinates are measured on an arbitrary scale but

it is possible to use distances between the coordinates as phenotypes for five udder conformation traits. These five traits are: (1) front teat placement; (2) rear teat placement; (3) distance between front and rear teats; (4) udder balance and (5) udder depth. We decided to use the average distance between the coordinates in the analyses. Each average was based on registrations performed from 30 to 60 days after calving, and only cows with at least 10 completed milkings in that period were kept in the data set.

In addition, records on four udder conformation traits scored by professional classifiers were extracted from the Danish cattle database. Due to computational limitations, only every fourth herd without AMS was included in the analyses and only data from 2007 and onwards were used.

The final data set contained information on 2 591 first parity Holstein cows from AMS herds and 102 816 first parity Holstein cows from herds without AMS. In total, 1 490 cows with measures of teat coordinates also had udder conformation assessments.

### *Statistical analysis of udder conformation*

The AMS data and the linearly scored conformation data were analysed using bi-variate linear animal models by means of DMU (Madsen and Jensen, 2008). The model can be arranged in the following way:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where  $y_1$  and  $y_2$  were vectors of udder conformation records from milking robots and assessment records, respectively, and  $X_1$  and  $X_2$  were design matrices relating fixed effects in  $b_1$  and  $b_2$  to  $y_1$  and  $y_2$ . The fixed effects for AMS data and for assessment data were:

$$b_1 = \begin{bmatrix} hy \\ age \\ mc \end{bmatrix} \text{ and } b_2 = \begin{bmatrix} hys \\ age \\ mc \\ cla \\ ca \end{bmatrix}$$

where **hy** was the effect of herd-year group, **age** was the effect of age at calving in months,

and **mc** was the effect of month of calving. The effect of herd, year and six month season was included in **hys**, the effect of classifier and two month period was included in **cla**, and the effect of months between date of calving and date of assessment was included in **ca**.

The random effects of animal were included in **a<sub>1</sub>** and **a<sub>2</sub>** where the design matrices **Z<sub>1</sub>** and **Z<sub>2</sub>** relate records to the animal effects. The random residuals were **e<sub>1</sub>** and **e<sub>2</sub>**. The covariance structures for the random effects were:

$$\text{var} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} = \mathbf{G} = \mathbf{G}_0 \otimes \mathbf{A},$$

where

$$\mathbf{G}_0 = \begin{bmatrix} \sigma_{a1}^2 & \sigma_{a1,a2} \\ \sigma_{a1,a2} & \sigma_{a2}^2 \end{bmatrix}$$

and **A** is the additive relationship matrix.

$$\text{var} \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} = \mathbf{R} = \mathbf{R}_0 \otimes \mathbf{I},$$

where

$$\mathbf{R}_0 = \begin{bmatrix} \sigma_{e1}^2 & \sigma_{e1,e2} \\ \sigma_{e1,e2} & \sigma_{e2}^2 \end{bmatrix}$$

and **I** is the identity matrix.

### Data description of milking speed

The milking robot measures among other things milk yield and milking time per milking. A 14 days moving average calculated by the milking robot was until recently used as the official milk yield in connecting with milk recording. We decided to use this average milk yield and the fat and protein percentages from the first milk recording after first calving in the calculation of fat and protein flow (kg per minute). We decided also to calculate the average milking time as a 14 days moving average so that the time frame for the average milk yield and the average milking time is the same. The average milking time is calculated per 24 hours, and each milking counts equally much.

In addition, records on fat and protein flow from herds without AMS were extracted from the national database. These records are based on measures of milk yield and milking time from TruTest milk meters and fat and protein percentages from the first milk recording after first calving.

The data set contains information on first parity Holstein cows that were between 22 and 34 months old when they calved. For inclusion of the records in the analyses, the first milk recording should be in the interval from 30 to 240 days after first calving. Records without date of milk recording, average milk yield, average milking time, fat percentage or protein percentage were deleted. In addition, the average milk yield should be at least 15 kg of milk.

After editing, the data set contained 4 050 cows from AMS herds and 272 043 cows from herds without AMS. None of the cows had information on both types of fat and protein flow. Finally, records on assessments of milking speed were merged to the data set. About 900 of the cows from the AMS herds and about 47 000 of the cows from the herds without AMS had assessments of milking speed.

### Statistical analysis of milking speed

Data were analysed using the DMU package (Madsen and Jensen, 2008). A tri-variate linear animal model was fitted where **y<sub>1</sub>**, **y<sub>2</sub>** and **y<sub>3</sub>** were vectors of flow records from milking robots, assessment records and flow records from TruTest milk meters, respectively. The model can be arranged in the following way:

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \mathbf{y}_3 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{X}_3 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \\ \mathbf{b}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_3 \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{a}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix}$$

where **X<sub>1</sub>**, **X<sub>2</sub>** and **X<sub>3</sub>** were design matrices relating fixed effects in **b<sub>1</sub>**, **b<sub>2</sub>**, and **b<sub>3</sub>** to **y<sub>1</sub>**, **y<sub>2</sub>**, and **y<sub>3</sub>**. The fixed effects for fat and protein flow and for assessment of milking speed were:

$$\mathbf{b}_1 = \mathbf{b}_3 = \begin{bmatrix} \mathbf{hys} \\ \mathbf{age} \\ \mathbf{mc} \\ \mathbf{cmr} \end{bmatrix} \text{ and } \mathbf{b}_2 = \begin{bmatrix} \mathbf{hys} \\ \mathbf{age} \\ \mathbf{mc} \\ \mathbf{ca} \end{bmatrix}$$

where **hys** was the effect of herd, year and six month season. The effect of age at calving in months was included in **age**, the effect of month of calving was included in **mc**, the effect of months between date of calving and date of first milk recording was included in **cmr**, and the effect of months between date of

calving and date of assessment was included in **ca**.

The random effects of animal were included in **a**<sub>1</sub>, **a**<sub>2</sub> and **a**<sub>3</sub> where the design matrices **Z**<sub>1</sub>, **Z**<sub>2</sub> and **Z**<sub>3</sub> relate records to the animal effects. The random residuals were **e**<sub>1</sub>, **e**<sub>2</sub>, and **e**<sub>3</sub>. The covariance structures for the random effects were:

$$\text{var} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{a}_3 \end{bmatrix} = \mathbf{G} = \mathbf{G}_0 \otimes \mathbf{A},$$

where

$$\mathbf{G}_0 = \begin{bmatrix} \sigma_{a1}^2 & \sigma_{a1,a2} & \sigma_{a1,a3} \\ \sigma_{a1,a2} & \sigma_{a2}^2 & \sigma_{a2,a3} \\ \sigma_{a1,a3} & \sigma_{a2,a3} & \sigma_{a3}^2 \end{bmatrix}$$

and **A** is the additive relationship matrix.

$$\text{var} \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix} = \mathbf{R} = \mathbf{R}_0 \otimes \mathbf{I},$$

where

$$\mathbf{R}_0 = \begin{bmatrix} \sigma_{e1}^2 & \sigma_{e1,e2} & 0 \\ \sigma_{e1,e2} & \sigma_{e2}^2 & \sigma_{e2,e3} \\ 0 & \sigma_{e2,e3} & \sigma_{e3}^2 \end{bmatrix}$$

and **I** is the identity matrix.

## Results and discussion

### *Genetic parameters for udder conformation*

The objectively measured traits show higher heritabilities than the corresponding subjectively scored traits (Table 1).

**Table 1.** Heritabilities ( $h^2$ ) for and genetic correlations ( $r_g$ ) between (1) front teat placement; (2) rear teat placement; (3) distance between front and rear teats; (4) udder balance and (5) udder depth measured in milking robots or scored by classifiers with standard errors in parentheses. Distance between front and rear is not scored by classifiers.

| Trait | $h^2$       | $h^2$       | $r_g$       |
|-------|-------------|-------------|-------------|
|       | AMS         | Assessments |             |
| 1     | 0.46 (0.06) | 0.31 (0.01) | 0.92 (0.04) |
| 2     | 0.38 (0.05) | 0.32 (0.01) | 0.94 (0.04) |
| 3     | 0.46 (0.09) | -           | -           |
| 4     | 0.44 (0.07) | 0.22 (0.01) | 0.90 (0.04) |
| 5     | 0.65 (0.06) | 0.42 (0.01) | 0.94 (0.02) |

The genetic correlations are all high ( $r_g \geq 0.90$ ) which indicate that traits scored by classifiers are almost the same as the corresponding traits measured by robots. Thus, measurements of teat coordinates may be a nice supplement to assessments of udder conformation. However, it is important to bear in mind that measurements from milking robots cannot replace all assessments made by the classifiers as the classifiers in addition to ten linear udder conformation traits also score seven body traits and five feet and leg traits.

### *Genetic parameters for milking speed*

The heritability for flow measured in milking robots is higher than the heritability for flow measured by means of TruTest milk meters (Table 2). The reason may be that the average milk yield and the average milking time from milking robots are based on 14 days moving averages whereas these two averages from TruTest milk meters are based on measures from a single day. On the other hand, fat percentages from milking robots may be less accurate than fat percentages from TruTest milk meters because the interval between two milkings can vary in the robot (Peeters and Galesloot, 2002). Both heritabilities for fat and protein flow are high compared to the heritability for assessment of milking speed. It may be attributable to the fact that flow is based objective measurements.

The genetic correlations between the three traits are high (Table 2). Thus, there is reason to believe that information from milking robots, TruTest milk meters and assessments can be combined and used in the genetic evaluation of milking speed.

Today, an average of 1 to 7 observations from TruTest milk meters is used in the genetic evaluation (Team genetic evaluation, 2011). The heritability estimate increases as the number of observations increases and therefore the phenotypic data are weighted. If Nordic Cattle Genetic Evaluation (NAV) decides to use flow observations from milking robots in the genetic evaluation it is necessary to weigh these observations as well.

**Table 2.** Heritabilities for and genetic correlations between (1) fat and protein flow measured in milking robots, (2) scored by dairy farmers or measured by means of (3) TruTest

milk meters in connection with milk recording with standard errors in parentheses.

| Trait | Heritability | 2           | 3           |
|-------|--------------|-------------|-------------|
| 1     | 0.63 (0.07)  | 0.91 (0.05) | 0.94 (0.03) |
| 2     | 0.20 (0.02)  | -           | 0.91 (0.02) |
| 3     | 0.41 (0.01)  | -           | -           |

The use of flow observations from milking robots may have limited effect on the estimated breeding values of proven bulls because there are already many observations from TruTest milk meters and assessments. However, by using flow observations from milking robots, all cows from AMS herds will be genetically evaluated for milking speed which is of importance for owners of AMS herds.

### Conclusion

According to these preliminary results it is possible to use information on teat co-ordinates and fat and protein flow from milking robots in

the joint Nordic genetic evaluation of udder conformation and milking speed, respectively.

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