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







Outline

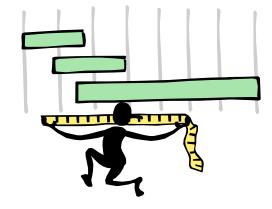
- Background and data collection
- Udder conformation
 - Teat co-ordinates
- Time usage
 - Fat and protein flow





Advantages of data from milking robots

- Repeated measurements of a variety of traits
- Objective measurements
- Measured on all cows in milk
- Measured over more lactations



Data is available – why not use them?



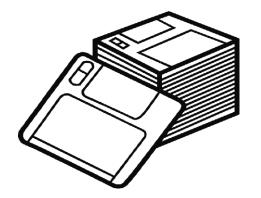
Data collection from AMS herds

- Collected by technicians in connection with milk recording
- Data are subsequently transferred to the national cattle database
- At present only data from Lely's milking robots
- Danish Cattle Federation collaborates with Lely in transferring data in real time – long-term strategy



How to handle repeated measurements

- Great many observations
- Average of the variable in question over a period of time



 Presumably more sophisticated methods to utilize the information to the full

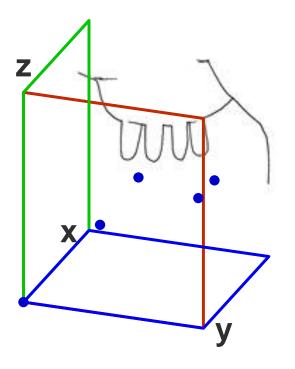


Udder conformation

- 130 000 Danish cows are classified per year
 - O The majority of the cows are 1st parity cows
- Wish for EBVs based on later parities
- Possibility to apply information on teat co-ordinates in the genetic evaluation?



Teat co-ordinates



- Front teat placement
- Rear teat placement
- O Distance, front rear
- Udder balance
- Udder depth



Data set and choice of model

- The udder conformation study is based on Holstein 1st parity data
 - 2 591 cows with AMS data
 - AMS data from February '11 to May '12
 - O Avg. of obs. 30-60 DIM
 - 102 816 classified cows
 - Year > 2006
 - 1490 cows having both

Model – udder conformation

Bi-variate linear animal model

$$AMS = HY + AGE + MO + a + e$$

Assessment =
$$HYS+AGE+MO+CLA+CA+a+e$$

Where

HY = herd*year, HYS = herd*6 month, AGE = age at calving, MO = calving month, CLA = classifier*2 month, CA = distance calving-assessment, a = additive genetic effect, and e = residual



Heritabilities and genetic correlations

| Trait | h ² (S.E.) - AMS | h² (S.E.) – CLA | r _g (S.E.) |
|------------------------|-----------------------------|-----------------|-----------------------|
| Front teat placement | 0.46 (0.06) | 0.31 (0.01) | 0.92 (0.04) |
| Rear teat placement | 0.38 (0.05) | 0.32 (0.01) | 0.94 (0.04) |
| Distance, front - rear | 0.46 (0.09) | - | - |
| Udder balance | 0.44 (0.07) | 0.22 (0.01) | 0.90 (0.04) |
| Udder depth | 0.65 (0.06) | 0.42 (0.01) | 0.94 (0.02) |

- High heritabilities
 - AMS> Classifiers assessments
- High genetic correlations



Partial conclusion – Udder conformation

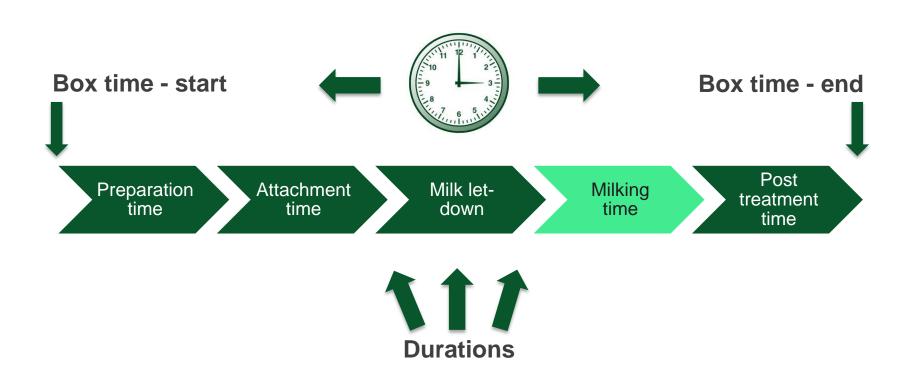
- Teat co-ordinates from robots will be included in the genetic evaluation in the future
- More reliable indices for later lactations
- More reliable indices for cows not classified
- Cheaper registrations

Fat and protein flow in kg per minute

- Fat and protein flow is already included in joint Nordic routine evaluation for milkability
 - Milkmeters (DK) or assessed by dairy farmers
- Data from milking robots are not yet included in the genetic evaluation
- Possibility to add information on fat and protein flow from milking robots in routine evaluation?

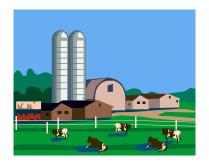


Time usage



Data set and choice of model

- The flow study is based on Holstein 1st parity data
- 4 050 cows with F+P flow from AMS
 - 900 with assessments
- 272 043 cows with F+P flow from milkmeters
 - 47 000 with assessments
- No cows with both types of F+P flow
- AMS data from May '05 to February '11



Calculated F+P flow AMS

- One observation per cow
 - First milk recording 30-240 DIM
- 14 days moving average of milk yield per milking calculated in the robot
- Fat and protein percentages from milk recording



14 days moving average of milking time

Model – Fat and protein flow

Tri-variate linear animal model

Where

HYS = herd*6 month, AGE = age at calving, MO = calving month, CM = distance calving-milkrecording, CA = distance calving-assessment, a = additive genetic effect, and e = residual

Genetic parameters for flow

- h² for flow from robots and milk recording are high
- h² for assessments and flow from milk recording are very close to previous estimates
- High genetic correlations between the traits
- Heritabilities and genetic correlations (S.E.)

| | h² | Assessments | Flow, milkmeter |
|-----------------------|-------------|-------------|-----------------|
| Flow (F+P), AMS | 0.63 (0.07) | 0.91 (0.05) | 0.94 (0.03) |
| Assessments | 0.20 (0.02) | - | 0.91 (0.02) |
| Flow (F+P), milkmeter | 0.41 (0.01) | - | - |



Partial conclusion - Flow

- It is possible to use flow from robots in the genetic evaluation
- Limited effect on the EBVs of the bulls
 - There are already many observations from electronic milkmeters
- Cows from AMS herds will be genetically evaluated



Conclusions

- According to the preliminary results it is possible to use:
 - Teat co-ordinates in the genetic evaluation of udder conformation
 - Fat and protein flow from milking robots in the genetic evaluation of milking speed