Genetic evaluation of in-line recorded milkability from milking parlor and automatic milking systems

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Background

❑ Measures the cows' ability to let down milk and to be completely milked

❑ Selection against slow milking cows
- Save time
- Efficient use of equipment

❑ Genetic evaluation based on subjective scoring

❑ Objective observations from AMS
- high heritabilites and repeatabilites for average flow rate (AFR) and box time (BT)

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Objectives

❑ Could data from AMS and CMP be jointly used for genetic evaluation?

   - Estimate genetic correlations between
      - milking systems

      - lactations
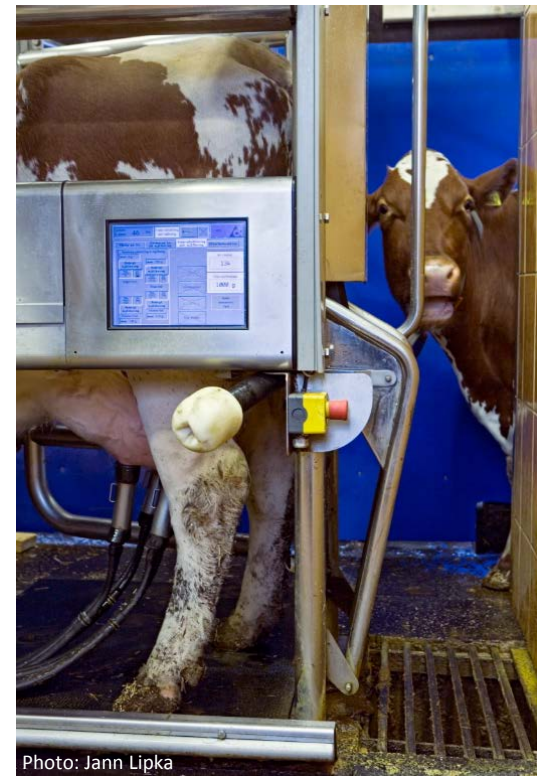   - traits

❑ Compare models for analyzing data

Photo: Jann Lipka

Data

- ❑ 72 herds with CPM
  - 19 000 cows, 704 000 observations
  - Year 2007-2011
  - 2 days/month
  - Milking time (MT), milk yield (MY)

- ❑ 19 herds with AMS (DeLaval)
  - 3 800 cows, 2 220 000 observations
  - Year 2004-2009
  - each milking
  - AFR, BT, MY
  - Per udder quarter

- ❑ Lactation number 1-3

- ❑ Swedish Holstein (SH) and Swedish Red (SR)

❑ Genetic correlations in CMP- and AMS-data between:
- lactations
- traits

Model included effects of:
- herd-year-season, lactation month, milk yield
- permanent environment (pe), additve genetic (a), residual (e)

We found:

	Lact 1 – Lact 2+3
AMS	0.93-0.99
CMP	0.97-0.98

❑ Genetic correlations in CMP- and AMS-data between:
- lactations
- traits

Model included effects of:
- herd-year-season, lactation month, milk yield
- permanent environment (pe), additve genetic (a),
residual (e)

We found:

	Lact 1 – Lact 2+3	AFR – MT(BT)	MT - BT
AMS	0.93-0.99	-0.93- -1.00	0.93-1.00
CMP	0.97-0.98	-0.94 - -0.99	-

❑ Genetic correlations between CMP- and AMS-data

Model included effects of:
- herd-year-season, lactation month, lactation no, milk yield
- pe, a, e

We found:

Trait in AMS	Trait in CMP	SH	SR
AFR	AFR	0.97	0.98
MT	MT	0.98	1.00
BT	AFR	-0.98	-0.94
BT	MT	0.99	0.93
AFR	MT	-0.96	-0.99
MT	AFR	-1.00	-0.95

❏ Genetic parameters in joint CMP- and AMS-data

Repeatability model included effects of:
- herd-year-season, lactation month, lactation no,
  system, milk yield(system)
- pe,a, e

Random regression models included the same effects
+ 1-4 order of Legendre polynomials of DIM for a and pe

We found:

	AFR			MT		
	σ^2_a	h^2	Rep.	σ^2_a	h^2	Rep.
SH	0.19	**0.49**	0.83	0.93	**0.38**	0.71
SR	0.11	**0.44**	0.77	0.69	**0.41**	0.77

Conclusions

❑ High genetic correlations between AMS and CMP
  → potential for joint use of data

❑ High genetic correlations between lactations, and high repeatabilites within lactation
  → enough to include a few records from 1st lactation

❑ High genetic correlations between traits
  → enough to include either AFR or MT(BT)

Thank you for your attention!