Genotype by environment interaction for activity-based estrus traits in Danish Holstein

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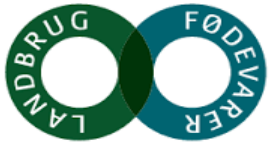
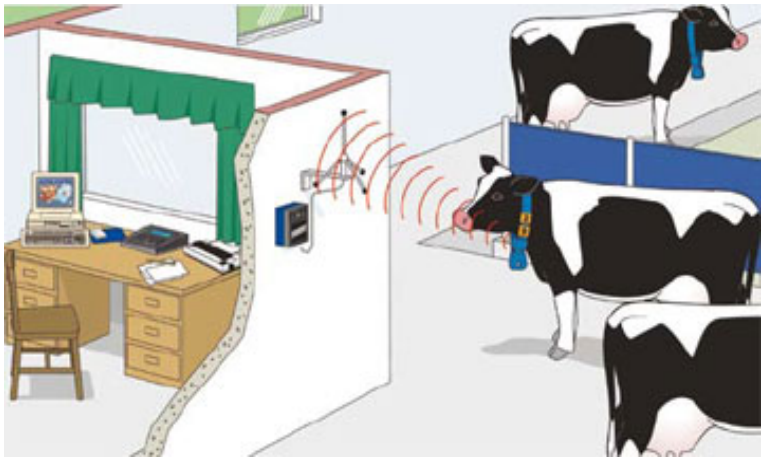


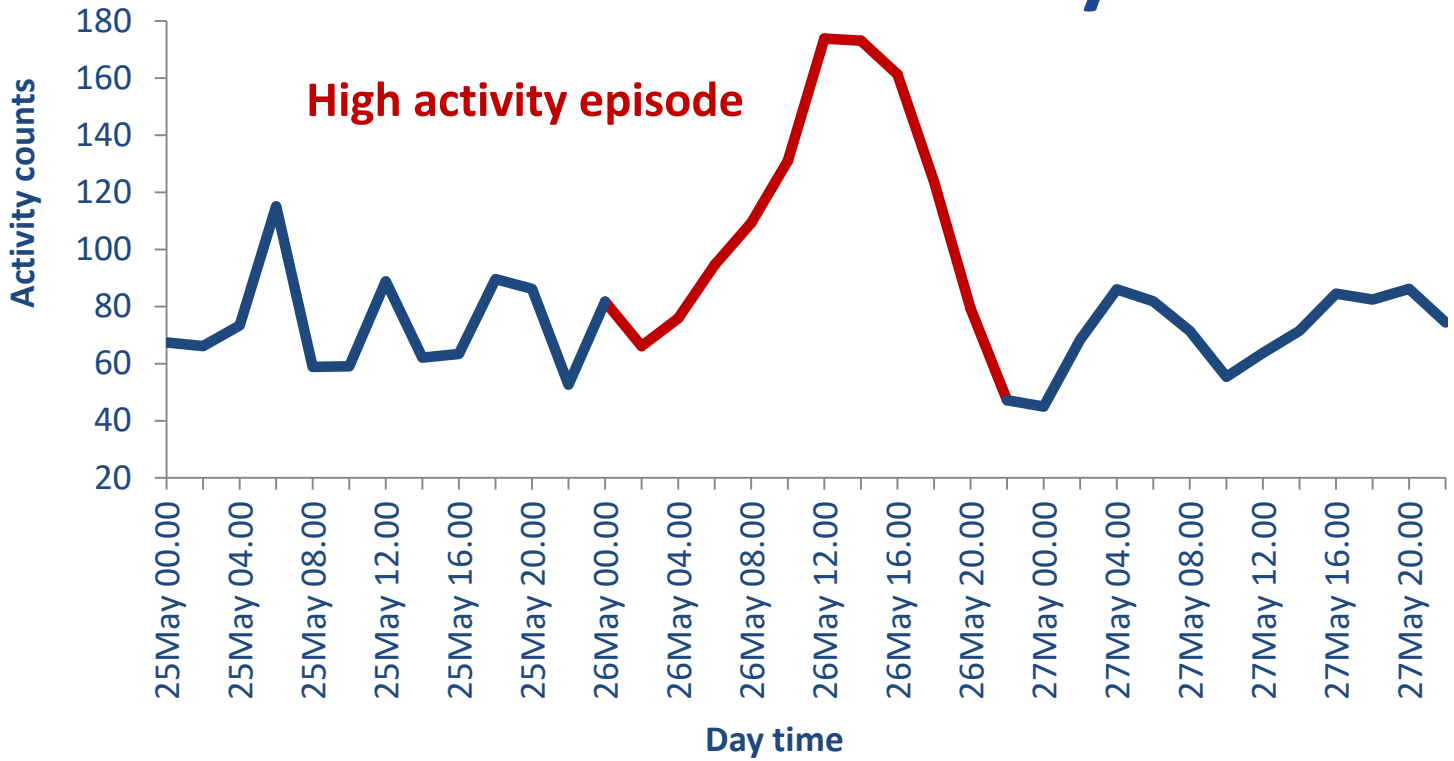
SEGES

Activity-based estrus traits



- Using activity monitor devices (pedometer/ activity tags) that use the behavioral changes to detect estrus in dairy cows.

The raw activity profile one day before and after the estrus day



Interval from calving to first high activity (CFHA)

- Reflects the ability of cow to return to cyclic after calving.
- Less biased compared to the Interval from calving to first insemination (CFI). (h^2= 0.16 vs 0.07) ☺
- Highly correlated with CFI (r_g=0.96).

Duration of high activity (DHA)

- The interval in hours between the episode started until the episode ended (h^2= 0.02).

Strength of high activity (SHA)

- The average of the highest 2 activity values (h^2= 0.05)

(Løvendahl and Chagunda. 2009; Ismael et al., 2015)

Genotype by environment interaction in dairy cattle

- Few studies on fertility (Scaling effect).
- Traits are based on (AI) data (Farmer decisions ☹).
- The relationship between fertility and milk traits using measure that is free from human bias ☺.
- The change of genetic correlation between milk and fertility as a function of herd production level .

Objectives

- To estimate genetic parameters of fertility traits derived from activity tags as a function of production level to define the G×E effect.
- To estimate the genetic correlation between CFHA and the energy corrected milk as a function of production level.

Data

- **Estrus traits for 11,522 first parity cows housed in 125 herds.**
- **Test-day records from 1st to 3rd lactation.**
  - **Test days close to dim 70 ± 15 days were selected, because it is close to the peak milk yield.**
  - **Herd solutions of ECM70 used as an environmental descriptor in random regression model (RRM).**
- **ECM70 records for 10,009 first parity cows.**

Analysis

- Fixed effects model to obtain herd solutions for ECM70 to be used as an environmental descriptor.

$$y_{ijk} = \mu + h_i + p_j + ymc_k + e_{ijk}$$

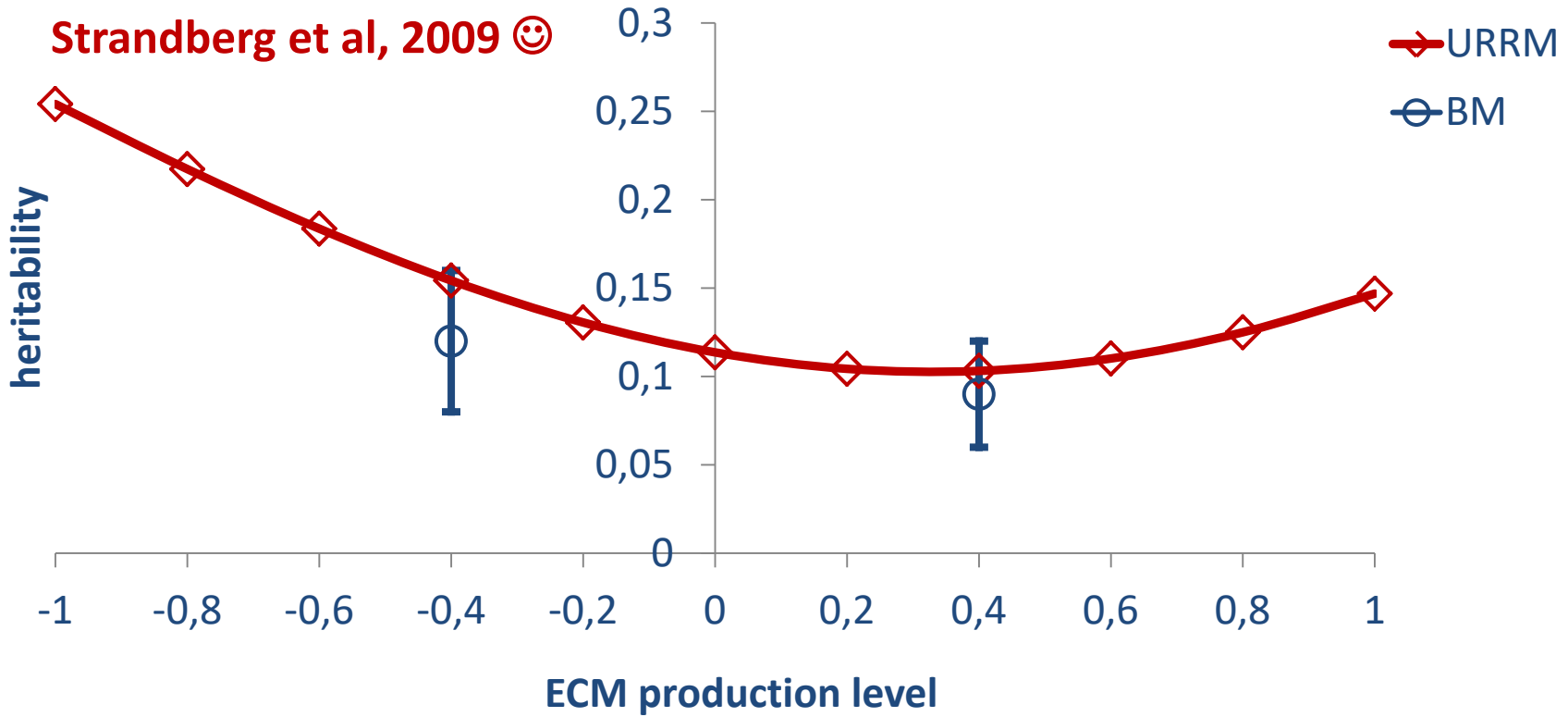
- Herd solutions were standardized from -1 to +1.
- Univariate RRM to estimate the variance components, for each trait. Bivariate RRM analysis to estimate genetic correlations between the CFHA and ECM70.

$$y_{ijk} = \mu + h_i + b(AGE) + ym_j + a_{0k} + a_{1k}PL + e_{ijk}$$

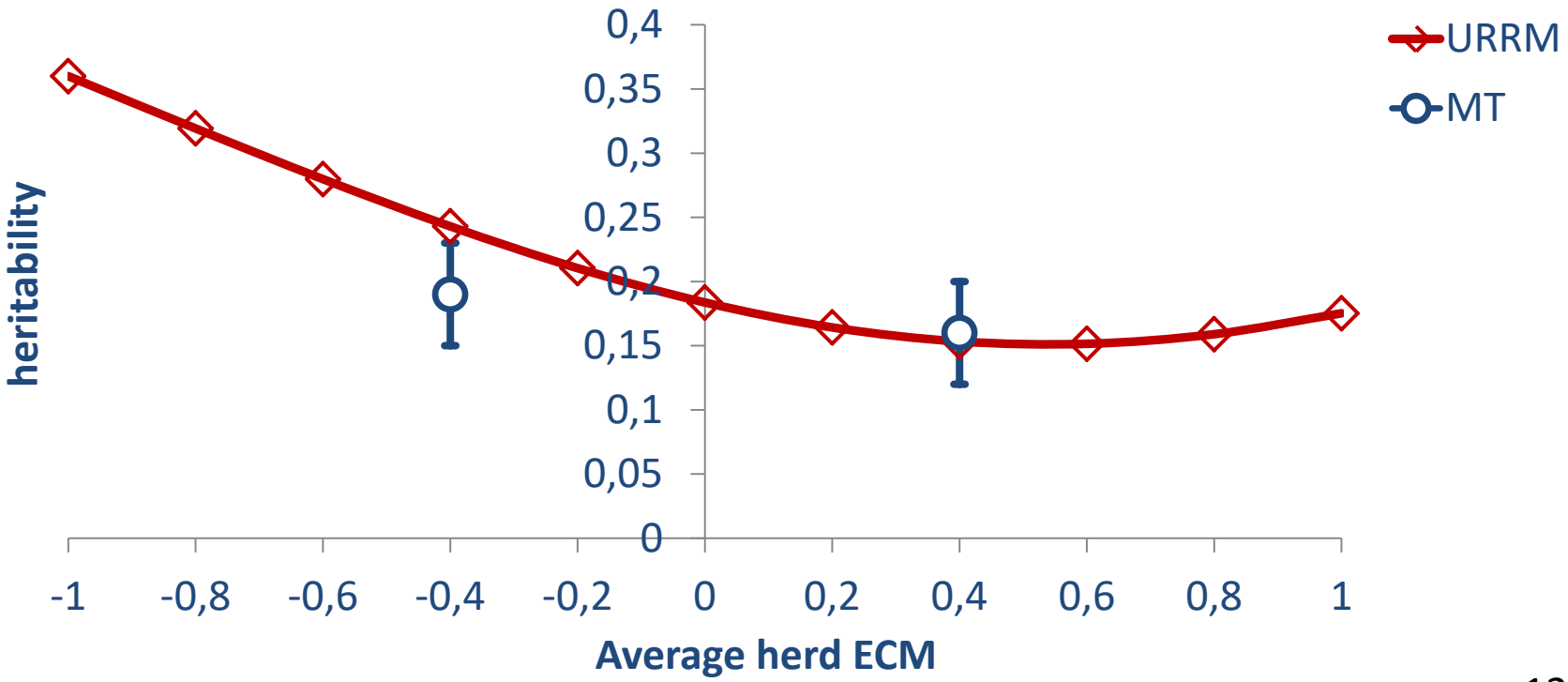
- Fixed effects of Herd, age at first calving (Fixed regression), and year month of episode
- Additive genetic effect or level (Random)
- Additive linear effect of PL or slope (Random)
- Residual (Random)

For validation of the RRM, a bivariate model (BM) where the production environment was categorized into low or high (the lowest and highest third of production environment) where the trait values were considered as 2 separate traits

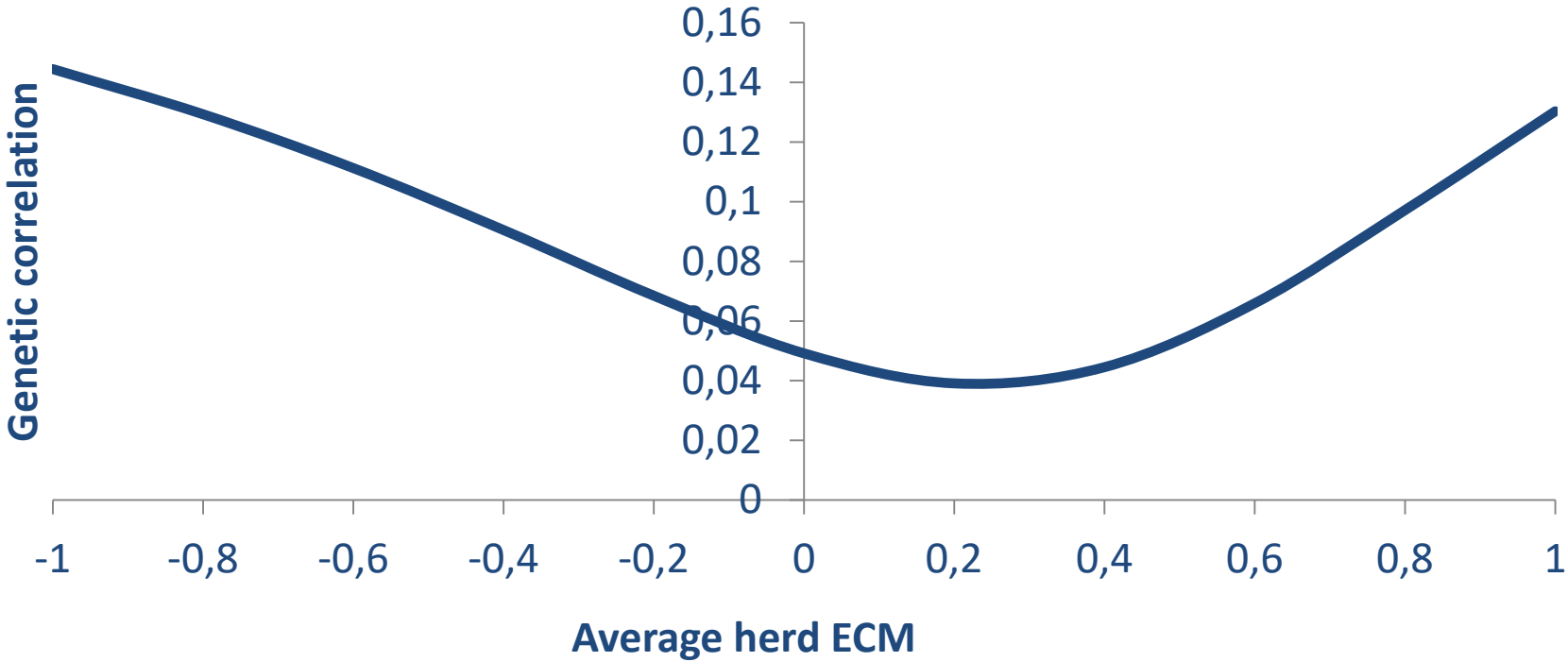
Heritability of CFHA



Heritability of ECM70



Genetic correlation between CFHA and ECM70



Genetic correlations from RRM and BM

Traits	r_g BM	r_g RMM
CFHA	0.90 (0.16)	0.74
DHA	0.84 (0.46)	1.00*
SHA	0.08 (0.34)	0.22
ECM70	1.00 (0.09)	0.80
CFHA and ECM70 (Low)	0.29 (0.20)	0.09
CFHA and ECM70 (high)	-0.13 (0.23)	0.04

Conclusions

- **No significant G×E found for ECM70, CFHA, and DHA regarding to production environment.**

- **The unfavorable relationship between milk and fertility decreased by improving the production level. More data required for further validation especially for the BRRM.**