

Genetic parameters for a multiple-trait linear model conception rate evaluation

*K. Muuttoranta¹, A-M. Tyrisevä¹, E.A. Mäntysaari¹,
J.Pösö², G.P. Aamand³, J-Å. Eriksson⁴,
U.S. Nielsen⁵ and M. H. Lidauer¹*

¹ Natural Resources Institute Finland,

² Faba Co-op, ³ Nordic Cattle Genetic Evaluation,

⁴ Växa Sweden, ⁵ SEGES Cattle

STØTTET AF

mælkeafgiftsfonden



Background



Nordic Cattle Genetic Evaluation (DK, SWE, FIN)

First common fertility evaluation
for Nordic dairy cattle (2005)

Updated fertility model (2015)

sire model



animal model

repeatability
model



multivariate
multilactation model

Objectives of the study



Non-return rate → conception rate in the evaluation

Model for variance component estimation needed

Variance components for conception rate

Obstacles of the study



11 complex traits in the same analysis

Modeling conception rate in a multiple trait context

- repeated observations

Sampled data for analyses

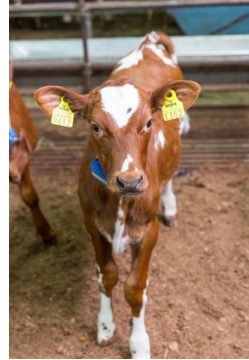


Photo: Erkki Oksanen/Luke

From Swedish Red dairy cattle heifers and cows

400 herds with min. 8 first-calvers annually

101 315 females with records

10 397 sires with daughters

Traits



- 1. Conception rate [0 or 1] outcome of each AI**
CR0, CR1, CR2, CR3
(heifers, 1st, 2nd and 3rd parity)
- 2. Interval from the first to the last service [days]**
IFL0, IFL1, IFL2, IFL3
- 3. Interval from calving to the first service [days]**
ICF1, ICF2, ICF3

Model

Multivariate multilactation sire model

- 11 traits: heifers + cows (1. – 3. parities)
- CR as repeated observations within parities, permanent environment as random effect

Model

Fixed effects:

- herd*birth year (heifers) or herd*calving year (cows)
- year-month effect:
 - year month of insemination for CR
 - year-month of 1st insemination for IFL
 - year-month of calving for ICF
- heifers' first insemination age
- i^{th} insemination for CR

Model

Fixed effects:

- herd*birth year (heifers) or herd*calving year (cows)
- year-month effect:
 - year month of insemination for CR
 - year-month of 1st insemination for IFL
 - year-month of calving for ICF
- heifers' first insemination age
- **i^{th} insemination for CR**

Model

Random effects:

- sire
- permanent environment (for all 11 traits)
- residual,
where residual variances for interval traits were fixed to 2% of the phenotypic variance during REML estimation

Validating "ith insemination" effect by simulation

Data structure in CR

cow	i th AI	CR
100	1	0
100	2	0
100	3	0
100	4	0
100	5	0
100	6	0
100	7	1

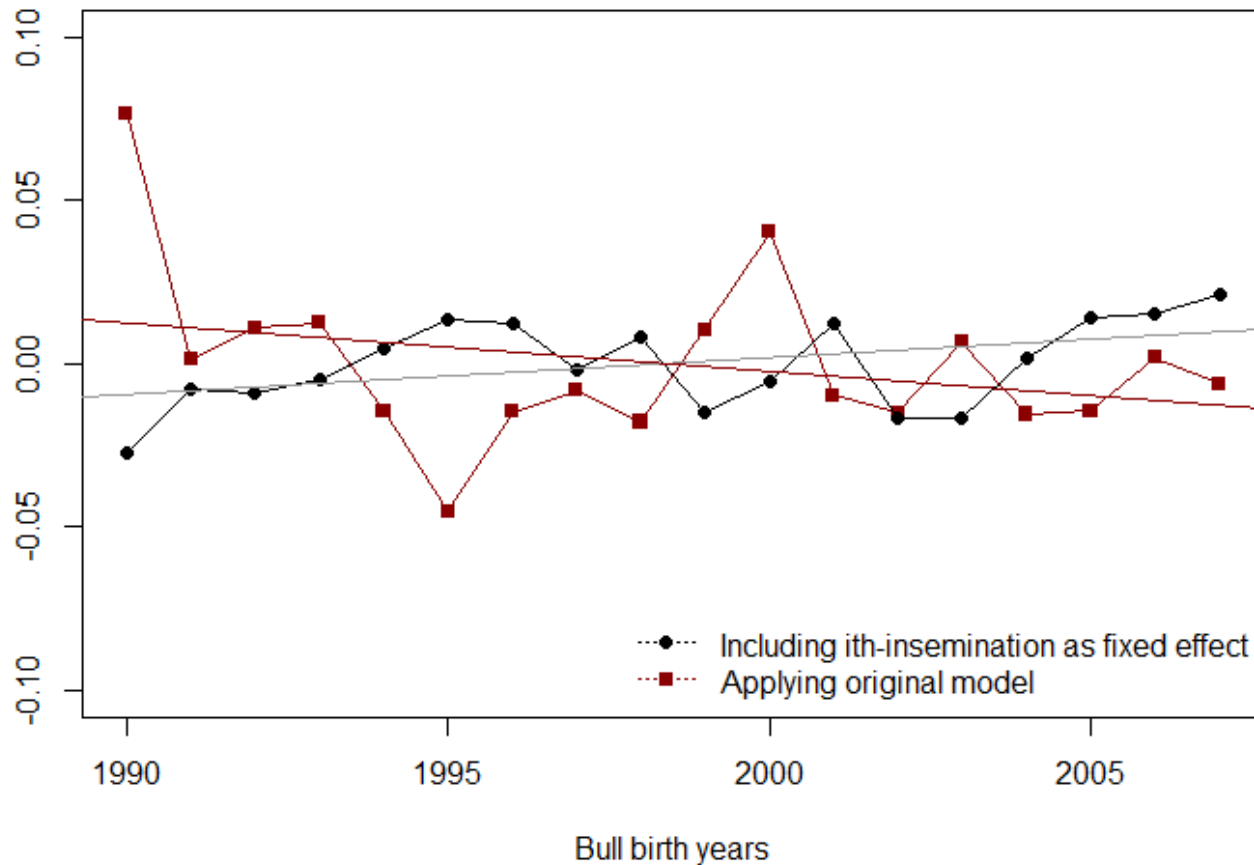
cow	i th AI	CR
101	1	1

cow	i th AI	CR
102	1	0
102	2	1

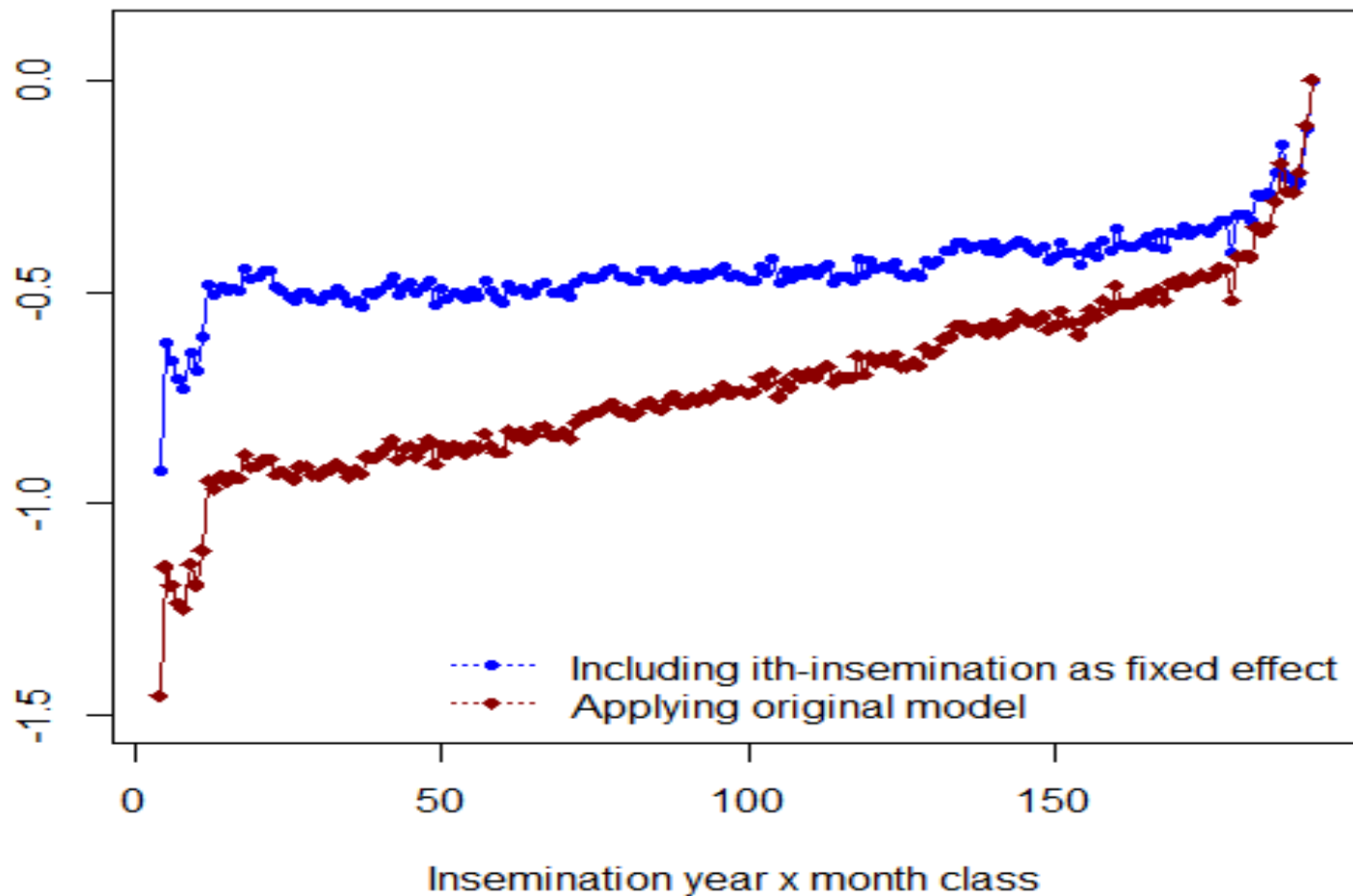
Simulation of conception rate data

- True breeding values & observations simulated for cows with real pedigree
- Based on single trait animal model ($h^2=0.1$)
- CR observations simulated for observed scale
 - probability of success $p=0.6$
 - repeated observations until success (max. 10 observations per cow)
- Herd x year and insemination year x month effects simulated to be 0.0
- 5 data replicates

Based on simulation study: genetic trends biased if i^{th} insemination effect excluded



Based on simulation study: environmental trends biased if i^{th} insemination effect excluded



Analyses

- MC-EM REML applied of variance component estimation using the **MiX99** software package

Solving Large Mixed Model Equations

VCE results



Heritabilities

	Conception rate	Interval from first to last AI	Interval from calving to first AI
Heifers	.017	.020	-
1 st parity cows	.017	.024	.049
2 nd parity cows	.021	.037	.025
3 rd parity cows	.024	.041	.032

Genetic and phenotypic correlations within traits:

CR



	CR0	CR1	CR2	CR3
CR0		.65	.43	.69
CR1	.03		.90	.95
CR2	.03	.05		.92
CR3	.02	.05	.06	

CR are binomial observations with a variance structure depending on the number of repeated trials service period.

Genetic and phenotypic correlations within traits:

ICF



	ICF1	ICF2	ICF3
ICF1		.85	.88
ICF2	.10		.88
ICF3	.08	.11	

Conclusions

- Inclusion of i^{th} insemination is crucial, otherwise
 - h^2 values and genetic correlations inflated
 - trends biased
- Expectation of successful AI affected by the number of previous, unsuccessful AI
- Multiple trait analysis for low-heritable traits was possible



Kaarina Matilainen: "Single-step genomic evaluation for fertility in Nordic Red Dairy Cattle" EAAP 2016, 31th Aug

Thank you!