Threshold and linear model estimates of genetic and residual correlations between CM, SCC and production traits

CG2 Session 5

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Udder health

- Clinical mastitis
  - frequent and expensive disease
- Finland
  - Primary reason – culling
  - 21% - of all culled in 2003

Genetic evaluation

- MT evaluation - Accurate VC estimates essential
- Binary nature of CM
  - not taken into account
- Linear model
  - most estimates
- Threshold model - Theoretically appropriate
- Literature – r_g linear model involving binary trait
  - Underestimation reported
- Finland – New GE model for CM
  - VC estimates from suitable methodologies

Objective

- Estimate genetic and residual correlations between CM, SCC and production traits using threshold and linear model

Traits

- **SCC** – Lactation mean of log transformed ($\log_e$scc) test-day somatic cell count (1000cells/ml)
- **CM (0 / 1)** - Vet. records/culling due to udder diseases (7 days before and 150 days after calving)
- **305-d prod. traits** - milk, protein and fat yield

Data

- Finnish National health + prod.
- 119,000 1st lact. Ayrshire cows
- First crop daughters
- Sires - at least 20 daughters
  - In total 1269 sires

Model

1. Linear model

- Linear model used for CM, SCC, prod. traits
- CM considered as a continuous trait
- VC estimated using AI-REML procedure
  - DMU package (Madsen and Jensen, 2002)

Model

2. Threshold model

- CM - binary (threshold) & SCC, prod. traits - Gaussian
- A threshold-liability model (Gianola, 1982) – CM
- Multivariate Bayesian approach
  - (Korsgaard, et al. 2003)
- MCMC computations
  - Chain of 50,000 iterations, after burn-in of 5000
  - All post burn-in samples - inference posterior features

General model

$$\begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} X_{h1} & 0 \\ 0 & X_{h2} \end{bmatrix} \begin{bmatrix} hy_1 \\ hy_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} s_1 \\ s_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where

y is vector of observable continuous trait (SCC and production traits) and unobserved liabilities to CM

ß is vector of systematic effects

hy is vector of herd-3-year of calving effects

s is vector of sire genetic effects

e is vector of residual effects and

X, X_h and Z are corresponding incidence matrices

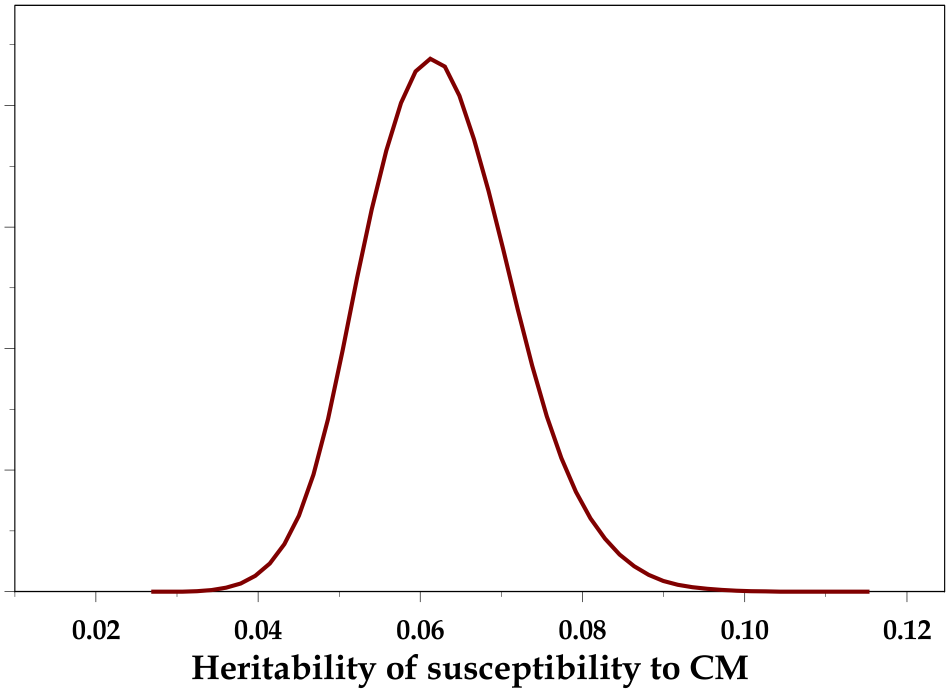
RESULTS

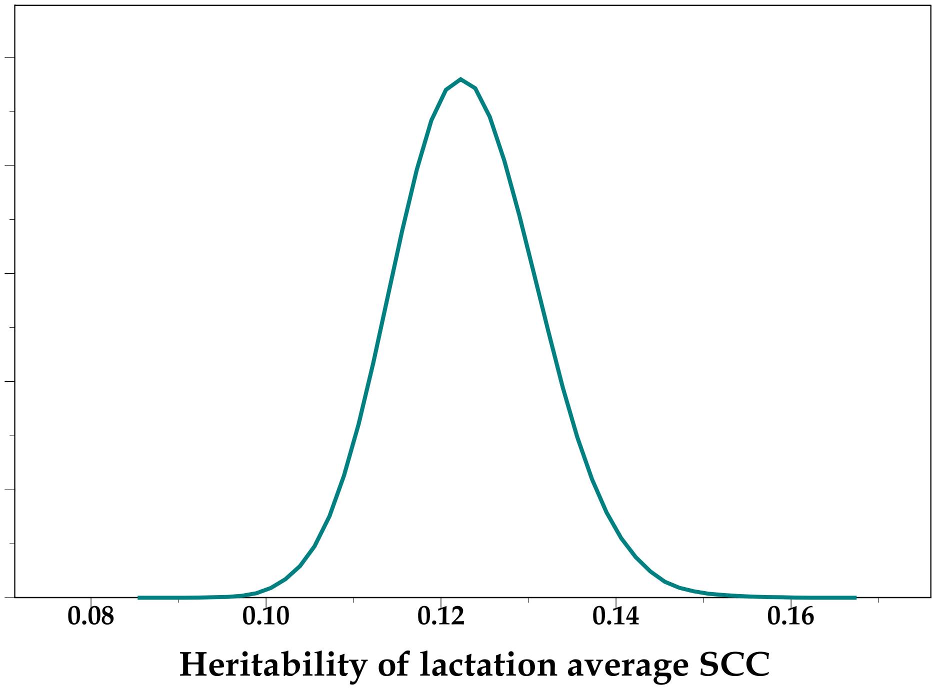
CM and SCC

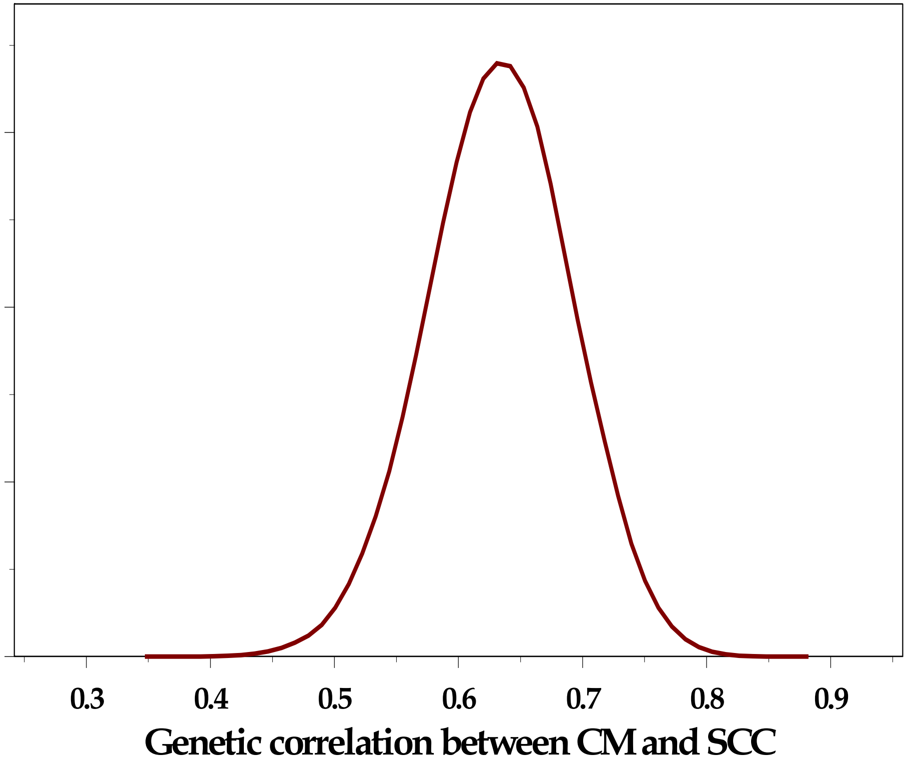
Estimates of parameters from bivariate analysis of CM and SCC

Methods		CM	SCC
Linear	CM	0.020	0.628
	SCC	0.060	0.123
Threshold	CM	0.061	0.634
	SCC	0.109	0.123

Heritabilities; on the diagonal, Genetic correlation; upper diagonal, Residual correlations; lower diagonal


0.02
0.04
0.06
0.08
0.10
0.12
Heritability of susceptibility to CM


0.08
0.10
0.12
0.14
0.16
Heritability of lactation average SCC


0.3
0.4
0.5
0.6
0.7
0.8
0.9
Genetic correlation between CM and SCC

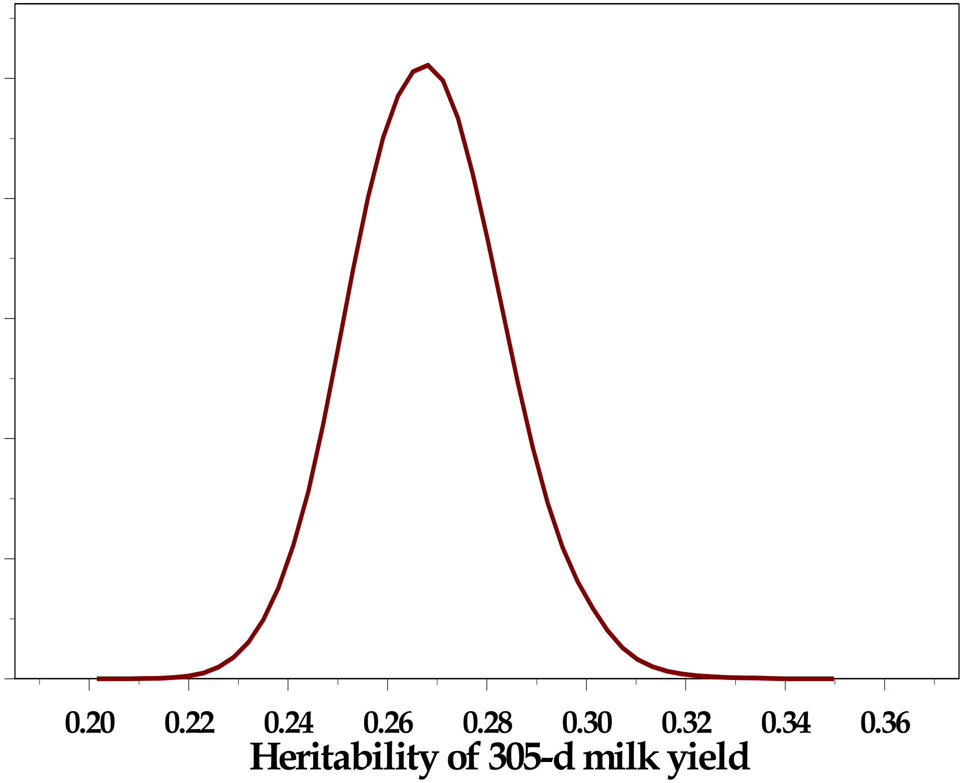
RESULTS

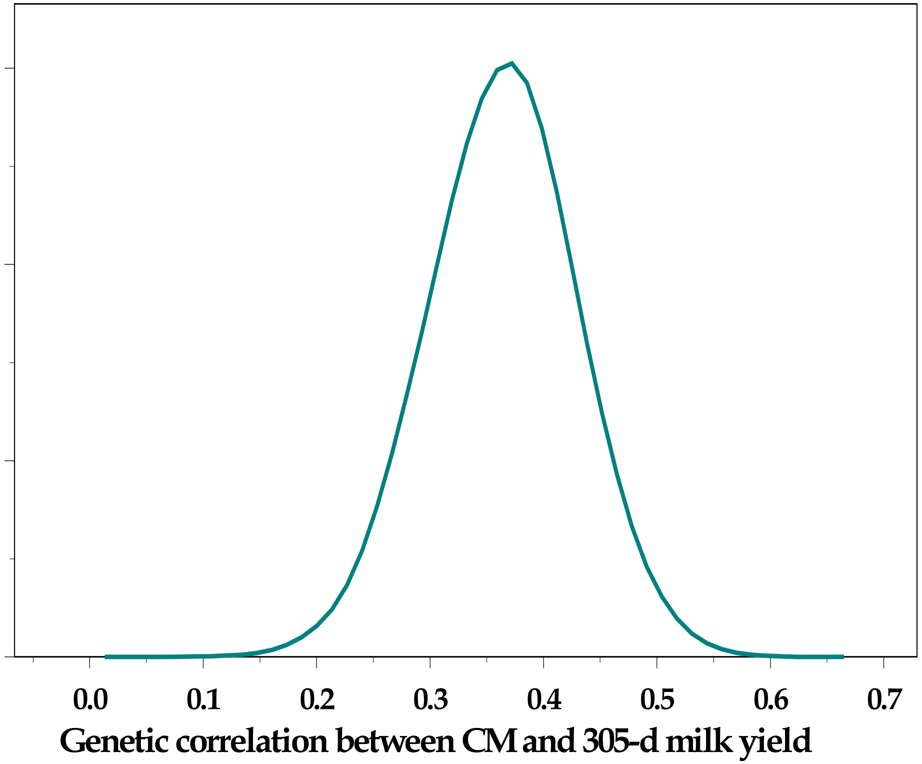
CM and 305-d milk yield

Estimates of parameters from bivariate analysis of CM and 305-d milk yield

Methods		CM	305-d MY
Linear	CM	0.020	0.346
	305-d MY	-0.021	0.268
Threshold	CM	0.061	0.363
	305-d MY	-0.037	0.268

Heritabilities; on diagonal, Genetic correlation; upper diagonal, Residual correlations; lower diagonal


0.20
0.22
0.24
0.26
0.28
0.30
0.32
0.34
0.36
Heritability of 305-d milk yield


0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Genetic correlation between CM and 305-d milk yield

Heritability of CM and continuous traits from linear and threshold models

Traits	Methods	
	Linear-Linear	Threshold-Linear
CM	0.020	0.062
SCC	0.123	0.123
Milk	0.268	0.267
Protein	0.222	0.222
Fat	0.227	0.227

Genetic correlation between CM, SCC and 305-d production traits

	Methods	
Traits	Linear-Linear	Threshold-Linear
CM – SCC	0.628	0.634
CM – Milk	0.361	0.362
CM – Protein	0.316	0.318
CM – Fat	0.294	0.302

Residual correlations between CM, SCC and 305-d production traits

	Methods	
Traits	Linear-Linear	Threshold-Linear
CM – SCC	0.060	0.109
CM – Milk	-0.021	-0.037
CM – Protein	-0.015	-0.027
CM – Fat	-0.025	-0.045

Conclusions

- NO significant difference in genetic correlation estimates from the two models
- Lower estimates of residual correlation from the linear model
- The low correlation estimate may indicate the need for alternative definition of CM trait