Session CG.2.7.
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Genetic correlations between clinical mastitis, milk fever, ketosis, and retained placenta within and between the first three lactations of Norwegian Red (NRF)

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Introduction

- Clinical mastitis (**CM**), milk fever (**MF**), ketosis (**KET**), and retained placenta (**RP**) are among the most frequent diseases affecting dairy cattle
- Of all veterinary treatments in dairy cows (Norway 2003): **44% CM**, **9% MF**, **9% KET**, and **5 % RP**
- Several studies have reported heritability estimates but very few studies of the *genetic associations* between these diseases

Objective

- Infer heritability and genetic correlations between CM, MF, KET, and RP within and between the first three lactations of Norwegian Red (NRF)

Data

- Daughters of 2411 NRF sires
  - Progeny-tested 1978-1998
  - First-crop daughters only
- First calving in herd-5-year classes with at least 10 first-lactation cows
- Records of 372,227 cows
  - of which 247,692 had a 2nd lactation, and 147,051 had a 3rd lactation

Data

- For each cow, all cases of veterinary treated CM, MF, KET, and RP in the first three lactations were included.
- Within each lactation, absence or presence of each of the four diseases was scored as “0” or “1”, respectively, based on whether or not the cow had at least one veterinary treatment recorded in the interval:

  -15 to 120 d for CM and KET

  -15 to 30 d for MF

  0 to 5 d for RP

Table 1. Mean frequency of clinical mastitis (CM), milk fever (MF), ketosis (KET) and retained placenta (RP), by lactation.

	1st lactation	2nd lactation	3rd lactation
No of cows	372,227	247,692	147,051
Mean CM frequency[1], %	15.8	19.8	24.2
Mean MF frequency, %	0.1	1.9	7.9
Mean KET frequency, %	7.5	13.0	17.2
Mean RP frequency, %	2.6	3.4	4.3

Methods

- Bayesian approach using MCMC methods
- A 12-variate (3 lactations×4 diseases) threshold liability model assuming that each disease was a different trait in each lactation
- Same model as used in Heringstad et al., 2004. J. Dairy Sci. 87:3038-3046

Model

$$\boldsymbol{\lambda} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_{\mathbf{h}}\mathbf{h} + \mathbf{Z}_{\mathbf{s}}\mathbf{s} + \mathbf{e}$$

where

λ : a vector of the unobserved liabilities;

β : a vector of systematic effects (season×yr of calving and age at calving (1st lact.), mo×yr of calving and calving interval (2nd and 3rd lact));

h : a vector of herd-5-year effects;

s : a vector of sire transmitting abilities;

e : the vector of residual effects; and

$\mathbf{X}$, $\mathbf{Z}_{\mathbf{h}}$, and $\mathbf{Z}_{\mathbf{s}}$: the corresponding incidence matrices

- Residuals were correlated within lactation and independent between lactations: $\mathbf{e} \sim N(\mathbf{0}, \mathbf{R_0} \otimes \mathbf{I})$

$$\mathbf{R_0} = \begin{bmatrix} 1 & r_{1,2} & r_{1,3} & r_{1,4} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & 1 & r_{2,3} & r_{2,4} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & 1 & r_{3,4} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & & 1 & r_{5,6} & r_{5,7} & r_{5,8} & 0 & 0 & 0 & 0 \\ & & & & & 1 & r_{6,7} & r_{6,8} & 0 & 0 & 0 & 0 \\ & & & & & & 1 & r_{7,8} & 0 & 0 & 0 & 0 \\ & & & & & & & 1 & 0 & 0 & 0 & 0 \\ & & & & & & & & 1 & r_{9,10} & r_{9,11} & r_{9,12} \\ & & & & & & & & & 1 & r_{10,11} & r_{10,12} \\ & & & & & & & & & & 1 & r_{11,12} \\ & & & & & & & & & & & 1 \end{bmatrix}$$

Priors

- Independent proper uniform priors assigned to each element of $\boldsymbol{\beta}$
- Multivariate normal priors assigned to effects of herd-5-year and sire transmitting abilities:

$$\mathbf{h} \sim N(\mathbf{0}, \mathbf{H}_0 \otimes \mathbf{I}) \qquad \mathbf{s} \sim N(\mathbf{0}, \mathbf{G}_0 \otimes \mathbf{A})$$

- Inverse Wishart prior distributions used for the 12×12 (co)variance matrices of herd-5-year ($\mathbf{H}_0$) and sire effects ($\mathbf{G}_0$)
- Bounded uniform priors assigned to non-zero residual correlations

Results

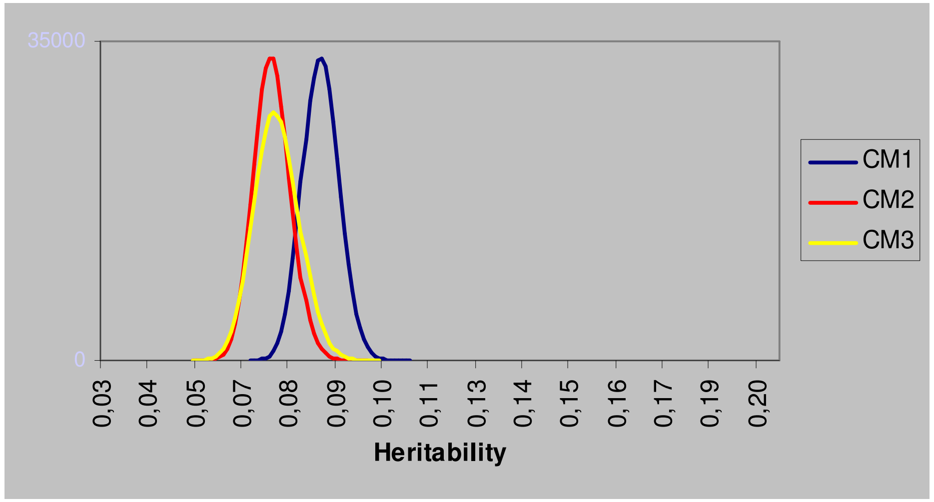
Heritability

- Posterior means:
  - CM: 0.07 - 0.08
  - MF: 0.09 - 0.13
  - KET: 0.14 - 0.16
  - RP: 0.08

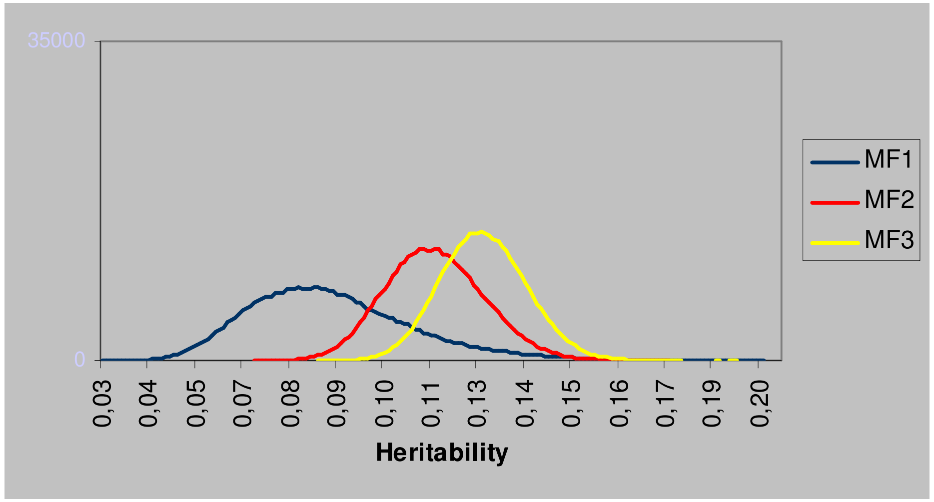
- Posterior SD: 0.005 – 0.021

Posterior distributions of heritability of liability to

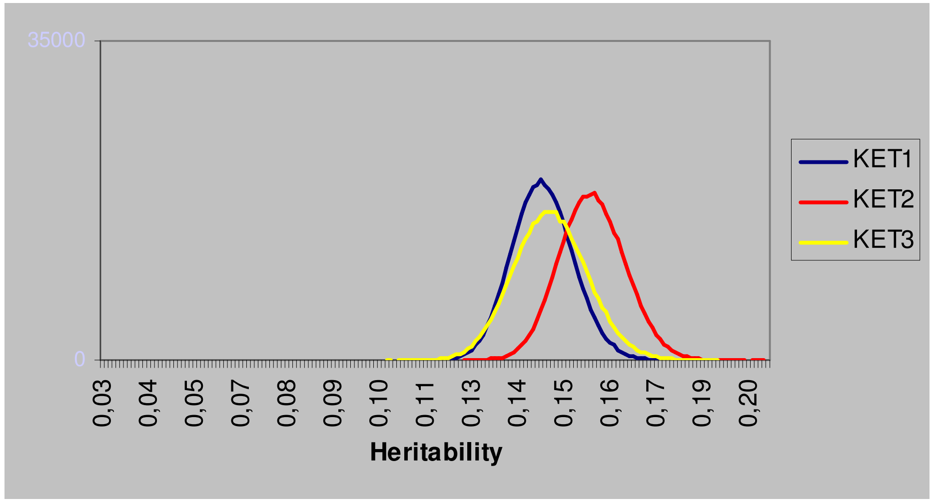
Clinical mastitis



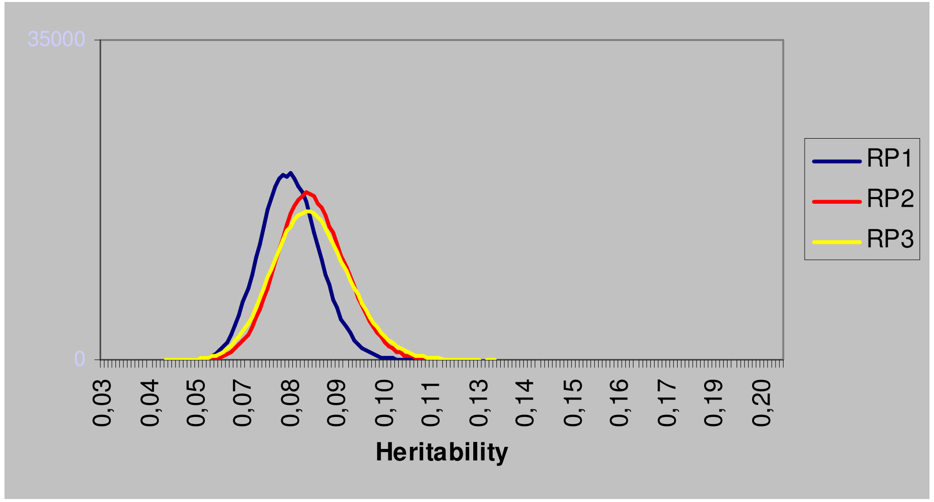
Milk fever



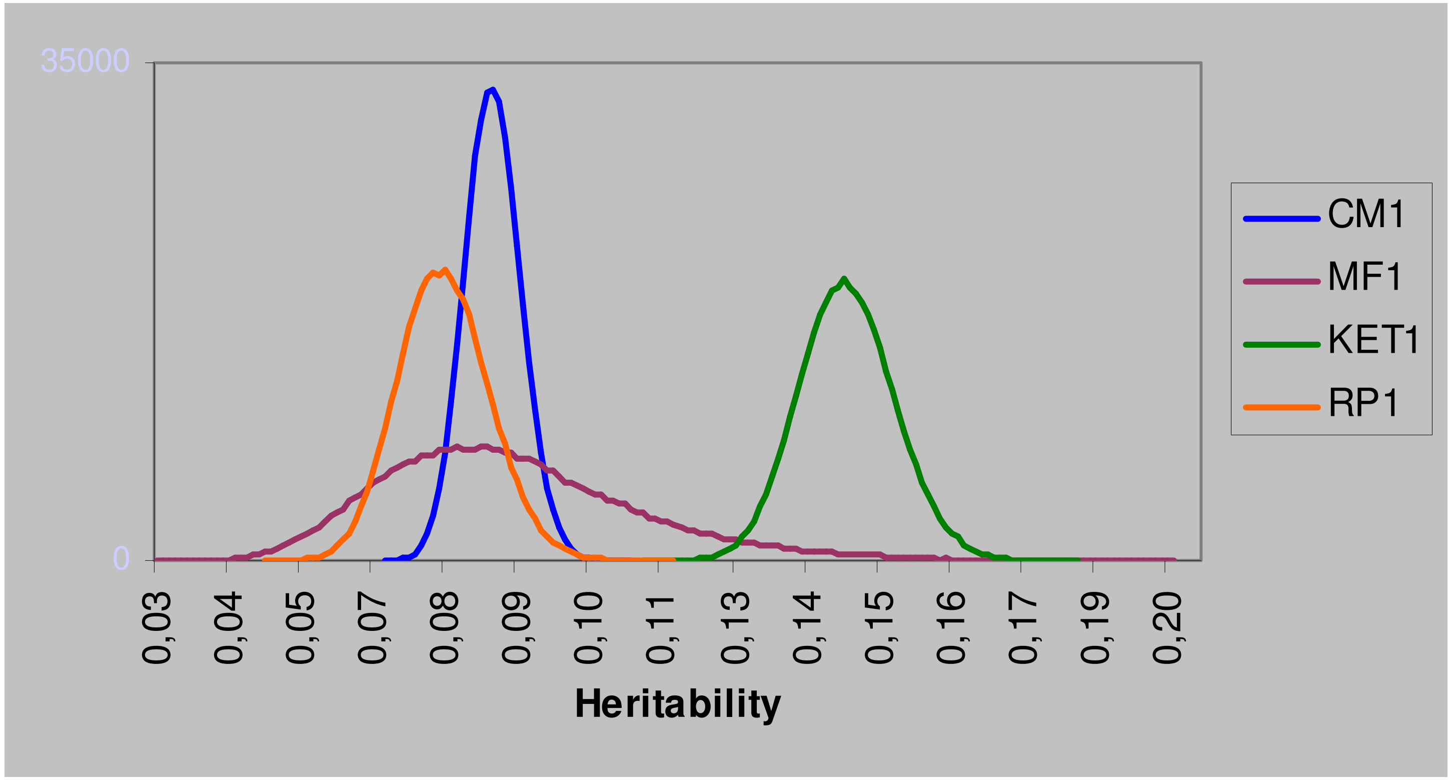
Ketosis



Retained placenta



Posterior distributions of heritability of liability to clinical mastitis (**CM**), milk fever (**MF**), ketosis (**KET**), and retained placenta (**RP**) in first lactation



Genetic correlations

Table 2. Posterior means of genetic correlations between liability to clinical mastitis (CM*i*), milk fever (MF*i*), ketosis (KET*i*), and retained placenta (RP*i*) in the first three lactations (*i*=1, 2, 3)

	MF1	KET1	RP1	CM2	MF2	KET2	RP2	CM3	MF3	KET3	RP3
CM1	.12	.26	.16	**.73**	.17	.20	.16	**.67**	.16	.16	.05
MF1		.19	-.04	.13	**.29**	.22	-.09	.14	**.19**	.22	-.10
KET1			.07	.17	.40	**.83**	.07	.25	.32	**.77**	.03
RP1				.19	.14	.04	**.55**	.19	.17	.04	**.59**
CM2					.18	.11	.22	**.73**	.16	.08	.10
MF2						.35	.16	.22	**.71**	.33	.15
KET2							.00	.19	.23	**.86**	-.03
RP2								.22	.21	-.02	**.65**
CM3									.22	.16	.11
MF3										.24	.18
KET3											-.05

Bold blue indicate genetic correlations between the same disease in different lactations

Italic indicate that |posterior mean| - 2SD < 0

Genetic correlations within disease between lactations

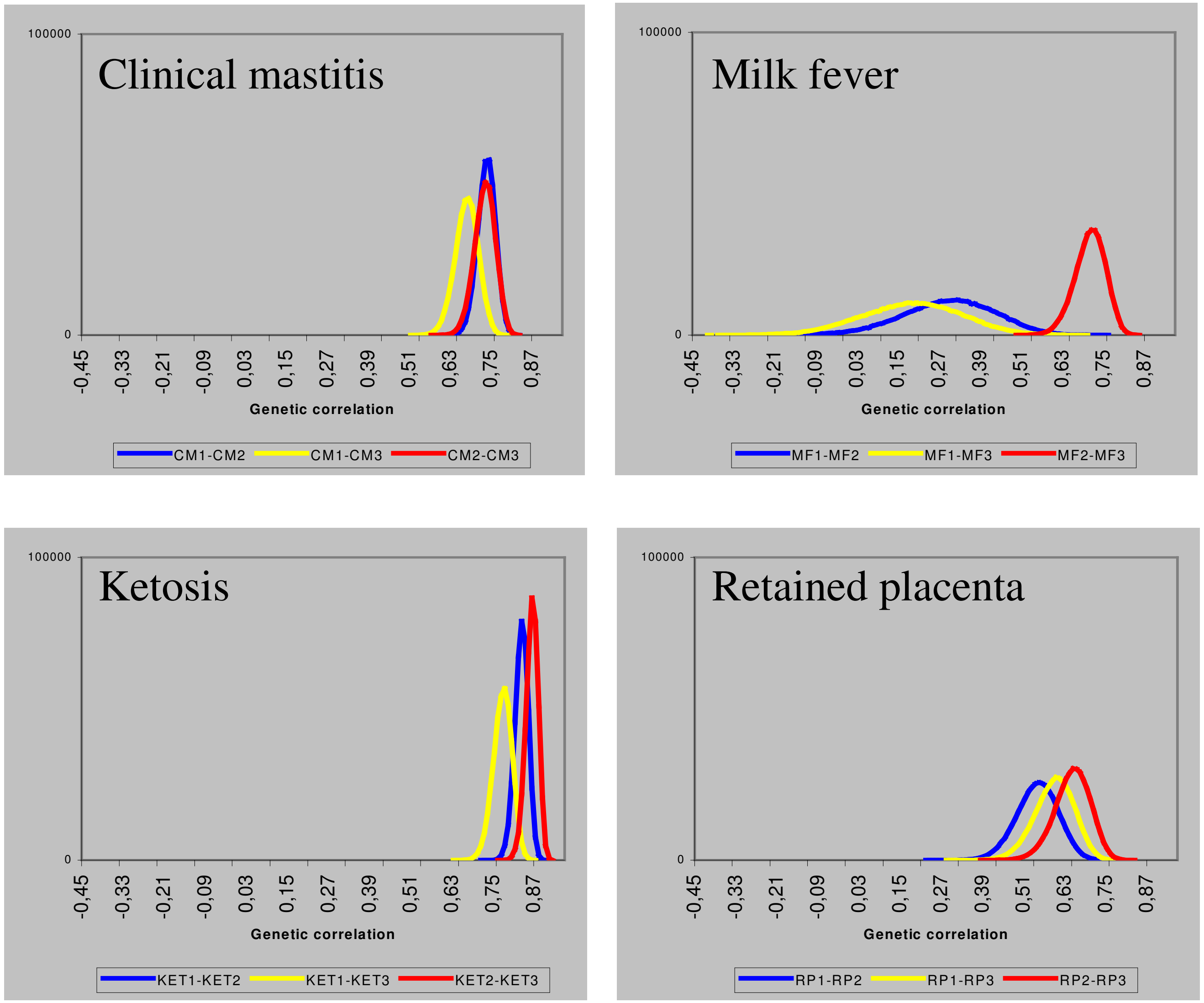
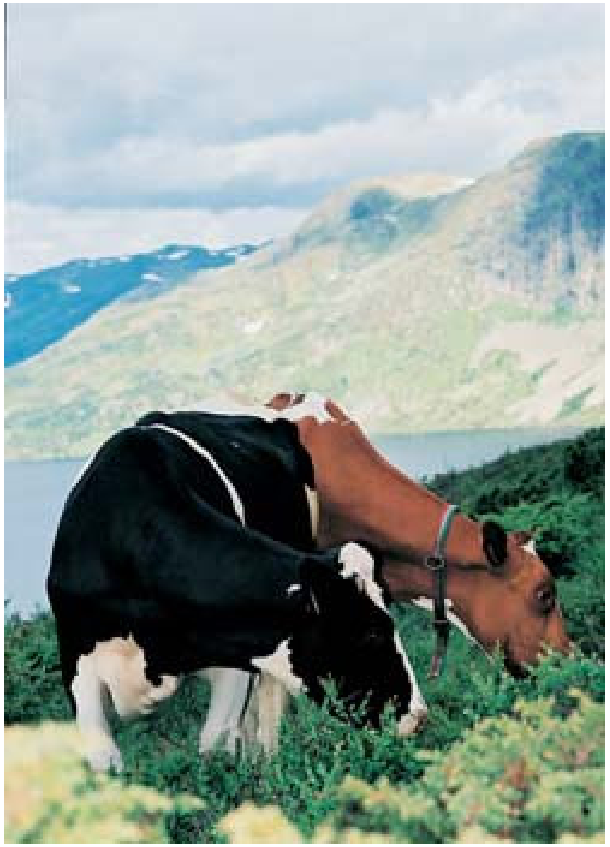


Figure 6. Posterior distributions of the genetic correlations between liability to clinical mastitis (CMi), milk fever (MFi), ketosis (KETi), and retained placenta (RPi) in lactation i=1,

Genetic correlations between diseases

Traits	Range posterior means
CM-MF	0.12 - 0.22
CM-KET	0.08 - 0.26
CM-RP	0.05 - 0.22
MF-KET	0.19 - 0.40
MF-RP	-0.10 - 0.21
KET-RP	-0.05 - 0.07



Highest KET1-MF2:	0.40
Lowest MF1-RP3:	-0.10

Genetic correlations

- Posterior means range from –0.10 to 0.86
- Higher within disease between lactations than between diseases
- Genetic correlations suggest:
  - MF different trait in first and later lactations
  - KET may be considered the same trait in all three lactations
- All genetic correlations between RP and other diseases were small
- Genetic correlations involving MF1 had high SD

Genetic correlations

- Low or moderate genetic correlations between diseases (from –0.10 to 0.40)
  - Very different diseases
    - CM is an infection of the udder
    - MF and KET are metabolic diseases
    - RP is a fertility disorder
- All genetic correlations that could be considered to be different from 0 were positive
  - there may exist some general disease resistance or robustness with a genetic component

Heringstad, B., Y. M. Chang, D. Gianola, and G. Klemetsdal. 2005. **Genetic analysis of Clinical Mastitis, Milk Fever, Ketosis, and Retained Placenta in the first three lactations of Norwegian Red (NRF) cows with a Multivariate Threshold Model**. Journal of Dairy Science (accepted).

Thank's!