Strategy for estimation of variance components for the joint Nordic yield evaluation

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Introduction

- **Since 2006 joint Nordic yield evaluation**
  - Countries

    Denmark, Finland, Sweden
  - For each breed own evaluation

    Red Cattle, Holstein, Jersey
  - Three biological traits

    Milk, protein, fat
  - Lactations

    1, 2, 3 (3+ for Finland)
  - Evaluation model

    Multiple-trait random regression animal model with 27 traits

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Introduction

- **Meta-model approach**
  - Test-day records
    - **Denmark**
    - **Finland (bimonthly records for protein and fat yield)**
  - 305-day records
    - **Sweden**
  - Model for additive genetic effects
    - **Genetic correlation of one across countries**
    - **Different heritabilities and variances across countries**

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Introduction

- **Next generation of joint Nordic yield model**
  - Test-day records for all countries
    - **For Sweden 305-d records are upgraded by TD records**
  - New variance components for all countries and breeds
    - **Variance components for Swedish traits needed**
    - **Variance components for Finnish traits were estimated in 1997**
    - **Variance components should be estimated by same method for all countries and breeds**
- **Variance component analysis by Bayesian method**
  - Challenges
    - **Large number of parameters to be estimated**
    - **RR models are highly over-parameterized**

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Aim of this study

- **Find suitable model for the variance component analysis**

- **Find size and number of data samples**

- **Bayesian inference - post-Gibbs analysis**

Chosen model for VC analysis

- **Fixed effects**
  - herd$\times$2-years-calving period
  - calving age
  - days carried calf
  - 3rd ord. Leg. + $e^{-0.04}$ nested within 2-years-calving period

- **Random effects**
  - herd$\times$test-day
  - lin. Leg.+ quad. Leg. + $e^{-0.04}$ nested within herd$\times$2-years-calving
  - 2nd ord. Leg. + $e^{-0.04}$ for non-genetic animal effect
  - 2nd ord. Leg. + $e^{-0.04}$ for additive genetic animal effect
  - 12 residual classes (from DIM 8: 3$\times$ 2 weeks, 3$\times$ 3 weeks, 3$\times$ 7 weeks, 3$\times$ 5 weeks)

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Bayesian inference

- **Gibbs sampler implementation in the DMU package**
- **Priors**
  - Fixed effects
    - **Flat priors**
  - Random effects
    - **Wishart distributions**
    - **Prior values from analysis with records from ~1000 cows**
    - **Proper priors: degree of belief was dimension of covariance matrix + 2**
- **Chain length**
 - 110,000 samples
  - First 10,000 samples discarded

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Find size and number of data samples

- **Reasonable data sets**
  - 9 traits per analysis (milk, protein, fat, and 3 lactations)
    - **1971 parameters to be estimated**
  - Data edits
    - **About 20000 cows with observations**
    - **A sampled herd should have at least 10 first calvers / year**
    - **12 years of data**
- **Are heritabilities different across countries?**
  - Analysis on first lactation only should be sufficient
    - **"only" 279 parameters to be estimated**
    - **2 samples per country and per breed**

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Variance components for Nordic Red Cattle
First lactation daily genetic variances for milk yield
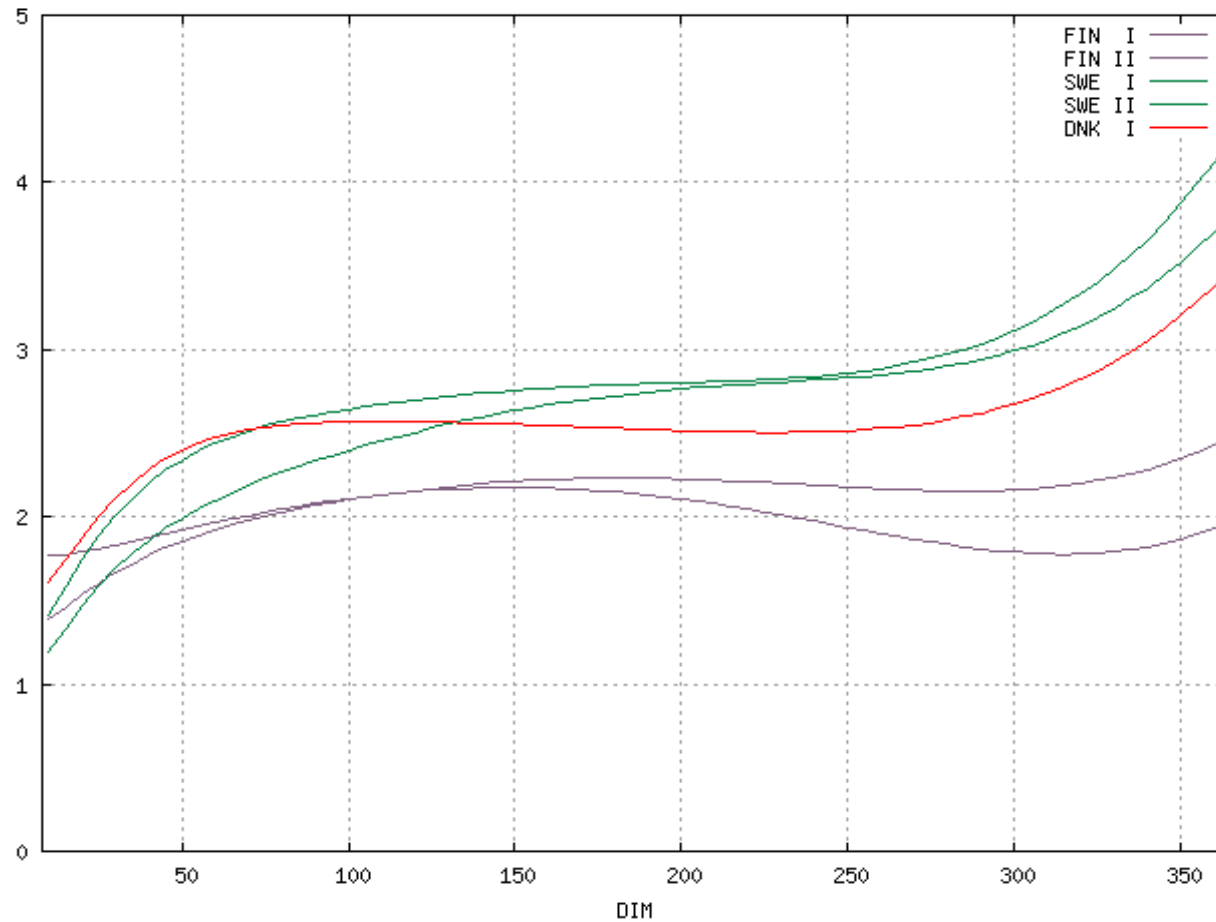
Variance components for Nordic Red Cattle

First lactation daily pe+residual variances for milk yield
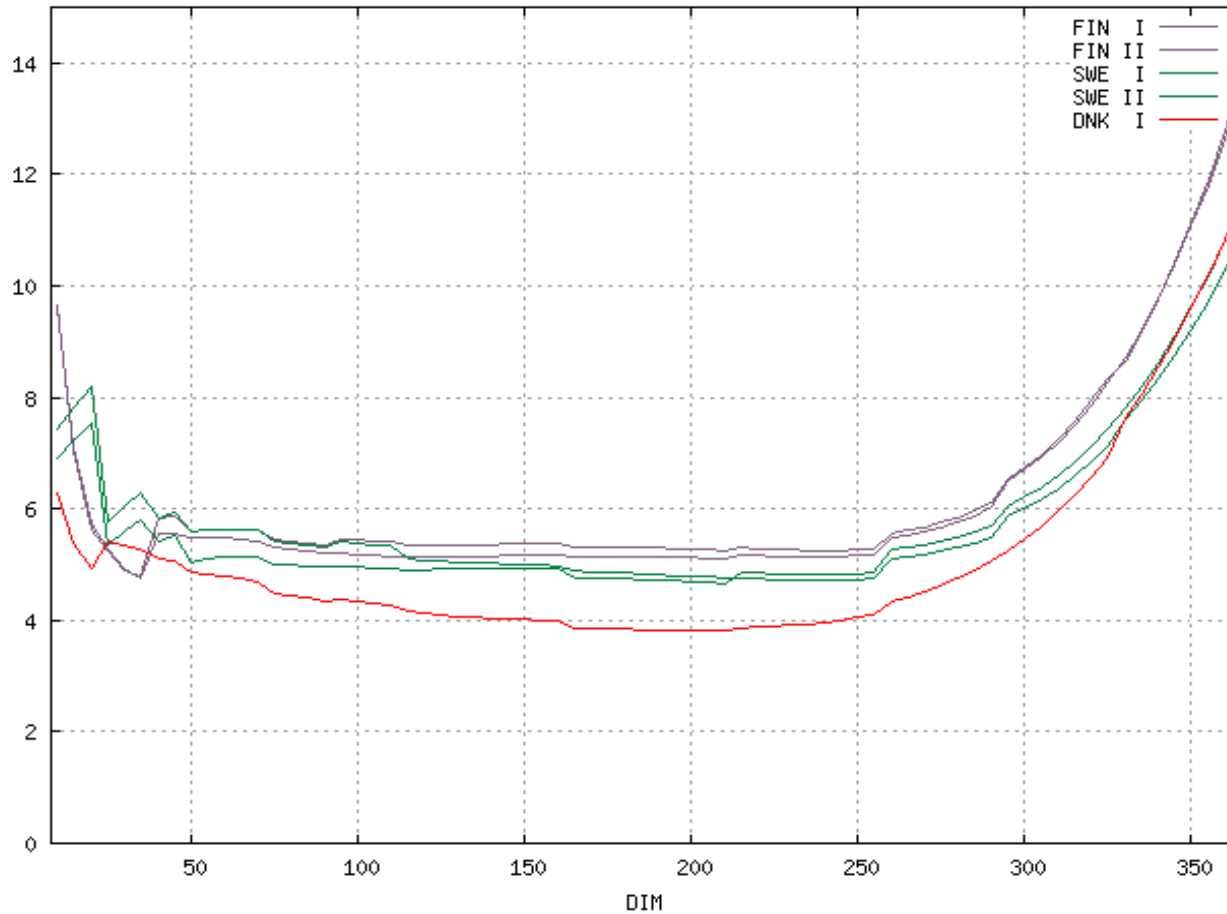
Heritability estimates for Nordic Red Cattle

First lactation daily heritabilities for milk yield
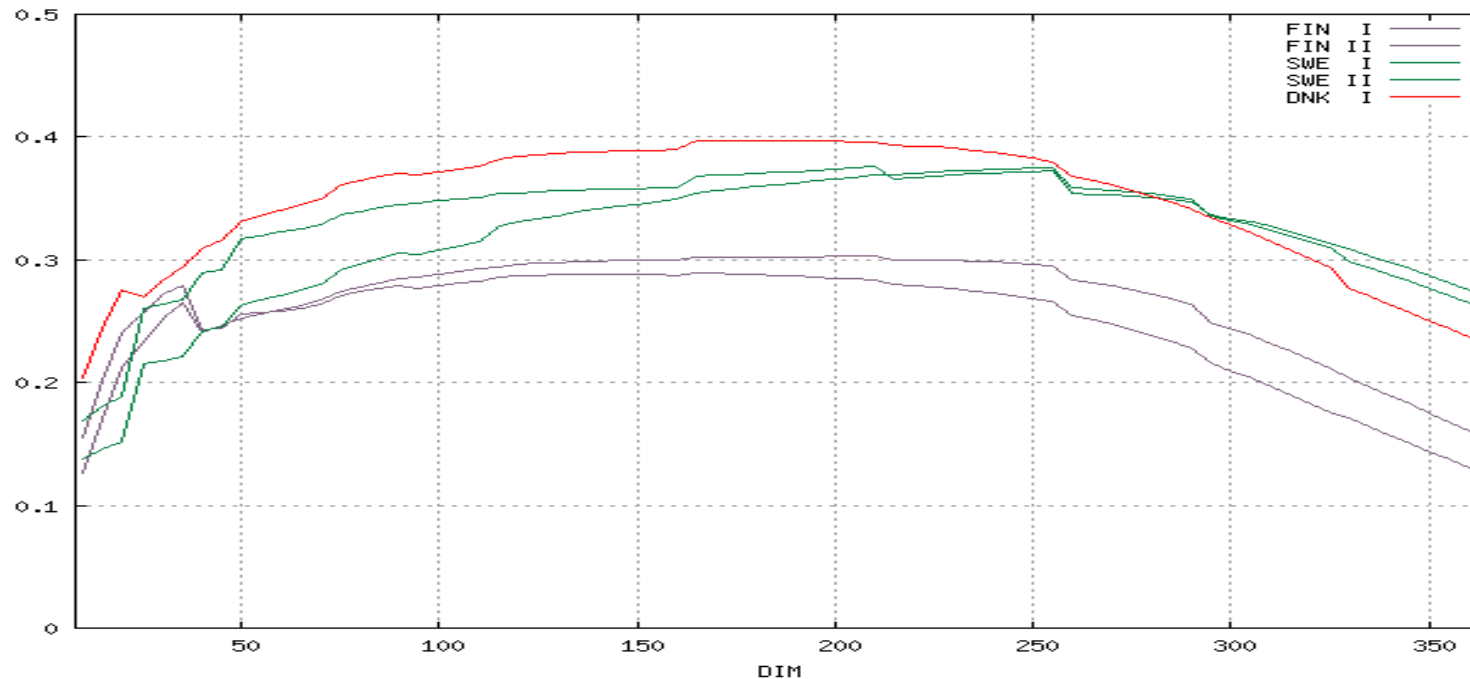
- **Results**

    - Results very similar from samples within the countries

    - Genetic correlations between different DIM and traits were very similar within and across the countries

    - Differences in heritabilities across the countries

Heritability estimates for Nordic Red Cattle

First lactation on 305d basis

	Samples				
	Denmark	**Finland**		**Sweden**	
	I	I	II	I	II
Milk	**0.48**	**0.35**	**0.36**	**0.41**	**0.42**
Protein	**0.44**	**0.31**	**0.31**	**0.38**	**0.41**
Fat	**0.43**	**0.34**	**0.33**	**0.37**	**0.42**

- **Conclusions**

  6 samples to be analyzed:

  Red Cattle (DNK, FIN, SWE)

  Holstein (DNK, SWE)

  Jersey (DNK)

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Post-Gibbs analysis from a 9-traits analysis

- **Convergence of Gibbs sampler**
  - By method of batching
  - Estimation of posterior sample size
- **Parameters analyzed**
  - (Co)variance components
  - Derived parameters
    - **Correlations**
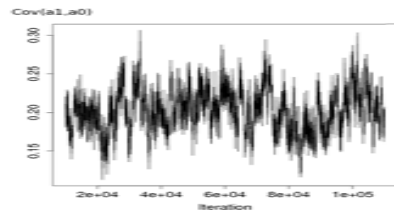   - **Daily heritabilities**
    - **305d heritabilities**

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Post-Gibbs analysis

- **Poor mixing properties for several variance components**
- **Much longer burn-in is needed**

Trace plots of genetic (co)variance components for 1st lact. protein yield

intercept   (Chain length of trace plots: 100,000)
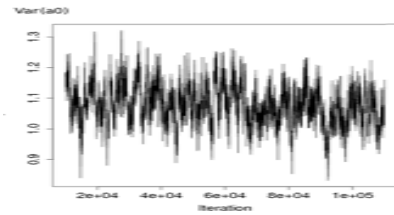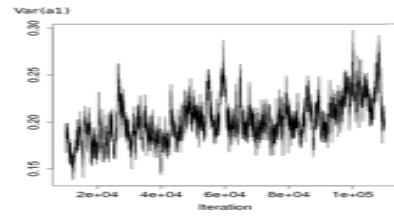
linear
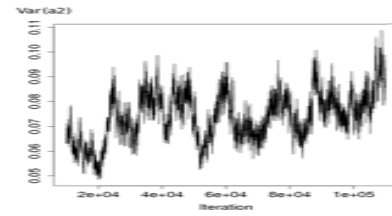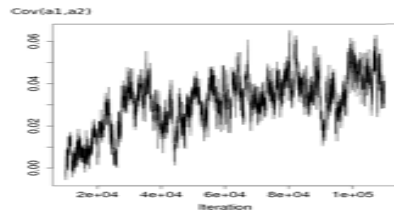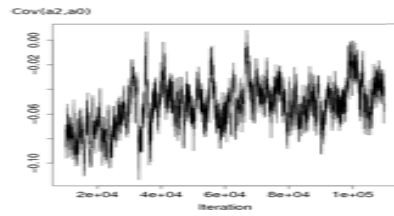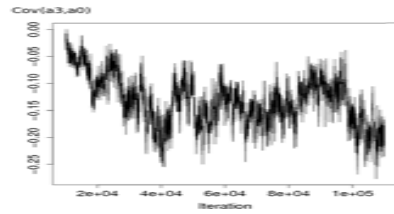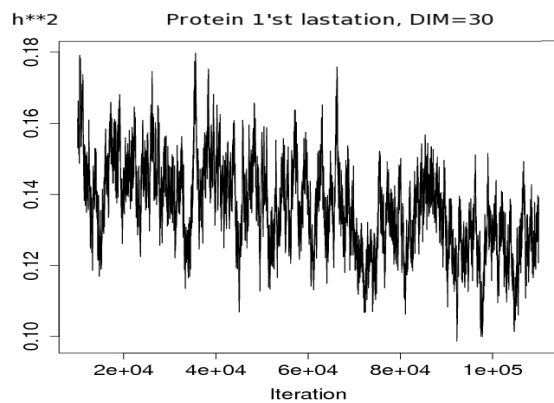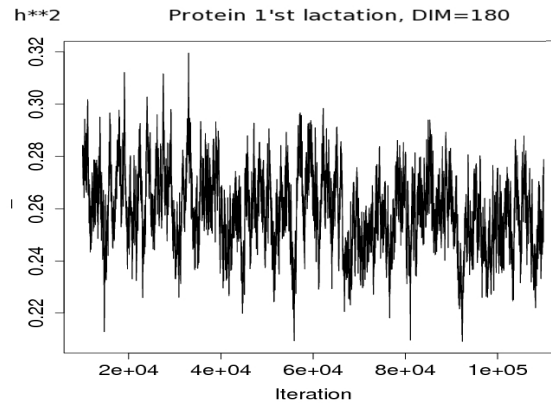
quadratic
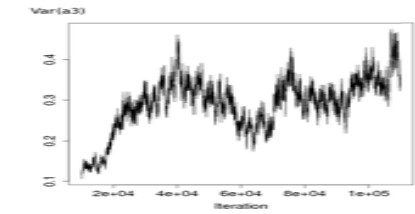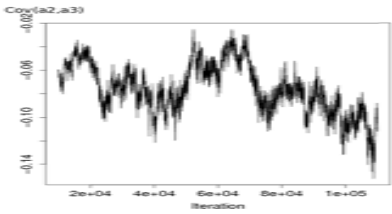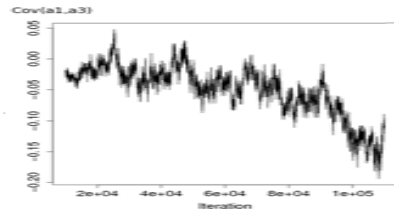
e$^{-0.04}$

Post-Gibbs analysis

- **Functions of (co)variance components have better mixing**

Trace plots for h², 1st lactation protein yield at DIM 30, 180 and 300

DIM 30   **DIM 180**   **DIM 300**

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Post-Gibbs analysis

- **The problem is most apparent in the 3rd lactation**

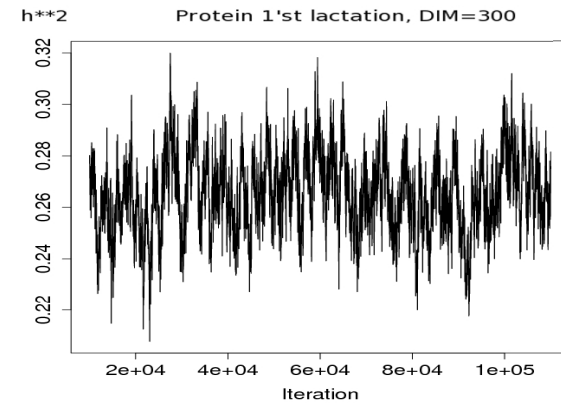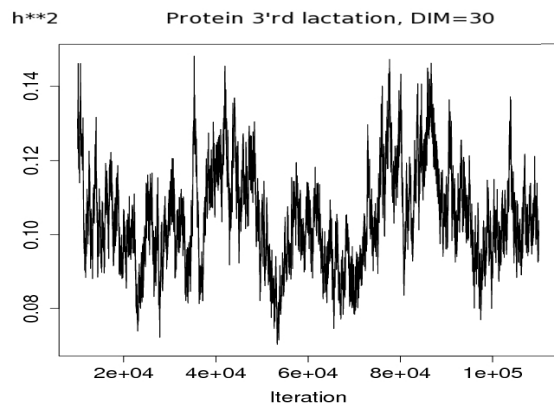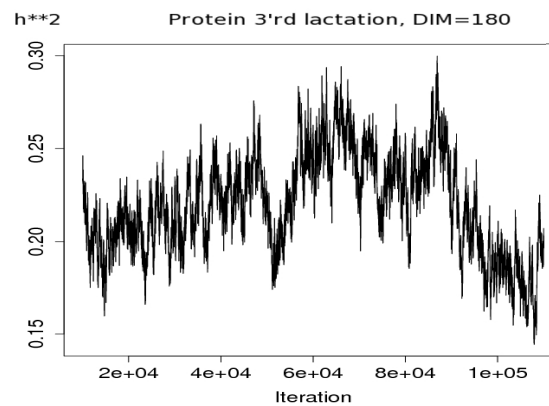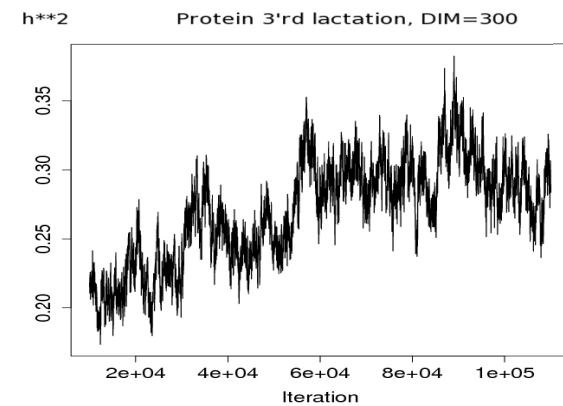**Trace plots for h², 3rd lactation protein yield at DIM 30, 180 and 300**

DIM 30　　　　**DIM 180**　　　　**DIM 300**

Post-Gibbs analysis

Posterior means and standard deviations for h², phenotypic and genetic correlation

Trait	h2	ESS*	Milk 1	Prot. 1	Fat 1	Milk 2	Prot. 2	Fat 2	Milk 3	Prot. 3	Fat 3
Milk 1st	.42(.02)	90.2		.87(.01)	.48(.03)	.92(.02)	.77(.02)	.32(.04)	.89(.02)	.69(.04)	.26(.05)
Prot. 1st	.39(.02)	85.5	.92(.01)		.65(.02)	.76(.03)	.90(.02)	.48(.04)	.77(.03)	.86(.03)	.46(.05)
Fat 1st	.43(.02)	152.6	.72(.01)	.80(.01)		.41(.08)	.64(.03)	.92(.01)	.43(.03)	.63(.04)	.89(.02)
Milk 2nd	.30(.02)	60.5	.58(.01)	.53(.01)	.36(.01)		.81(.01)	.38(.04)	.93(.02)	.70(.04)	.28(.05)
Prot. 2nd	.27(.02)	60.1	.52(.01)	.60(.01)	.46(.01)	.92(.01)		.62(.03)	.79(.03)	.91(.03)	.55(.04)
Fat 2nd	.36(.02)	63.9	.34(.01)	.43(.01)	.62(.01)	.23(.01)	.83(.01)		.37(.05)	.59(.04)	.93(.02)
Milk 3rd	.29(.03)	30.5	.53(.01)	.48(.01)	.33(.01)	.57.01)	.54(.01)	.38(.01)		.81(.02)	.37(.05)
Prot. 3rd	.28(.03)	29.9	.44(.01)	.52(.01)	.41(.02)	.51(.01)	.61(.01)	.48(.02)	.93(.02)		.63(.03)
Fat 3rd	.35(.03)	35.7	.29(.02)	.38(.02)	.55(.01)	.24(.02)	.46(.01)	.61(.01)	.76(.01)	.85(.01)	

* ESS=effective sample size for h²

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Conclusions

- Genetic correlations were very similar across samples from different countries for same breed
- **Heritabilities differed for same breeds across countries**
- One sample per breed $\times$ country was sufficient
- **Gibbs sampler analysis showed pure mixing properties for single VC in the 9-traits analysis**
- Mixing properties were better for derived functions
- **VC analysis for reduced rank matrices is recommended**

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