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VERSITÄT

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Generating test-day methane emissions as a basis for genetic studies with random regressions

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Background

- Greenhaus gas (GHG) emissions
  - CO_2, N_2O, and CH_4
  - global climate change
  - inefficient use of dietary energy
- The dairy cattle sector (FAO, 2010)
  - 4% of GHG emissions
  - 52% contribution of methane emissions (ME)
- Methods to measure ME
  - respiration chamber
  - sulfur hexafluoride tracer
  - mobile laser methane detector

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www.extension.org/pages/67580/effects-of-corn-processing-method-and-dietary-inclusion-of-wet-distillers-grains-with-solubles-wdgs-#.U_Sar2M8gWY

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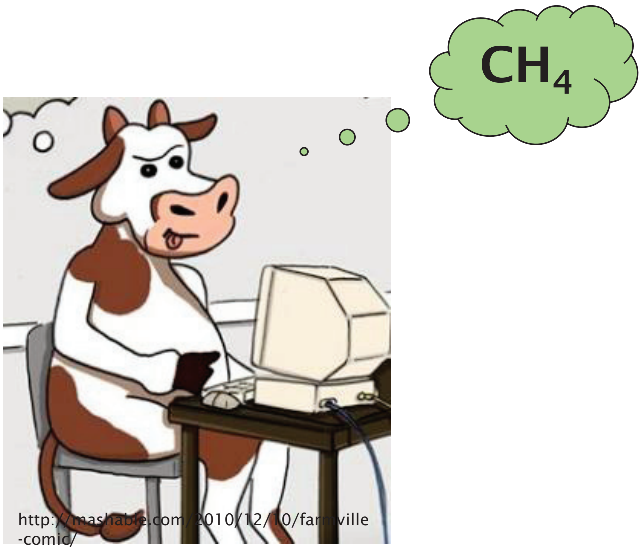
(Foto by Chagunda and Wall, 2012)

Aims of this study

- simulate and predict test-day ME using indicator traits
- estimate heritabilities for ME by DIM
- genetic correlations: test-day ME and test-day production traits by DIM
- genetic correlations: test-day ME and fertility traits by DIM
  tesy-day ME and clinical mastitis by DIM
- evaluate breeding program designs
  - progeny testing program
  - genomic breeding programs

1. Simulation and prediction of test-day ME



http://mashable.com/2010/12/10/farmville-comic/

Data

- Real data
  - 7804 test-day records
  - 916 first lactation Brown Swiss cows
  - 41 low input farms in mountainous regions in Switzerland
- Test-day production traits
  - Milk yield (MY), fat percentage (Fat%), protein percentage (Pro%), milk urea nitrogen (MUN)
- Conformation traits
  - Wither height (WH), hip width (HW), body condition score (BCS)
- Fertility traits
  - Calving interval (CI), days open (DO), stillbirth (SB)
- Health trait: clinical mastitis (CM)

Predict methane emissions - equation 1

$$ME1 = (10.0 + 4.9 \times MY + 1.5 \times BW^{0.75}) \times 0.0132$$

(Kirchgeßner et al., 1995)

Test-day MY

$$BW = 439 + 0.2 \times DIM + 4.2 \times HH + 29.2 \times HW + 0.3 \times HW^2 + 33.5 \times BCS$$

(Enevoldsen et al., 1997)

Predict methane emissions - equation 2

$$ME2 = FI \times 18.4 / 0.005565 \times 0.006 \times \left[1 + \left(2.38 - LI\right) \times 0.04\right]$$

(de Haas et al., 2011)

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$$\begin{aligned} FI = {} & 15.28 + 0.008 \times (BW - 603) \\ & + 0.2389 \times (ECM - 20) - 0.005874 \times (ECM - 20)^2 \\ & + 0.305 \times (Con - 2.88) \\ & + 0.959 \times (ECR - 5.41) \\ & - 0.0028 \times (DIM - 112) + 1.142 \times (\ln(DIM) - 4.33) \\ & + 0.0443 \times (Mon - 6.36) - 0.019776 \times (Mon - 6.36)^2) \end{aligned}$$

(Schwarz and Gruber, 1999)

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Simulation

		Milk urea nitrogen (in mg/dl) < 25.14	Milk urea nitrogen (in mg/dl) > 25.14
Protein %	< 3.418	No concentrate 4.5 MJ NEL/kg DM	No concentrate 6 MJ NEL/kg DM
Protein %	> 3.418	10% concentrate ~ *N(1.78, 0.41)* 4.5 MJ NEL/kg DM	10% concentrate ~ *N(1.78, 0.41)* 6 MJ NEL/kg DM

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Simulation

Level of intake: can be calculated based on FI and BW

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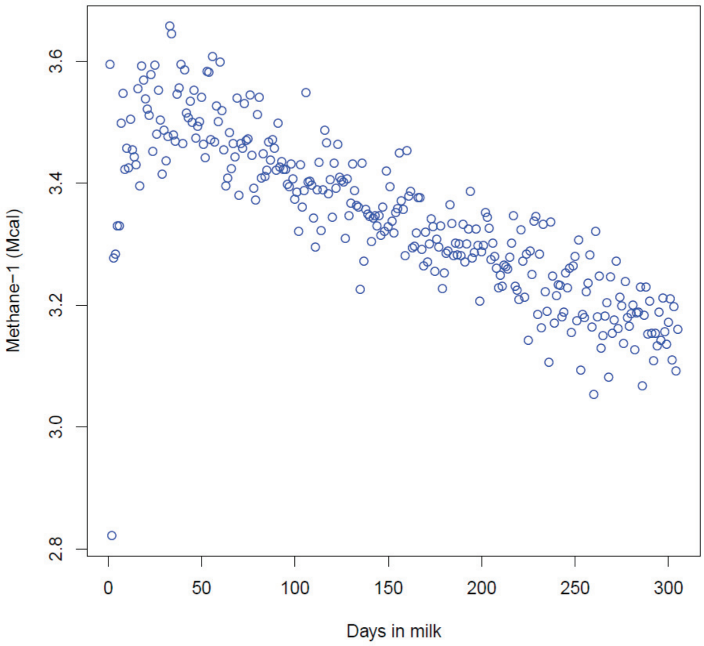
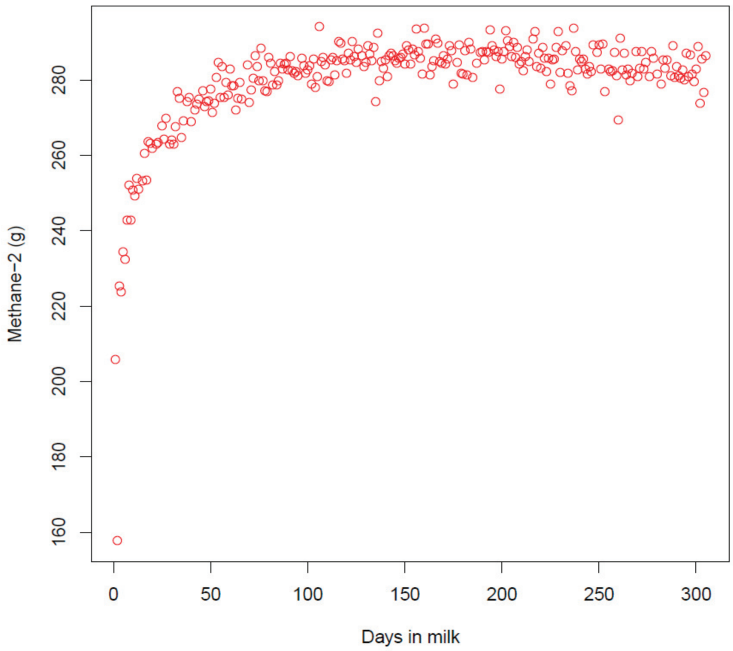
Predicted ME1(in Mcal) and ME2 (in g)

- **Phenotypic correlation between ME1 and ME2: 0.63**





2. Heritabilities for test-day ME

Bivariate random regression models

DMU package (Madsen and Jensen, 2012)

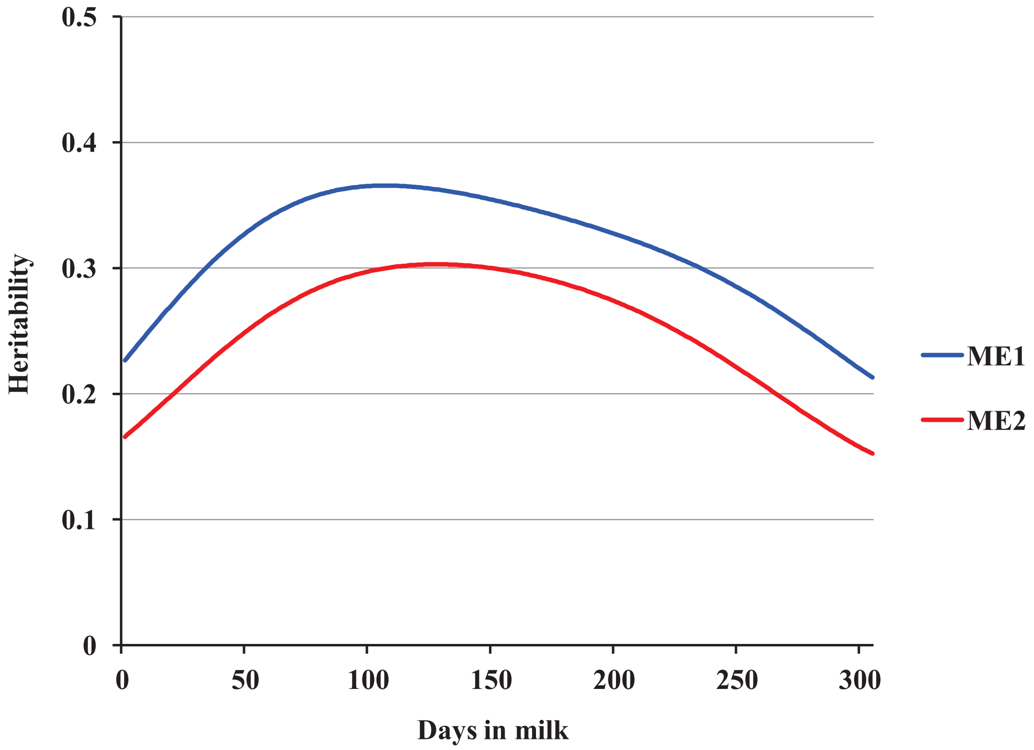
Fixed effects → $\mathbf{Xb}$; PE → $\mathbf{Zp}$

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Qu} + \mathbf{Zp} + \mathbf{e}$$

$\mathbf{y}$: Vector of the test-day methane ME1 and ME2; $\mathbf{Qu}$: Ad

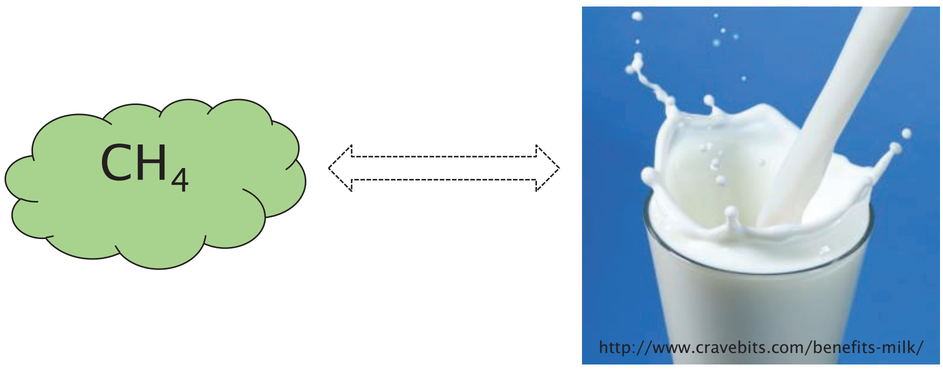
- Fixed effects
  - Farm
  - Test-year-season
  - Fixed regression with Legendre polynomials 3 (LP 3)
- Time dependent covariate
  - DIM 1- 305
- LP 2 for additive genetic and permanent environment effects

Daily heritabilities for methane emissions

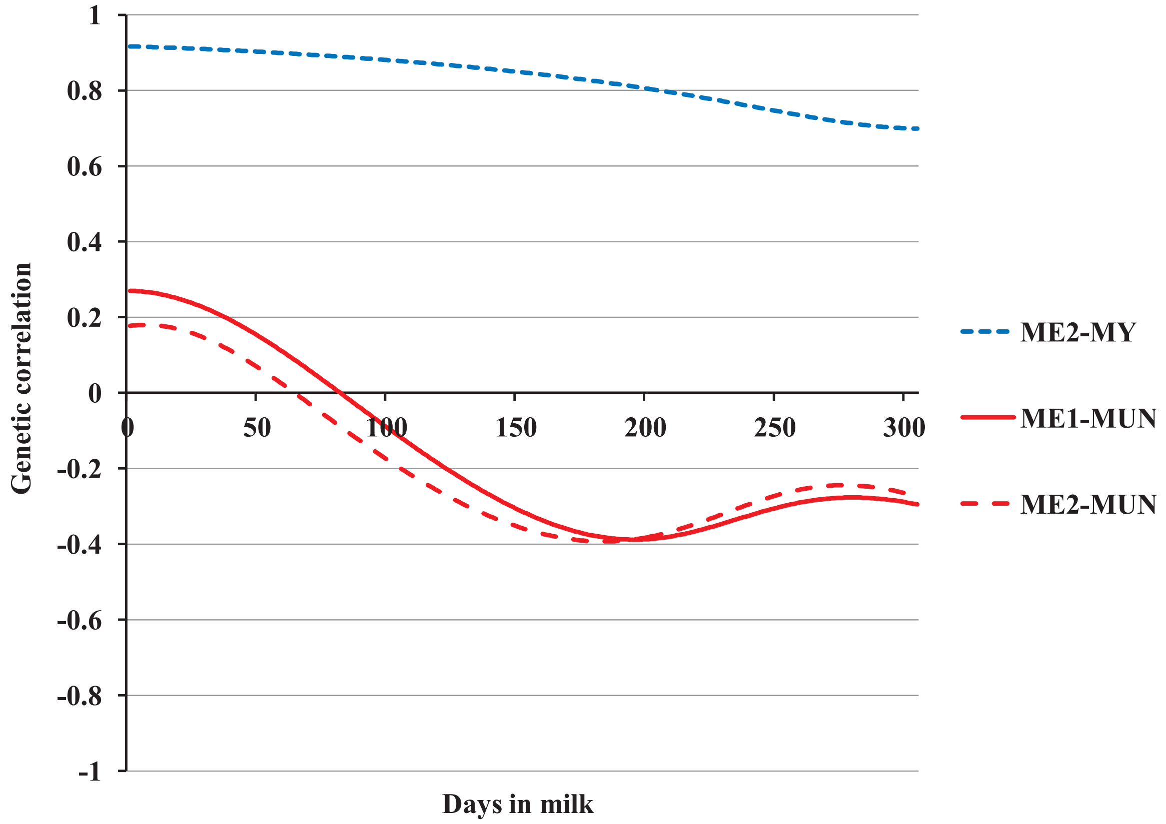


3. Genetic correlations:

- **test-day ME and test-day production traits**

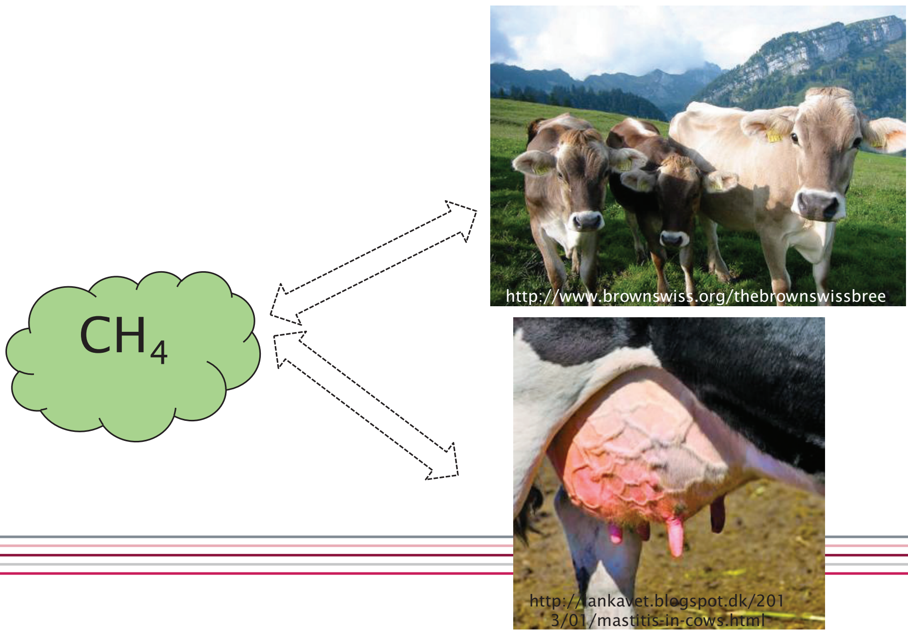


Genetic correlations



4. Genetic correlations:

- **test-day ME and fertility traits**
- **test-day ME and clinical mastitis**

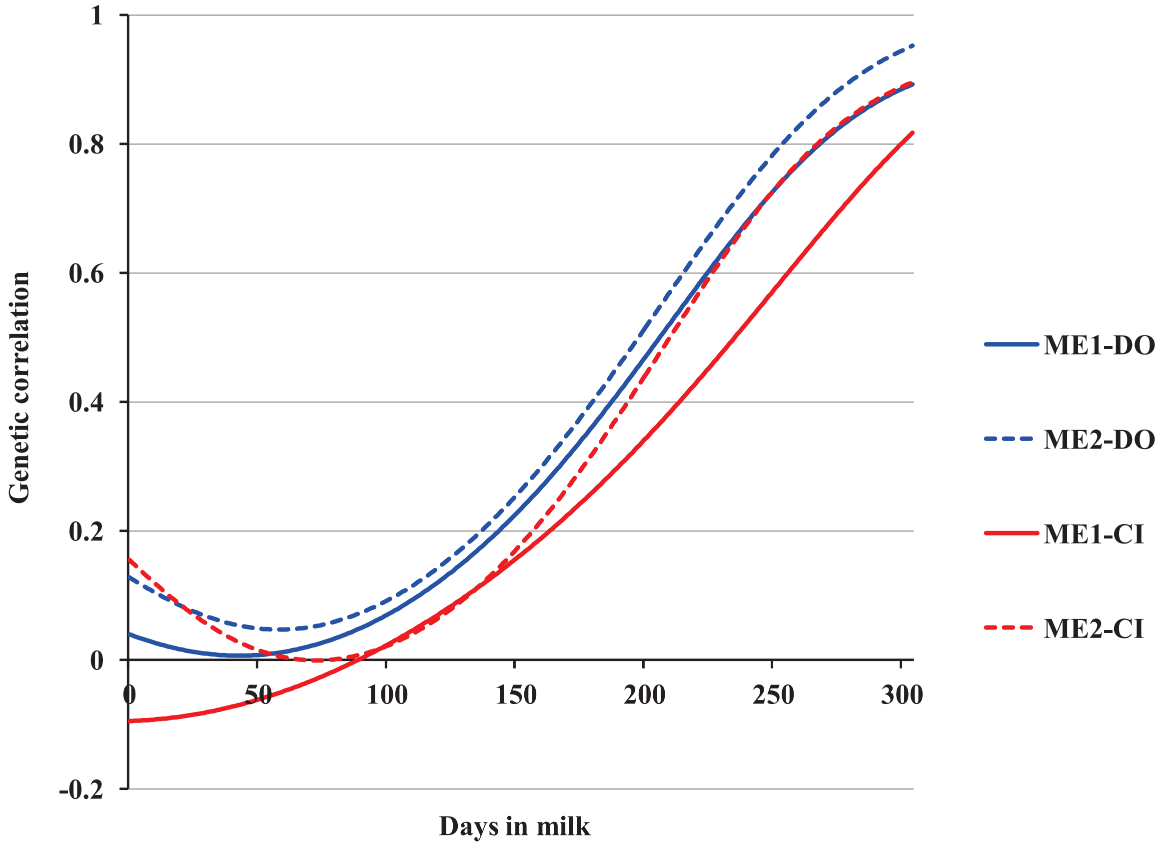


Bivariate random regression and single trait models (DMU package)

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1\mathbf{b}_1 + \mathbf{Z}_1\mathbf{a}_1 + \mathbf{W}\mathbf{p} + \mathbf{e}_1 \\ \mathbf{X}_2\mathbf{b}_2 + \mathbf{Z}_2\mathbf{a}_2 + \mathbf{Q}\mathbf{s} + \mathbf{e}_2 \end{bmatrix}$$

- Dependent variables
  - y_1: test-day ME1 or ME2
  - y_2: fertility traits or clinical mastitis
- Fixed effects
  - b_1: farm, test-year-season, LP 3
  - b_2: farm, calving-year-season, sex of the calf for SB
- Random effects
  - a_1: additive genetic effect with LP 2
  - p: permanent environment effect with LP 2
  - a_2: additive genetic effect
  - s: service sire effect for CI and SB

Genetic correlations



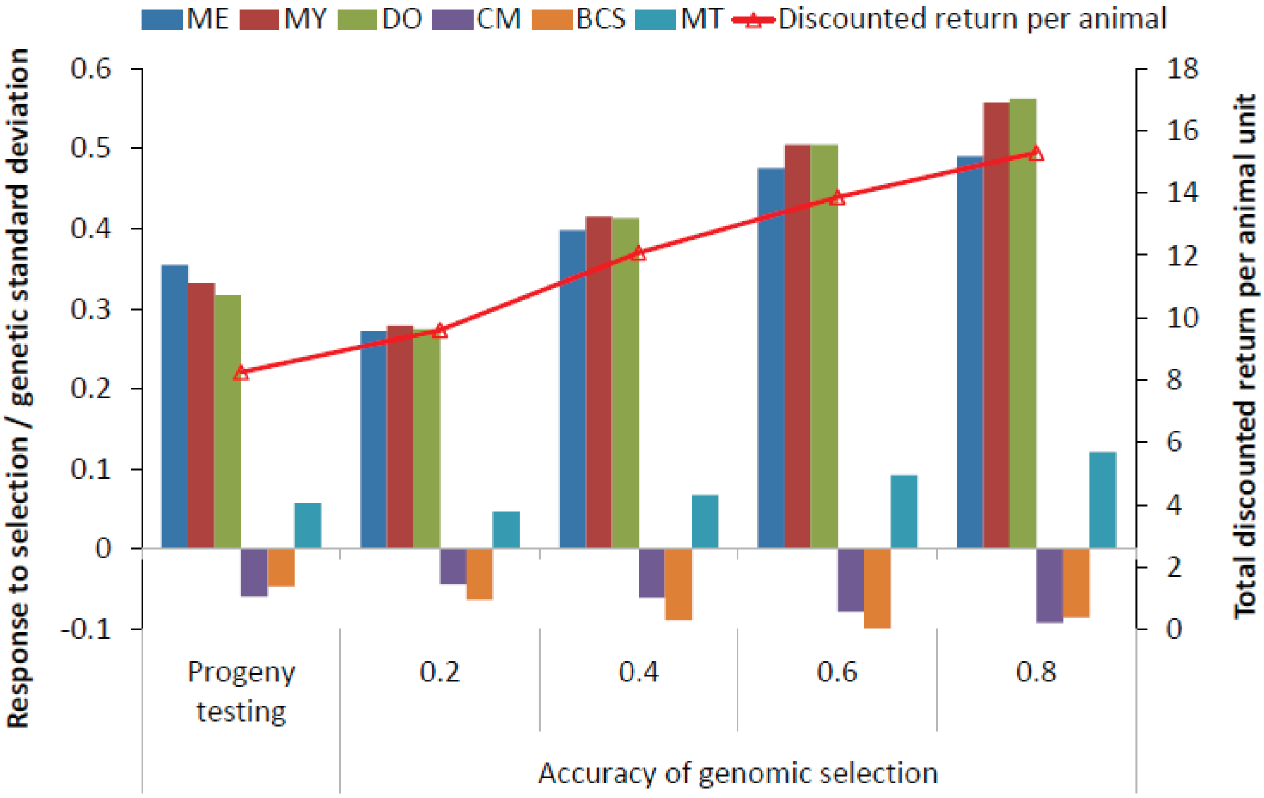
5. Breeding program

- progeny testing
- genomic breeding programs

Evaluation of breeding programs

ZPLAN+ (Täubert et al., 2010)

Economic weight for milk yield was five times higher than for other traits



Proeny testing and genomic breeding program with different accuracy

Conclusions

- Methane emissions can be predicted when combining real data with deterministic equations and stochastic simulations
- Moderate heritabilities for methane emissions
- Genetic correlation between methane emissions and
  - milk yield: antagonistic
  - fertility traits: positive
- Genomic breeding program is better
  - response to selection
  - discounted return per animal

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LowInputBreeds

Thank you for your attention!

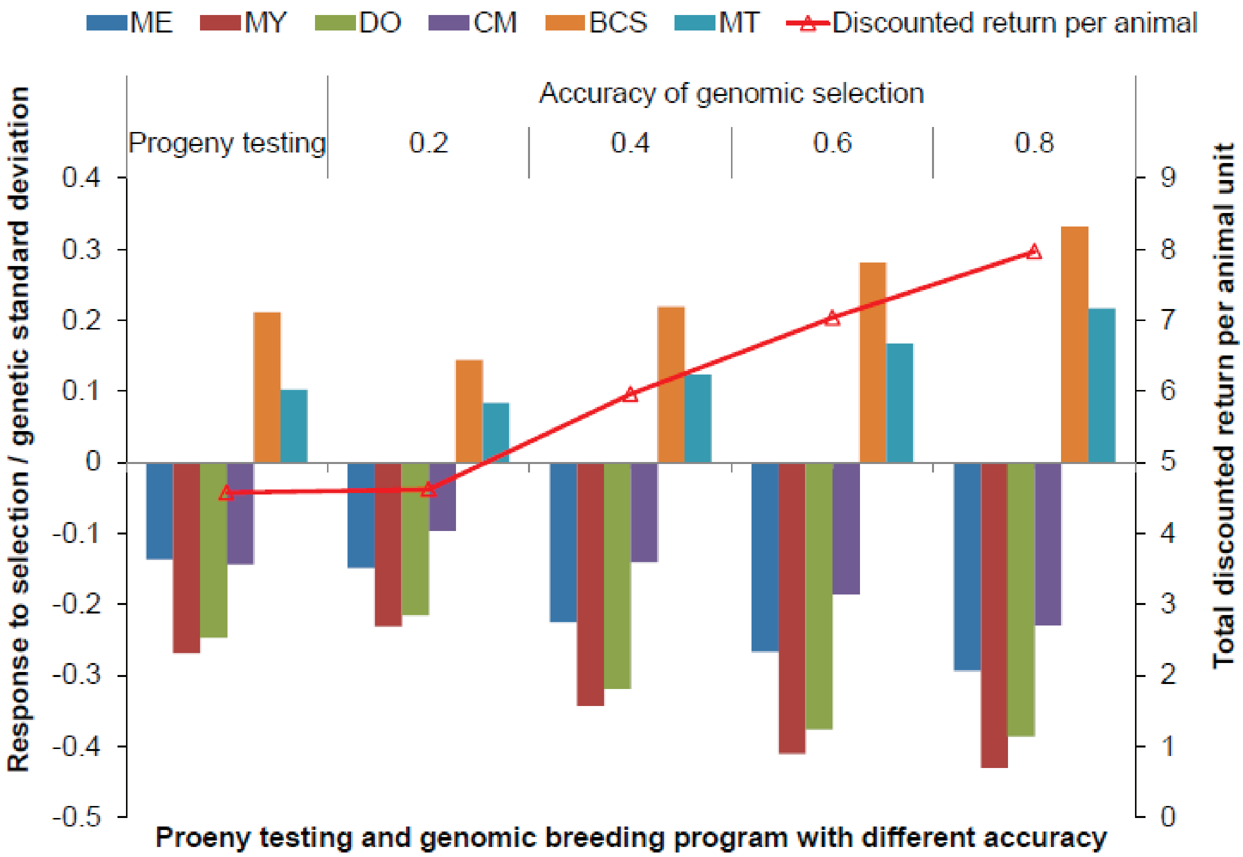
Characteristics of breeding programs

	Progeny testing	Genomic selection
Milking cow	25'000	25'000
Bull dam	250	250
Bull calves	125	125
Test bull	50	--
Proven bull	5	10
Elite bull	1	1
Bull sire	80% proven bull 20% elite bull	97% proven bull 3% elite bull
Cow sire	40% test bull 50% proven bull 10% elite bull	-- 67% proven bull 33% elite bull

Heritabilities and correlations among the traits

Trait	ME	MY	DO	CM	BCS	MT	Economic value
Methane emission (ME)	0.44	0.89	0.86	0.03	0.35	x	-6.84
Milk yield (MY)	0.92	0.34	0.93	0.04	-0.4	0	0.60 / 3.00
Days open (DO)	0.10	0.12	0.03	-0.18	-0.4	-0.03	-0.10
Clinical mastitis (CM)	0.02	0.01	0.02	0.10	-0.26	0.19	-1.66
Body condition score (BCS)	0.25	-0.01	-0.08	-0.01	0.15	x	6.11
Milking temperament (MT)	x	0	x	-0.67	x	0.04	8.01
Phenotypic SD	0.22	2.88	60.57	1.91	0.42	0.62	

Equal economic weight was assumed for the six traits



Total genetic gain of a bull per generation