Robust dairy cows:

where management and genetics meet

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Outline

- Preface: robustness what is new?

- Why is there a demand for robust cows?

- Tools to improve robustness

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Definition of robustness

"A robust dairy cow is a cow that is able to maintain homeostasis in the commonly accepted and sustainable dairy herds of the near future "

Jan ten Napel et al. 2005

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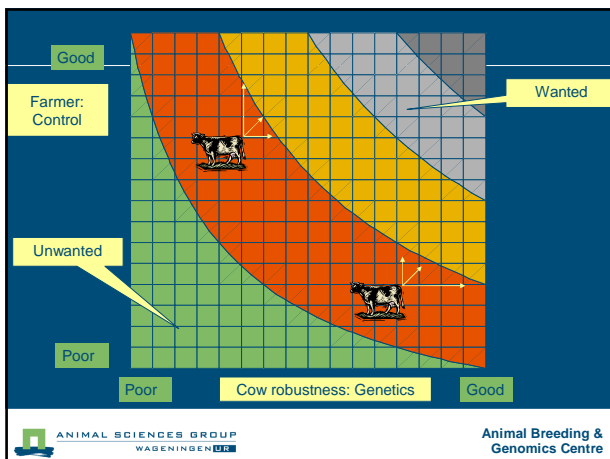Animal Breeding &
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What is new? Paradigm shift

- Control paradigm: avoiding environmental disturbances to happen
  - ←"Good management, pathogen free, ideal climate..."

- Improving robustness
  - ←"relying on animal (genetics) or system to cope"

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Good

Farmer:
Control

Wanted

Unwanted

Poor

Poor | Cow robustness: Genetics | Good

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Why more robust cows (now)?

- Wanted:
  - Demands: Health, welfare, longevity and food safety

- Global trends in dairy production
  - Reduced margins
  - Scale enlargement
  - Less (skilled) labour available per animal
  - Constraints: Antibiotics use or regulations

- Slight reduction in genetic ability due to single trait selection for production

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Why more robustness (now)?

- Control paradigm has reached its limits
  - "we cannot do much better, are more likely to do worse in future"

→ Rely even more on ability of systems and animals to deal with disturbances

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- Need for:

Innovative and practical breeding tools for improved dairy products from more robust dairy cattle

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EU-project with partners in:
- The Netherlands
- Belgium
- Ireland
- Scotland
- Sweden

www.robustmilk.eu

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RobustMilk:

- Bring research data on robustness traits (energy balance, fertility, SCC) together in database

- Tools that allow refocusing multitrait selection: 1
  - Measuring EB during milk recording? 2
  - Statistical tools on existing data? 3
  - Genomic selection tools? 4

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1) multi-trait selection

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1) multi-trait selection

- Include health & welfare traits in breeding goal

- Scandinavian countries set example

- Since 1990's most breeding goals/indices adapted to include longevity, fertility and health traits (Miglior et al JDS 2005)

- More emphasis on robustness → tools required

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1) Multi-trait selection

- Holstein population
  - +25d CIV
  - -6.5% NR

- Stabilised using multi-trait selection?

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1) Multi-trait selection

- For example to reduce the effects of selection on negative energy balance and body condition score

Genetic Analysis of Body Condition Score of Lactating Dutch Holstein and Red-and-White Heifers

E.P.C. Koenen,* R. F. Veerkamp,† P. Dobbelaar,‡ and G. De Jong*
Selection for Economic Efficiency of Dairy Cattle Using Information on Live Weight and Feed Intake: A Review

The Relationship Between Genetic Merit for Yield and Live Weight, Condition Score, and Energy Balance of Spring Calving Holstein Friesian Dairy Cows on Grass Based Systems of Milk Production

Genetic Parameters for Level and Change of Body Condition Score and Body Weight in Dairy Cows

Energy Balance of Dairy Cattle in Relation to Milk Production Variables and Fertility

Genetic Correlation Between Days Until Start of Luteal Activity and Milk Yield, Energy Balance, and Live Weights

Genetic Correlations Among Body Condition Score, Yield, and Fertility in First-Parity Cows Estimated by Random Regression Models

Genetic Relationships among Body Condition Score, Body Weight, Milk Yield, and Fertility in Dairy Cows

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2) Measuring EB in milk with MIR?

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2) Measuring EB in milk with MIR?

- Fat% and protein% with mid-infra red spectrometry (MIR)

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2) Measuring EB in milk with MIR?

Milk Fatty acid composition and heritabilities

	Mean	CV%
C6-12	10.74	11
C14-16	44.24	6
C18u	21.58	11
C16:0	32.61	9
C18:2 cis-9,trans-11	0.39	28
Ratio SFA/UFA	2.80	13

Average milk fat content increased from 3.7% in 1950 to 4 increased from 25.5% to 32.6% while C18u decreased fro

Table 2: Number of records used (n), variability explained (R^2) and root mean square error (RMSE(MJ)) of the cross validation, and the number of factors used for the PLS model containing only MIR predictors or MIR predictors plus milk yield across the four energy balance measures when undertaken using AM, MD, and PM samples

		Only MIR predictors			MIR predictors + milk yield		
AM	n	R^2	RMSE	Factors	R^2	RMSE	Factors
Direct_EB	1199	0.41	25	18	0.50	23	17
EC	1199	0.25	1131	17	0.25	1134	17
CEE	1199	0.27	1211	17	0.33	1158	15
DEV_EB	1199	0.40	20	17	0.44	19	12
PM							
Direct_EB	1127	0.32	27	12	0.42	25	12
EC	1127	0.24	1129	16	0.24	1128	17
CEE	1127	0.20	1253	12	0.29	1178	8
DEV_EB	1127	0.38	21	10	0.44	19	14
MD							
Direct_EB	1148	0.35	26	16	0.43	25	15
EC	1148	0.23	1144	16	0.22	1148	16
CEE	1148	0.25	1212	14	0.32	1158	16
DEV_EB	1148	0.37	21	16	0.41	20	13

Gengler et al Gembloux, Berry et al Moorepark, Wall et al. Edinburgh

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2) Measuring EB in milk with MIR?

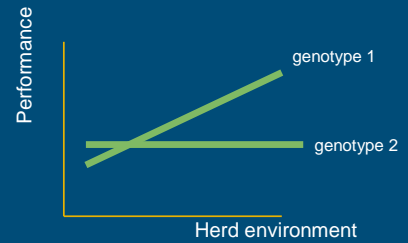- This research will provide easy and cheap measures of energy balance that can be used in management and breeding

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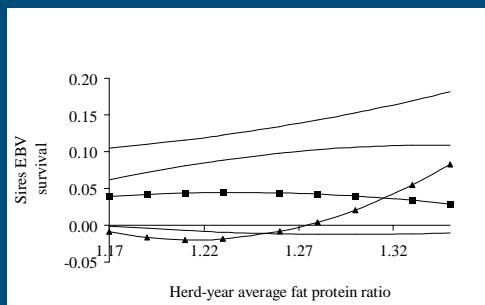
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3) Statistical tools on existing data?

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3) Statistical tools on existing data?

- Environmental sensitivity of genotypes

- Animals more sensitive, lower bandwidth to perform

Performance

genotype 1

genotype 2

Herd environment

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3) Environmental sensitivity - Macro

Sires EBV survival

0.20
0.15
0.10
0.05
0.00
-0.05

1.17   1.22   1.27   1.32

Herd-year average fat protein ratio

Calus et al

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3) Environmental sensitivity – Macro

Genetic correlation fertility and yield

0.50
0.40
0.30
0.20
0.10
0.00

Fertility farm

Production level farm

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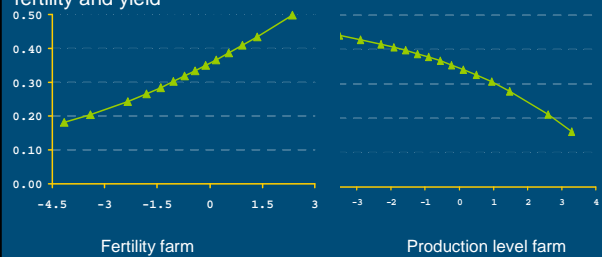
3) Environmental sensitivity – Macro

- This research should lead to selection tools that enable better matching of genetics and distinct environments

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3) Environmental sensitivity - Micro

- Not all environmental disturbances are known, measured or definable on a scale!

- What about unknown day to day disturbances, e.g. weather, feed, farmer.

- Micro environmental disturbances

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3) Environmental sensitivity - Micro

Bull A   Micro environment   Bull B

Son of Bull A   Son of Bull B

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3) Environmental sensitivity - Micro

$$P = \mu + A + E = \mu + A_m + \chi\sqrt{\sigma_E^2 + A_v}$$

$$\begin{pmatrix} A_m \\ A_v \end{pmatrix} \sim N\left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{G} \otimes \mathbf{A} \right) \qquad \mathbf{G} = \begin{bmatrix} \sigma_{A_m}^2 & \mathrm{cov}_{A_{mv}} \\ \mathrm{cov}_{A_{mv}} & \sigma_{A_v}^2 \end{bmatrix}$$

$$\chi \sim N(0,1)$$

Mulder, Bijma, and Hill, 2007; Genetics 175:1895-1910

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3) Environmental sensitivity - Micro

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3) Statistical models environmental sensitivity

- Selection for reduced micro-environmental sensitivity
  - Less sensitive to environmental disturbances → increased robustness

- These models should lead to breeding values for bulls for their environmental sensitivity at macro and micro level.

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4) Genomic selection tools?

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Use of DNA markers

- Advantage genetic markers:
  - Early information for the breeding
  - Select more reliable between sun's of the same sire

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Photos from HG

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Identifying the animals with profitable genes

- 1950: Phenotypic performance
- 1960: Daughter yield deviations from progeny test
- 1970: Phenotypic performance and pedigree information to produce breeding values bulls (BLUP)
- 1980: BLUP national scale and animal models
- 1990: Use of DNA markers: MAS approach
- 2005: **Whole Genomic Selection**

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Use of DNA markers: MAS approach

- Select DNA variation (markers) across the genome
- Genotype grandsire and sires and associate all markers with breeding values for profit traits to identify QTL
- Genotype offspring of sires for selected marker/QTL and practice Marker Assisted Selection.
- (Select new markers in same region to try and identify the gene where the mutation is (ca 250 genes).)

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Use of DNA markers: WGS approach

- Suggested in 2001
- Dramatic changes genotyping cost (€ 250):
  - a couple of markers 7 years ago,
  - few thousands markers in 2006
  - 50.000 in 2007
  - 600.000 in 2010
- Use all of them simultaneously, rather than finding the causal mutation!

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Use of DNA markers: WGS

1000+ reference animals with:
pedigree, phenotypic performance & 50.000 markers
↓
Estimate marker breeding values (calibrate markers)
↓
Accurate breeding value
young bulls and cows
also for animals with no records

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Robustmilk: can we use whole genome selection to select for traits that are difficult to measure on a large scale, for example energy balance?

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Start with NLK data only

- Experimental farm: 613 cows (1990-1997)
  - Feed intake (daily)
  - Body weight (weekly)
  - Milk production & milk contents (weekly)
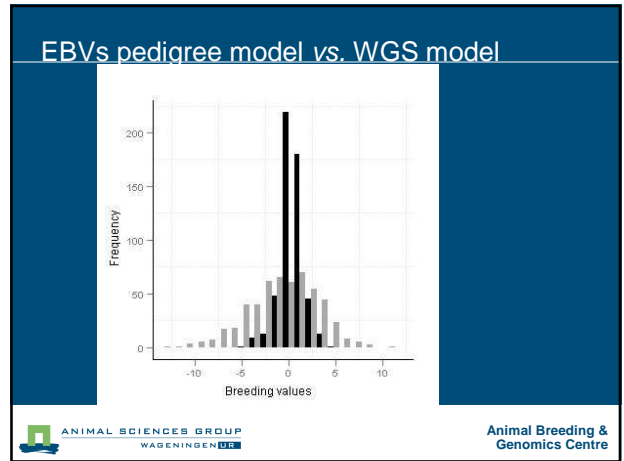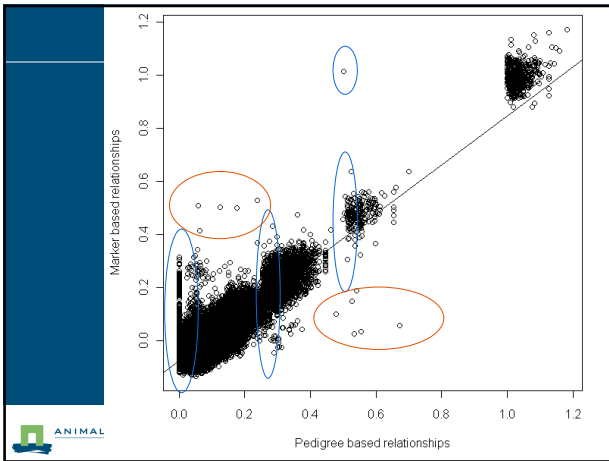- Blood samples: 588 cows (2009)
  - Illumina 50k Chip

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Genotyperen

54.001x

EBVs pedigree model *vs.* WGS model

Accuracies of predicting energy balance

	Phenotype	Breeding value
Pedigree	0.211	0.370
Pedigree + SNP	0.294	0.516
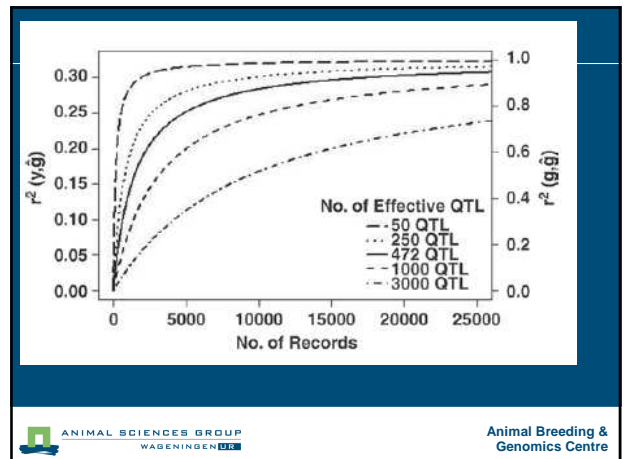
- In the future we will have breeding values for none routinely measured robustness traits, based on genomics prediction

Conclusions

- Robustness: Handling disturbances at system or animal level, versus control paradigm

- Genetic selection can make major contribution
  - multi traits selection is evolving
  - Measuring new traits (e.g EB by MIR) might help
  - Sensitivity for macro and micro disturbances
  - Genomic selection tools might ease selection