gembloux agro bio tech

Université de Liège

63rd Annual Meeting of EAAP 2012

Bratislava, Slovak Republic, August 27-31

Genetic variance in environmental sensitivity for milk and milk quality in Walloon Holstein cattle

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Introduction

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  - Economically desirable for some traits (e.g., increase of homogeneity of dairy products)

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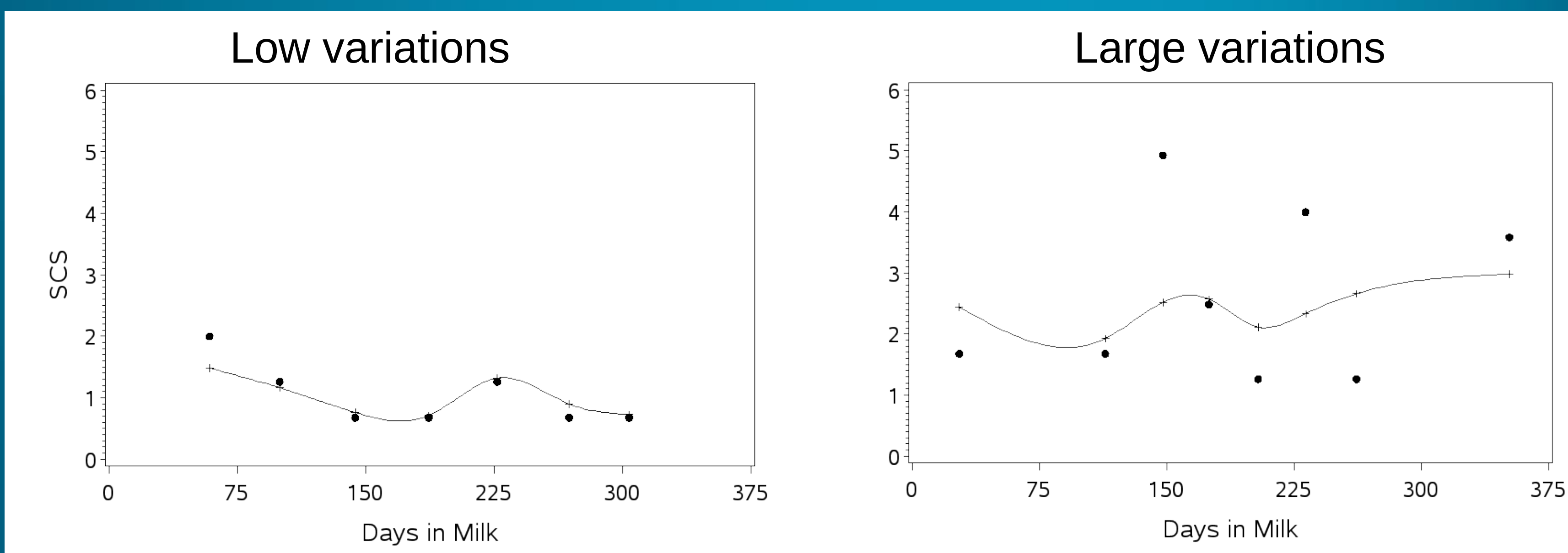
- Dairy cows robust to environmental changes
  - Economically desirable for some traits (e.g., increase of homogeneity of dairy products)
- But, variations of observations around the fitted curve during the lactation:



Introduction

- Dairy cows robust to environmental changes
  - Economically desirable for some traits (e.g., increase of homogeneity of dairy products)
- Environmental factors
  - Macro-environment
    - Identifiable (e.g., temperature)
  - Micro-environment
    - Unknown

➔ The genetic variance in micro-environmental sensitivity can be studied through genetic variance in residual variance (Hill and Mulder, 2010).

Introduction

- Potential interesting traits
  - Milk yield
  - Somatic cells score (SCS)
  - Milk fatty acids (**FA**) composition
    - Saturated FA (SFA)
      - Cholesterol, cardiovascular diseases (Haug et al., 2007)
    - Unsaturated FA (UFA)
      - Healthier for humans (Haug et al., 2007)
      - Milk fat quality properties (Palmquist et al., 1993)
    - C18:1 *cis-9*
      - Major UFA
      - Body fat mobilization in early lactation (Barber et al., 1997; Van Haelst et al., 2008)

        ➔ poor fertility performances (Bastin et al., 2012)

Aim

To study genetic heterogeneity of residual variance for milk yield, SCS, SFA, UFA and C18:1 *cis-9* separately

→ Estimation of variance components and breeding values (EBV_v) in the residual variance part

→ Using a double hierarchical generalized linear model (DHGLM; Rönnegård et al.,2010)

Data

- 26,887 Walloon Holstein first-parity cows
  - With a known sire
  - 747 herds
  - ≥ 5 cows / herd * test-day
  - ≥ 3 records / cow
  - 146,027 test-day records
    - Milk yield (kg), SCS
    - SFA (g/dL of milk), UFA (g/dL of milk), C18:1 *cis-9* (g/dL of milk)
- Pedigree
  - 86,410 animals
  - ≥ 10 cows with records / sire

Model

- Mean model

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{Z}\mathbf{p} + \mathbf{e}$$

Fixed effects

-Herd * test-day

-Lactation stage (classes of 5 DIM)

-Gestation stage

-Age at calving * season of calving * major lactation stage (classes of 73 DIM)

Model

- Mean model

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{Z}\mathbf{p} + \mathbf{e}$$

Random effects

-Additive genetic

-Permanent environmental

Random residuals

Model

- Mean model

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zu} + \mathbf{Zp} + \mathbf{e}$$

- Residual variance model

$$V(\mathbf{e}) = \exp(\mathbf{X}_v\boldsymbol{\beta}_v + \mathbf{W}_v\mathbf{h}_v + \mathbf{Z}_v\mathbf{u}_v + \mathbf{Z}_v\mathbf{p}_v)$$

Fixed effects

-Herd * calving year

-Lactation stage

-Gestation stage

-Age at calving * season of calving * major lactation stage

Model

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- Estimation of variance components and breeding values
  - DHGLM method (Rönnegård et al.,2010)
    - ➔ Iterations between the mean model and the residual variance model
  - Modified REMLF90 (Misztal, 2012)

Results

Trait	GCV	h^2_v
Milk yield	**0.17**	**$1.99*10^{-3}$**
SCS	**0.16**	**$3.47*10^{-3}$**
SFA	**0.12**	**$1.01*10^{-3}$**
UFA	**0.12**	**$3.57*10^{-3}$**
C18:1 *cis-9*	**0.12**	**$4.17*10^{-3}$**

- Low genetic coefficients of variation for residual variances (GCV; ≈ genetic SD of the residual variance model)
- In the lower range of GCV for other species (Hill and Mulder, 2010)

➔Presence of some genetic variance in environmental sensitivity

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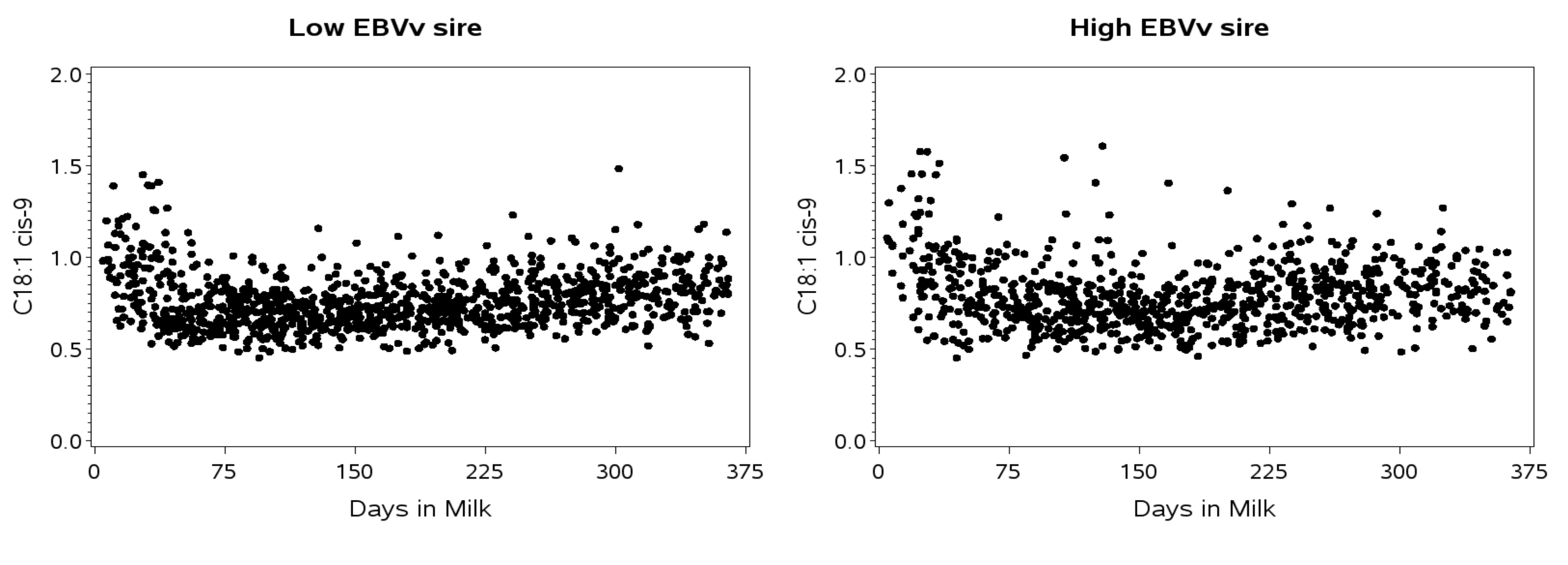
- Low heritabilities for residual variances (h^2_v)

➔ Lower than estimates in other species (0.02-0.05; Hill and Mulder, 2010)

➔ Accurate EBV_v estimated from a large data set with enough information per animal (Mulder et al., 2007)

Results



- Low EBV_v sire: less variation in observations within its daughters group than the high EBV_v sire

Results

	Variance components	Traits				
		Milk yield	SCS	SFA	UFA	C18:1 *cis-9*
Mean model	σ^2_p	1.11	0.70	0.41	0.14	0.11
	σ^2_u	0.57	0.15	1.34	0.30	0.20
Residual variance model	$\sigma^2_{h_v}$	0.13	0.18	0.14	0.20	0.19
	$\sigma^2_{p_v}$	0.53	0.95	0.42	0.33	0.30
	$\sigma^2_{u_v}$	$0.29*10^{-1}$	$0.25*10^{-1}$	$0.14*10^{-1}$	$0.15*10^{-1}$	$0.15*10^{-1}$

- Herd * test-day and permanent environmental effects

  ➔ Substantial contributions to heterogeneity of residual variance

  ➔ The DHGLM method may provide interesting information for management purposes in terms of variation.

Results

Pearson correlations between EBV and EBV_v

Milk yield	SCS	SFA	UFA	C18:1 *cis-9*
0.47	0.27	0.28	0.24	0.22

- Positive correlations
  - Higher EBV ➔ higher EBV_v ➔ ↑ residual variance

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  - Milk yield
    - Highest correlation

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- Positive correlations
  - Higher EBV ➔ higher EBV_v ➔ ↑ residual variance
  - Milk yield
    - Highest correlation
  - SCS
    - Selection of lower EBV would reduce the average level of SCS but also the residual variance of SCS, both involving fewer mastitis cases.

Results

Pearson correlations between EBV and EBV_v

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0.47	0.27	0.28	0.24	0.22

- Positive correlations
  - C18:1 *cis-9*
    - Desirable: high contents in milk with few variation during the lactation
    - But, selection of low EBV_v would decrease the average content in milk of this FA.

Results

Pearson correlations between EBV and EBV_v

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- Positive correlations
  - C18:1 *cis-9*
    - Desirable: high contents in milk with few variation during the lactation
    - But, selection of low EBV_v would decrease the average content in milk of this FA.
  - Correlations ≠ 1.00

    ➔ Selection feasible in a desired direction with proper weighting of both EBV in total merit indices

Conclusion

For all studied traits in the Walloon Holstein dairy cattle:

- Genetic and non-genetic heterogeneity of residual variance

- Genetic variance in environmental sensitivity

  ➔ Selection feasible to change micro-environmental sensitivity

- Substantial contributions of non-genetic effects

  ➔ Interesting information for management purposes in terms of variation

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Study supported by:

- Public Service of Wallonia (SPW-DGARNE; project D31-1273)
- European Commission, Directorate-General for Agriculture and Rural Development, under Grant Agreement 211708 (project Robustmilk)

This study has been carried out with financial support from the Commission of the European Communities, FP7, KBBE-2007-1. It does not necessarily reflect its view and in no way anticipates the Commission's future policy in this area.

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