Estimation of genetic variation in macro- and micro-environmental sensitivity

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- www.robustmilk.eu

Introduction

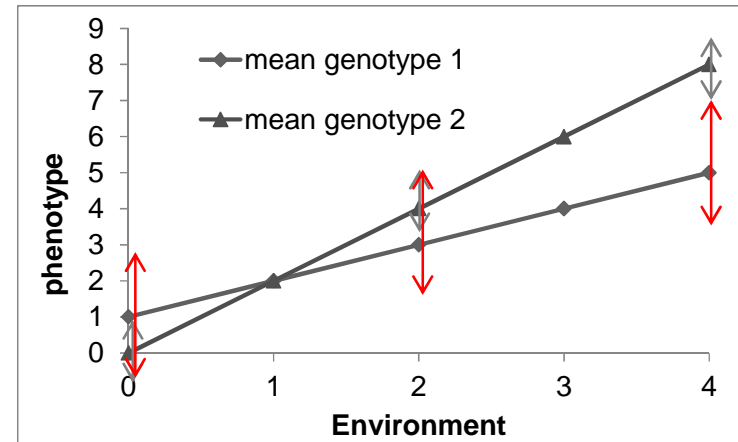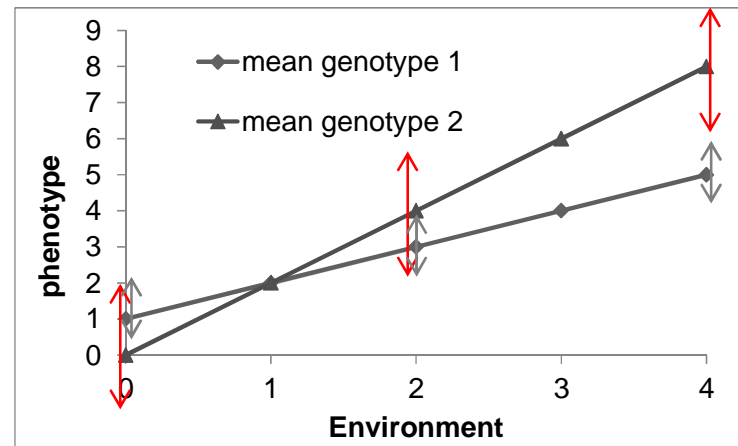What is macro- and micro-environmental sensitivity?

- ■ **Genetics of macro-environmental sensitivity**
  - ● Environmental change is known, e.g. feed, soil, herd
  - ● Measured as G x E (e.g. rg) or slope of a reaction norm

- ■ **Genetics of micro-environmental sensitivity**
  - ● Environmental change is unknown; can be animal specific
  - ● Measured as difference in environmental variance

Introduction

What is macro- and micro-environmental sensitivity?

- The genotype with the steepest slope has the largest variance

- The genotype with the steepest slope has the lowest variance

Introduction: empirical evidence

- Genetic variation in macro-environmental sensitivity
    - Genotype by environment interaction
    - Many studies have found non-unity genetic correlations
    - Significant variance in slope of reaction norm

- Genetic variation in micro-environmental sensitivity
    - Genetic heterogeneity of environmental variance
        - Hill and Mulder (2010)

- Not much known about relationship between both types of environmental sensitivity

Objective

- To develop a statistical method to estimate genetic parameters for macro- and micro-environmental sensitivity

- To investigate bias and precision of estimated genetic parameters in different designs using Monte Carlo simulation

The quantitative genetic model

Combine linear reaction norm with heterogeneous environmental variance

$$P = \mu + A_{int} + A_{sl}x + \exp(\sigma_E^2 + 0.5A_v)e$$

$$G = \begin{bmatrix} \sigma_{A_{int}}^2 & \sigma_{A_{int},A_{sl}} & \sigma_{A_{int},A_v} \\ & \sigma_{A_{sl}}^2 & \sigma_{A_{sl},A_v} \\ & & \sigma_{A_v}^2 \end{bmatrix}$$

A_{int} = breeding value for intercept
A_{sl} = breeding value for slope of linear reaction norm
A_v = breeding value for environmental variance

Statistical model

- DHGLM for heterogeneity of residual variance (Ronnegard et al., 2010)
  - Use of ASREML

- Sire model – most information comes from half-sibs in different environments

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zs}_{int} + \mathbf{Zs}_{sl}\mathbf{x} + \mathbf{e}$$

$$V(\mathbf{e}) = \exp(\mathbf{X}_v\mathbf{b}_v + \mathbf{Zs}_v)$$

- Adaptation of DHGLM: residual contains ¾ of genetic variance

Simulation

- Dairy cattle situation

- Sires with daughters that have phenotypes

- True herd mean simulated and used in statistical analysis

- 50, 100 or 200 sires

- 20, 50, 100 or 200 daughters per sire

- 100 cows per farm

- 3 levels of $\sigma^2_{A_{sl}}$ (0.025, 0.05 and 0.10)

- 3 levels of $\sigma^2_{A_v}$ (0.05, 0.10, 0.20)

- Correlations were varied; 0 and 0.5

Results

Genetic variances

100 sires with 100 daughters (averages of 100 replicates)

$\sigma^2_{A_{int}}$	$\hat{\sigma}^2_{A_{int}}$	SD($\hat{\sigma}^2_{A_{int}}$)
0.1	0.101	0.020
0.3	0.315	0.053
0.5	0.507	0.066

$\sigma^2_{A_{sl}}$	$\hat{\sigma}^2_{A_{sl}}$	SD($\hat{\sigma}^2_{A_{sl}}$)
0.025	0.026	0.008
0.050	0.053	0.014
0.100	0.104	0.021

$\sigma^2_{A_v}$	$\hat{\sigma}^2_{A_v}$	SD($\hat{\sigma}^2_{A_v}$)
0.05	0.053	0.029
0.10	0.115	0.061
0.20	0.186	0.065

- Variance components are unbiased
- Large sampling variance on $\hat{\sigma}^2_{A_v}$

Default parameters

$$\sigma^2_{A_{int}} = 0.3 \quad \sigma^2_{A_{sl}} = 0.05 \quad \sigma^2_{A_v} = 0.1 \quad \overline{\sigma^2_E} = 0.7$$

$$r_{A_{int},A_{sl}} = r_{A_{int},A_v} = r_{A_{sl},A_v} = 0$$

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Results

Genetic correlations

r_{A_{int},A_v}	$r_{A_{int},A_{sl}}$	r_{A_{sl},A_v}	$\hat{r}_{A_{int},A_v}$	SD	$\hat{r}_{A_{int},A_{sl}}$	SD	$\hat{r}_{A_{sl},A_v}$	SD
0.5	0	0	**0.554**	**0.155**	-0.028	0.136	-0.007	0.203
0	0.5	0	-0.010	0.200	**0.508**	**0.132**	-0.014	0.239
0	0	0.5	0.014	0.185	0.021	0.147	**0.558**	**0.208**

- Unbiased genetic correlations
- Large sampling variance

Default parameters

$$\sigma^2_{A_{int}} = 0.3 \qquad \sigma^2_{A_{sl}} = 0.05 \qquad \sigma^2_{A_v} = 0.1 \qquad \overline{\sigma^2_E} = 0.7$$

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Results

Design

$$r_{A_{int},A_{sl}} = r_{A_{int},A_v} = r_{A_{sl},A_v} = 0 \qquad \overline{\sigma_E^2} = 0.7$$

NS	ND	$\sigma_{A_{int}}^2$	SD	$\sigma_{A_v}^2$	SD	$\sigma_{A_{sl}}^2$	SD
		0.300		0.100		0.050	
100	20	0.301	0.057	0.120	0.113	0.063	0.038
100	50	0.309	0.051	0.099	0.060	0.056	0.020
100	100	0.315	0.053	0.107	0.046	0.054	0.015
100	200	0.301	0.046	0.093	0.024	0.053	0.009
50	100	0.312	0.079	0.107	0.064	0.053	0.018
100	100	0.315	0.053	0.107	0.046	0.054	0.015
200	100	0.301	0.033	0.099	0.028	0.053	0.009

Minimum design: 100 sires with 100 daughters each

Conclusion

- Method gives unbiased estimates of variance components

- Large sampling variance on genetic correlations

- Designs with at least 100 sires with each 100 daughters are required

- Application:
  - More insight in genetics of environmental sensitivity
  - Breeding more resilient animals
  - Next step: application of model to dairy cattle data

Thank you for your attention!!

Conclusion

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  - More insight in genetics of environmental sensitivity
  - Breeding more resilient/robust animals
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