

# Variance component and breeding value estimation for environmental sensitivity in dairy cattle

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## Background

Animal robustness, or environmental sensitivity, may be studied through individual differences in residual variance.

These differences appear to be heritable, and there is a need to fit models to predict breeding values explaining differences in residual variance.

## Aim

To estimate breeding values for environmental sensitivity (vEBV) in milk yield and somatic cell score, and their associated variance components, on a reasonably large dairy cattle data set having almost 1.7 million records.

The estimates are used to assess possibilities to select for robustness in Swedish Holstein dairy cattle.

**Table 1.** Estimated parameters for milk yield and somatic cell score in the exponential heterogeneity model (standard errors within brackets)

	Variance components	Milk yield	Somatic cell score
Mean Model	Genetic	8.78 (0.21)	0.28 (0.01)
	Perm. env.	12.40 (0.14)	1.03 (0.008)
Residual Variance Model	Genetic	0.049 (0.003)	0.046 (0.004)
	Perm. env.	0.37 (0.003)	0.61 (0.004)

## Material and Methods

Test-day somatic cell score and milk yield recorded between 2002 and 2009 from Swedish Holstein dairy cattle (Table 2) were analyzed univariately.

Variance components (VCE), ordinary breeding values and vEBVs were estimated using ASReml, applying the methodology for double hierarchical generalized linear models (Rönnegård et al. 2010 GSE 42:8). Estimation using ASReml took less than 7 days on a Linux server.

## Results

The VCE for milk yield (Table 1) were moderate to large with quite small standard errors.

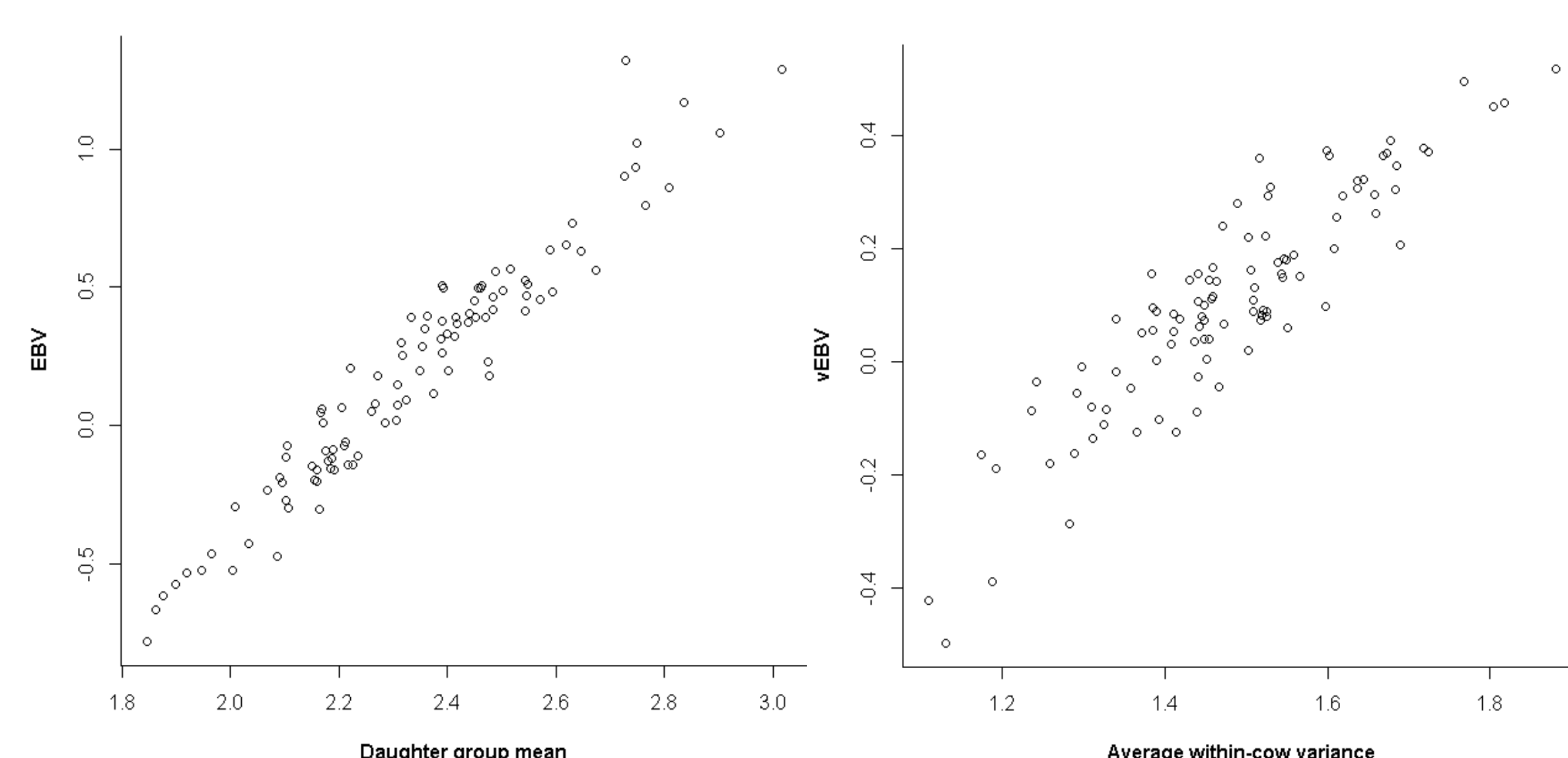
The VCE for somatic cell score were moderate (Table 1). The EBV and vEBV were clearly related to the empirical daughter group means and daughter group averages of within-cow variances (Figure 1).

The genetic standard deviations for environmental variance were 0.22 and 0.21, for milk yield and somatic cell score, respectively.

## Conclusion

A change in vEBV of one genetic standard deviation for one of these traits would alter the residual variance by 20% in Swedish Holstein.

Estimation of variance components, EBV and vEBV, is feasible for large dairy cattle data sets using standard variance component estimation software.



**Figure 1.** EBV and vEBV for somatic cell score plotted against daughter group means and daughter group averages of within-cow variances, respectively, for the 100 sires having largest daughter groups.

**Table 2.** Description of the Swedish Holstein Data

	Summary of all data	Milk yield		Somatic
		(liter/day)	cell score	
No. of records	1,693,154	Mean	29.13	2.36
No. of animals	177,411	Median	29.20	2.05
# herds	1,759	Variance	45.5	2.8
# herd-test-days	21,570			