

## HERD SPECIFIC RANDOM REGRESSION CURVES IN A TEST-DAY MODEL FOR PROTEIN YIELD IN DAIRY CATTLE

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### INTRODUCTION

Many dairy cattle organisations consider to introduce a test-day model for breeding value estimation for milk production traits. Several authors have used random regression models to estimate genetic parameters, which have the advantage that the covariance matrices are estimated directly from the data. However, some authors have reported increasing variances at the beginning and end of the lactation trajectory, which were not consistent with multi-trait results (van der Werf *et al.* 1998; Jamrozik and Schaeffer 1997; Pool 2000; Kettunen *et al.* 2000). To reduce this effect, Gengler and Wiggans (2001) have suggested to add a random effect of herd x lactation stage to the model. The aim of this study was to analyse the effect of herd specific random regression curves on the estimated genetic parameters in a test-day model for protein yield.

### MATERIAL AND METHODS

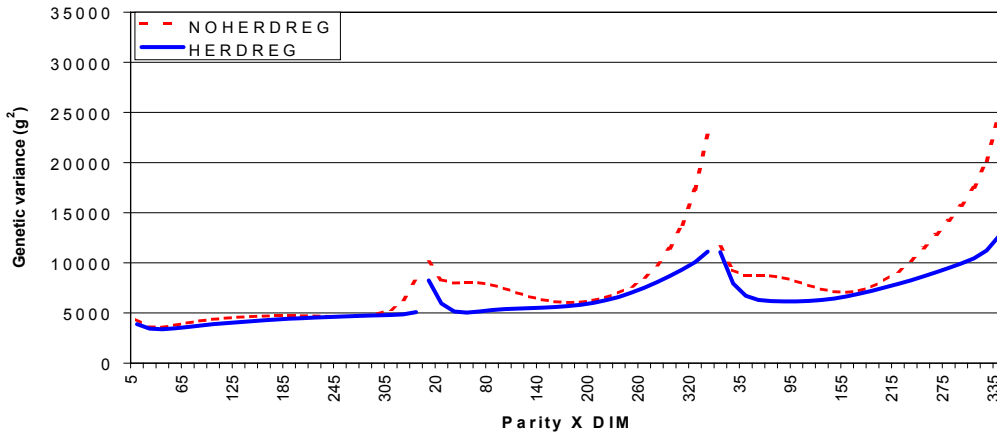
**Model without herd regression (NOHERDREG).** A data set of 498,724 test-day protein yield records from 23,700 Holstein cows on 490 herds was used (Pool 2000). This data set included only test-day yields from lactations 1, 2 and 3 between 5 and 335 days in milk (DIM). Lactations were required to have at least 6 test-day records of which one before DIM 80 and one after DIM 280. Herd-testdates (HTD) with less than 10 records were omitted and only records from cows with at least 9 paternal half sibs were used. Test-day records were analysed with a model including four fixed effects: year-season of calving, parity x age at calving, weekly classes of DIM and HTD. The additive genetic and the permanent environmental effects were modelled as random regression effects with fourth-order Legendre polynomials for every lactation. Using three lactations, this resulted in 15 genetic and 15 permanent environmental solutions per cow. Residuals were divided into 10 classes within lactation, to account for heterogeneous variances across lactation stages (de Roos *et al.* 2001).

**Model with herd regression (HERDREG).** A new, larger data set was used for this analysis, but with similar data edits. The data set comprised 857,255 test-day protein yield records from 43,990 cows on 544 herds (de Roos *et al.* 2001). Test-day records were analysed with a similar model as NOHERDREG, but including also a random regression effect to model herd specific production curves. The random regression of herd x 2-year of calving was modelled with fourth-order Legendre polynomials for every lactation, i.e. 15 coefficients per herd x 2-year.

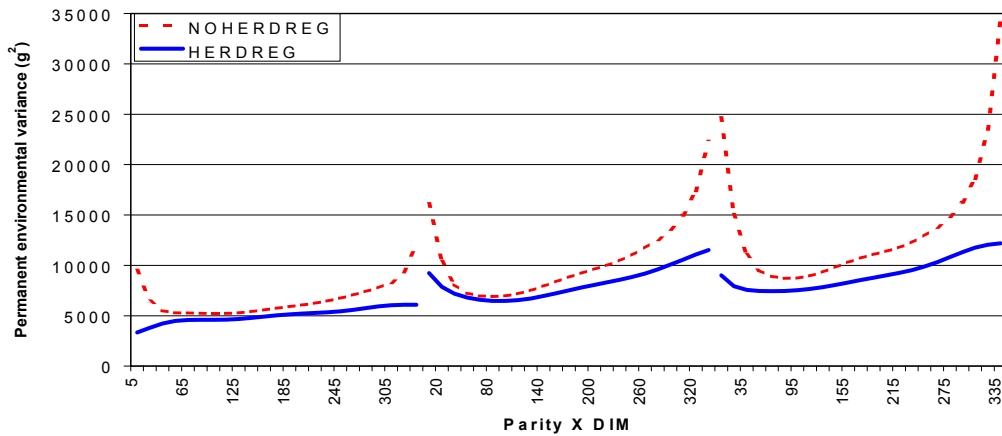
Parameters were estimated using Gibbs sampling techniques (Pool 2000).

**RESULTS AND DISCUSSION**

Genetic variances at the end of the lactation and around DIM 65 in lactation 2 and 3 were substantially lower for HERDREG than for NOHERDREG (Figure 1). Permanent environmental variances were lower for HERDREG, especially at the beginning and end of the lactation (Figure 2). This is much more consistent with studies where lactation parts have been analysed in a multiple trait model (van der Werf *et al.* 1998).



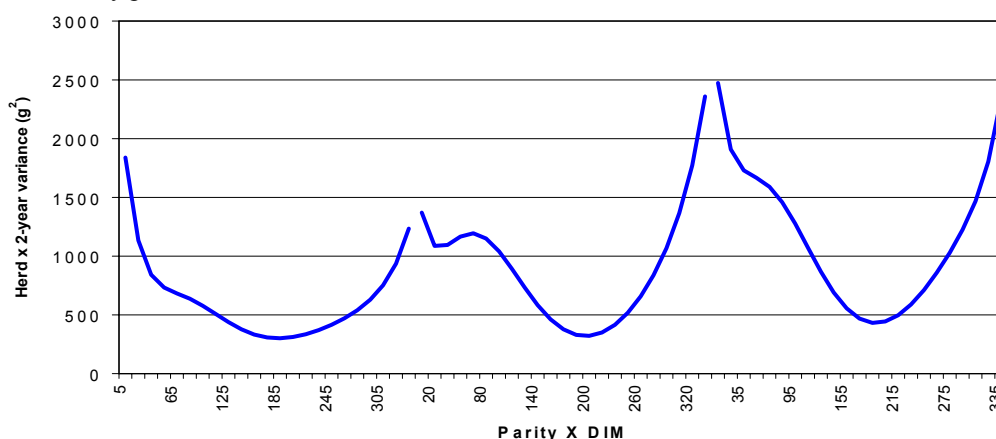
**Figure 1. Genetic variances for test-day protein yield across parity 1, 2 and 3 and DIM 5 until 335 for NOHERDREG and HERDREG**



**Figure 2. Permanent environmental variances for test-day protein yield across parity 1, 2 and 3 and DIM 5 until 335 for NOHERDREG and HERDREG**

Herd x 2-year variance was high at the beginning and at the end of the lactation (Figure 3) and correlations between beginning and end of the lactation were negative. This indicates that this effect primarily models persistency across herds, whereas the mean effect of herd is modelled with the HTD effect. Differences in persistency across herds may be caused by differences in

feeding systems, for example herds with flat feeding systems may have a ration that is nutritionally poor for fresh cows but rich for cows at the end of their lactation.



**Figure 3. Variances of herd x 2-year for test-day protein yield across parity 1, 2 and 3 and DIM 5 until 335**

Heritabilities of test-day protein yield were similar in lactation 1 but in lactation 2 and 3, HERDREG showed lower heritability around DIM 65 and at the end of the lactation. Genetic correlations between DIM 65 and DIM 335 were around 0.30 higher for HERDREG than for NOHERDREG. More research is needed to study the effect of the larger variances at the end of the lactation in NOHERDREG on estimated breeding values, particularly for cows with short lactations. Maybe, the higher variances at the end of the lactation are compensated by the lower genetic correlation with the beginning of the lactation and therefore do not have a large effect on estimated breeding values for 305-day yield.

The heritability for 305-day protein yield was between 0.44 and 0.47 for every lactation for NOHERDREG as well as HERDREG. However, genetic correlations between lactations were around 0.08 lower for HERDREG. The heritability for persistency, computed as yield at DIM 280 minus yield at DIM 60 and averaged over parities, was 0.42 for NOHERDREG and 0.18 for HERDREG. Genetic correlations between lactations for persistency were 0.10 (lactation 1 and 2) to 0.25 (lactation 2 and 3) lower for HERDREG than for NOHERDREG.

The inclusion of a random regression effect for herd x 2-year had large influence on genetic parameters. At the beginning of the lactation, it reduces the permanent environmental variance. At the end of the lactation, especially in lactation 2 and 3, it also severely reduces the genetic variance. This indicates that if the herd specific curves are not modelled separately, its variance will partly be absorbed by the genetic effect. This is also very likely given the fact that cows usually have their dam and progeny in the same herd, which makes it more difficult to distinguish genetic effects from herd effects. This causes an overestimation of the genetic variances, especially for persistency and an overestimation of genetic correlations across lactations.

An interesting subject for further research is that the difference in genetic and permanent environmental variance at the end of the lactation between NOHERDREG and HERDREG cannot completely be explained by the variance of the herd x 2-year effect. For example, at DIM 335 of lactation 3 the genetic variance is 25,000 g<sup>2</sup> for NOHERDREG and 13,000 g<sup>2</sup> for HERDREG and the permanent environmental variance is 34,000 g<sup>2</sup> and 12,000 g<sup>2</sup>, respectively, whereas the herd x 2-year variance in HERDREG is only 2400 g<sup>2</sup>. It has been questioned whether cows with only data in lactation 1 may cause the high variances at the end of lactation 2 and 3 in NOHERDREG, because their genetic and permanent environmental regression curves of lactation 2 and 3 have to be estimated from lactation 1 data. However, genetic and permanent environmental variances hardly changed for NOHERDREG when only cows with three lactations were used (unpublished data).

The effect of a different data set for NOHERDREG and HERDREG is not expected to have a large effect on the results, because de Roos *et al.* (2001) used the HERDREG data set also in another random regression model without herd specific regression curves and found very similar genetic parameters as in NOHERDREG.

As soon as genetic parameters with the HERDREG model are also obtained for test-day milk and fat yield, the random regression test-day model for the national genetic evaluation in The Netherlands will be extended with a herd specific random regression effect.

#### CONCLUSION

The inclusion of a herd specific random regression effect reduces the genetic and permanent environmental variances at the beginning and end of the lactation. The obtained pattern of genetic variances and correlations across the lactation are more consistent with results from multi-trait analyses. Therefore, it is recommended to include a herd specific random regression effect in the statistical model when variance components for test-day yield are estimated.

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