

## ESTIMATION OF GENETIC PARAMETERS FOR DAILY MILK PERFORMANCE OF EAST FRIESIAN MILK SHEEP BY RANDOM REGRESSION MODELS

A. Horstlick, H. Hamann and O. Distl

Institute of Animal Breeding and Genetics, School of Veterinary Medicine Hannover, Bünteweg 17p, 30559 Hannover, Germany

### INTRODUCTION

The East Friesian milk sheep originates from Northern Germany and North Holland. This milk sheep breed is well known for its high milk production capacity and prolificacy. After a dramatic decline of the population numbers of East Friesian milk sheep in the fifties to the seventies of the 20th century milk production with milk sheep is now increasing in Germany. However, genetic parameters and the development of breeding programmes have not been studied for East Friesian milk sheep. Therefore, the objective of this investigation is to estimate genetic parameters for milk yield traits, milk fat content, milk protein content and somatic cell score using random regression models.

### MATERIAL AND METHODS

**Data.** The milk performance data according to the official ICAR-protocol for method A were provided by the sheep breeding associations of Lower Saxony, Westphalia and Bavaria. The records were collected in 89 herdbook farms from 1992 to 2000. The data set included 7545 test day records of 918 East Friesian milk sheep with 1380 lactation records. The average daily milk performance was  $2.43 \pm 1.11$  kg milk,  $136 \pm 68$  g fat,  $115 \pm 51$  g protein,  $5.74 \pm 1.51$  fat percentage and  $4.84 \pm 0.79$  protein percentage. The average daily somatic cell score (SCS) was  $4.28 \pm 2.36$ . Nearly all milk sheep were lambing between January and March, whereby twins (55.6%) and triplets (24.5%) were most frequent. The lactation number of ewes varied from 1 to 11. The pedigree file contained a total of 4267 animals, of which 261 were sires and 630 dams. 52 granddams and 203 dams had own milk performance records. The average number of progeny per sire was only 3.5.

**Statistical analyses.** The variance-covariance components in dependence of test days were estimated by random regression models. The covariance functions between any two records measured at given test days were derived from orthogonal polynomials of fourth order (Kirkpatrick *et al.*, 1994). The analysis was performed by using DFREML, version 3.0 $\beta$  (Meyer, 1998).

The model for milk performance traits and somatic cell score was as follows:

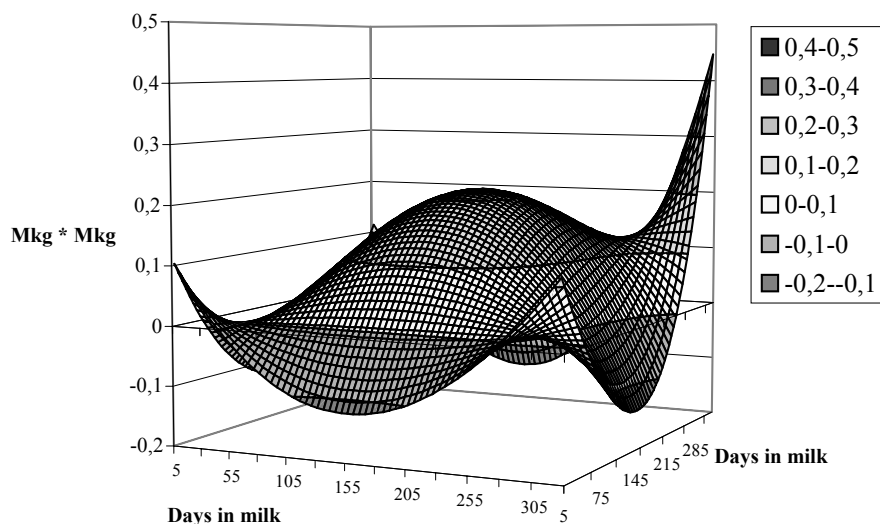
$$Y_{ijklmnopqrx} = \mu + R_i + S_j + J_k + L_l + T_m + H(R)_{in} + b_1 \text{DIM}_p + b_2 (\text{DIM}_p)^2 + b_3 \log \text{DIM}_p + b_4 (\log \text{DIM}_p)^2 + p_q [1 \ t \ t^2 \ t^3] + a_r [1 \ t \ t^2 \ t^3] + e_{ijklmnopqrs}$$

where  $Y_{ijklmnopqrx}$  represents the vector for milk performance traits and SCS and  $\mu$  a model dependent constant. The fixed effects were as follows: R = region (1-4), S = lambing season (1-3), J = lambing year (1-8), L = lactation number (1-5), T = test day (1-73), DIM days in milk,  $b_1 - b_4$  = fixed regression coefficients; herd within region (H(R), 1-89), the permanent environmental effect of the ewe (p, 1-918), the additive genetic effect of the animal (a, 1-4267) and the residual effect were treated as randomly distributed variables. Random regression coefficients of days in milk ( $t \ t^2$

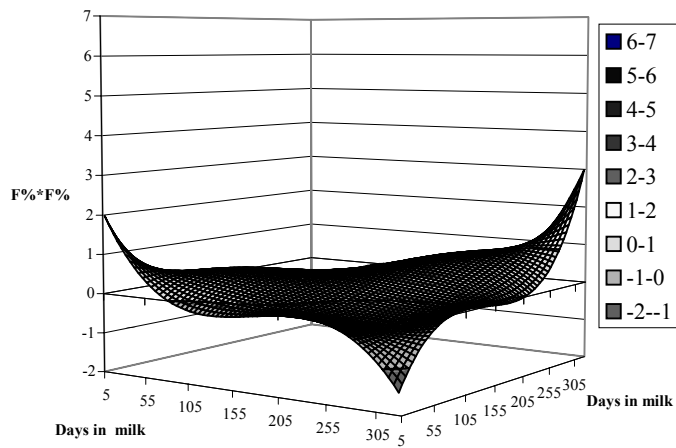
t<sup>3</sup>) on the permanent environment effect of the ewe and the additive genetic effect of the animal were modelled as orthogonal polynomials.

## RESULTS AND DISCUSSION

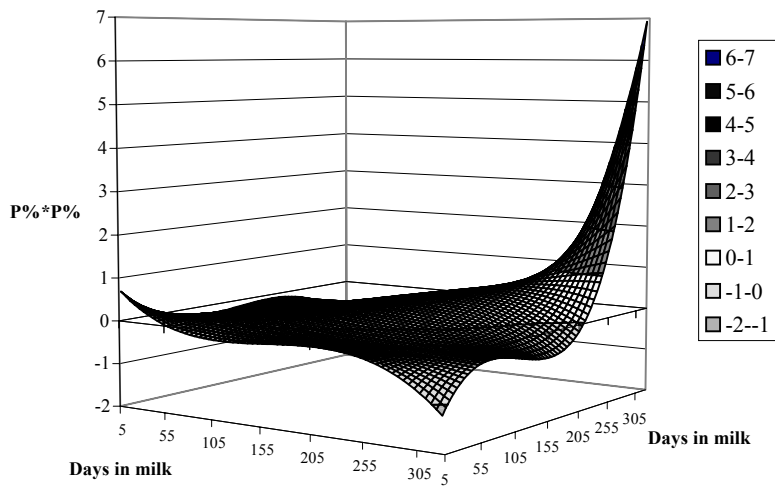
The additive genetic variance for milk yield varied between  $s_a^2 = 0.023$  and  $0.392 \text{ kg}^2$  (figure 1). The additive genetic covariances between test days ranged from -0.2 to 0.5. The additive genetic variance and covariance for milk fat and milk protein content are shown in figures 2-3. The average heritability estimates for daily milk yield were  $h^2 = 0.25 \pm 0.03$  (range: 0.03 to 0.70), for daily fat content  $h^2 = 0.46 \pm 0.09$  (range: 0.30 to 0.70), for daily protein content  $h^2 = 0.63 \pm 0.12$  (range: 0.44 to 0.92), and for SCS  $h^2 = 0.17 \pm 0.02$  (range: 0.14 to 0.37). The random regression models lead to higher additive genetic variances and heritability estimates as compared to the test day model with fixed regression for the same data set (Horstik *et al.*, 2001). The increase of the additive genetic variances for all traits analysed at the end of lactation may be due to the low number of test day records at this recording period. In order to avoid overestimation of additive genetic variances only herds with more than 20 records could be used in the random regression models. The estimates obtained for milk yield and fat content were in a similar range as reported by Barillet and Boichard (1987) for Lacaune sheep, whereas Baro *et al.* (1994) and Mavrogenis and Papachristoforou (2000) obtained higher estimates. The heritability estimates for protein content and SCS from random regression models were higher than those reported in literature (Barillet and Boichard, 1987 ; Baro *et al.*, 1994 ; El-Saied *et al.*, 1998).



**Figure 1. Additive genetic covariance functions of milk yield (Mkg) in dependence of the day of lactation**



**Figure 2. Additive genetic covariance functions of the fat content (F%) in dependence of the day of lactation**



**Figure 3. Additive genetic covariance functions of the protein content (P%) in dependence of the day of lactation**

## CONCLUSION

Additive genetic variances and heritabilities of daily milk performance traits and SCS recorded on dairy farms for East Friesian milk sheep are sufficiently high to achieve genetic progress. Random regression models can be used very efficiently for estimation of genetic parameters and for prediction of breeding values.

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