Genetic Parameter Estimates for Test Day Milk Yields of a Holstein-Friesian Herd in Turkey by a Random Regression Model

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A Random Regression Model allows the shape of the lactation curve to differ for each cow by the inclusion of random regression coefficients for each animal

Material and Methods

Data set comprised monthly 1506 test day milk yields of Holstein-Friesian dairy cattle obtained from Sarmisakli Farm, where is in Northwest region of Turkey. The cows were daughters of 56 sires and 119 dams, calved from 1987 through 1993. Total of 139 animals evaluated and there were 184 test date subclasses. Data were required to have at least 150d and at maximum 308d (11 x 28) long of first lactations.

Variance components were estimated by derivative-free REML (DFREML) using a Random Regression Model with the DXMRR statistical package. Additive genetic and permanent environmental (co)variances at the fixed regressions were modeled with the same order Legendre polynomial regressions. Residual variance was assumed to be constant throughout lactation. The following Random Regression Model was used in the analysis:

$$y_{ij} = HTD + \sum_{m=0}^{4} \beta_{im} Z_{ijm} + \sum_{m=0}^{4} \alpha_{im} Z_{ijm} + e_{ijk}$$

HTD :Fixed effect of test-date (assumed to be similar for all ages)
β_{im} :mth additive genetic random regression coefficients for animal i
α_{im} :mth permanent environmental random regression coefficients for animal i
Z_{ijm} :mth covariable for record j of cow i
e_{ij} :random residual effect
$Z_{ij} = (Z_{ij0} Z_{ij1} Z_{ij2} Z_{ij3} Z_{ij4})'$
$= (1\ c\ c^2\ d\ d^2)$ c:DIM(Days in Milk)/305 d:ln(305/DIM)

Significant differences in the fit of models were tested using a χ^2 test of the likelihood.

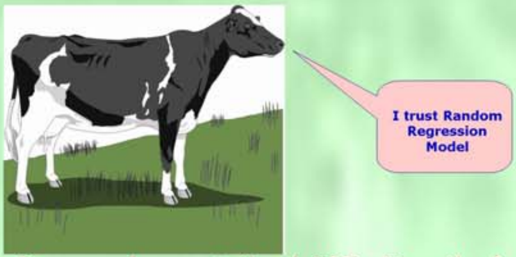
Results and Discussion

Table 1. Maximum log likelihood values for different orders of fit with ME=1

Order of Regression Model	Number of parameters	Log likelihood	Changes in Log likelihood	χ^2
2	7	-2752.14	-	-
3	13	-2659.44	93*	12.59
4	21	-2643.64	16	15.51
5	31	-2620.24	23*	18.31
6	43	-2616.20	4	21.03
7	57	-2610.32	6	23.68

* P<0.05

The third order polynomial gave the best fit when considering the largest changes in log likelihood.



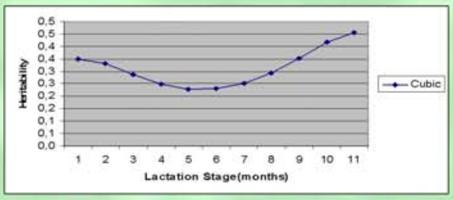


Figure 1. Heritability estimates of test day milk yields using third order of fit

Heritability estimates and co(variances) were found higher for yields at the beginning and end of lactation stages.

Table 2. Matrix of additive genetic (co)variances between test day milk yields (1-11)

8.73										
8.28	7.85									
7.99	7.59	7.33								
9.89	7.49	7.24	7.15							
7.97	7.56	7.31	7.22	7.28						
8.22	7.80	7.54	7.44	7.51	7.74					
8.64	8.20	7.92	7.82	7.89	8.13	8.56				
9.24	8.76	8.47	8.36	8.43	8.70	9.15	9.78			
10.01	9.49	9.18	9.06	9.14	9.43	9.91	10.59	11.48		
10.95	10.39	10.04	9.91	10.01	10.32	10.85	11.59	12.56	13.75	
12.07	11.45	11.07	10.93	11.03	11.37	11.95	12.78	13.85	15.15	16.70

Because of computational difficulties, the feasible analysis of the Random Regression Model depends on the order of fit and assumptions on measurement error structures. A constant error assumption, however, causes residual variance in early lactation to be underestimated. Underestimated error directly affects the estimates of total variance and hence the heritabilities of yields. This may partly explain the inconsistent of h^2 in early and late stages of lactation. Further investigations are needed on this topic.