

GENETIC PARAMETERS OF TEST DAY MILK YIELD FOR HOLSTEIN, BRUNA AND MODICANA BREEDS IN SOUTHEASTERN SICILY USING AN AUTOREGRESSIVE MULTIPLE LACTATION ANIMAL MODEL

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INTRODUCTION

The Consorzio Ricerca Filiera Lattiero-Casearia (Co.R.Fi.La.C.) is a dairy research center located in the province of Ragusa, Sicily, that focuses on milk production, manufacture and marketing of Ragusano cheese, and farmer outreach programs. Created with grant funding from the public sector, this Center was the natural response to the demand by dairy producers for research and extension education assistance to meet competitiveness challenges in the European community (Licitra *et al.*, 1998). Two main production systems characterize the dairy industry in this region. Herds of Modicana cows of modest size are generally managed under a traditional system based on pasture. Larger herds of higher yielding Brown Swiss (Bruna) and Holstein cows are managed under a more input-intensive system.

In this context, one priority for Co.R.Fi.La.C. was to genetically evaluate the local dairy breeds (Holstein, Bruna and Modicana) managed under these conditions. Therefore, objectives of this study were to estimate variance components and genetic parameters using autoregressive test day (TD) animal models. Given the acknowledged potential of these models (Carvalheira *et al.*, 1998 ; 2001) to reduce the size of residual variance components, it is expected that genetic differences among the animals will be amplified, thus providing more accurate estimates of individual genetic merit, larger additive genetic components of variance and heritabilities for daily milk yields. Estimates of systematic environmental effects were also of interest for evaluation of herd management and individual cow productivity.

MATERIAL AND METHODS

Data. The Italian Dairy Herd Improvement Association and the Co.R.Fi.La.C. provided the data for each breed for this study and consisted of: herd code, cow identification, test date, age at calving, lactation number (L), days-in-milk (DIM) and daily milk yield. The original data were for calvings from 1994 to 1999. The editing process was performed according to pre-defined criteria conforming the data for the genetic analysis following assumptions of the autoregressive test-day animal model (Carvalheira *et al.*, 2001). This included keeping only records from the first three L, deleting records that missed relevant information or that were considered outliers, and DIM less than 5 or greater than 305 days. Cows were deleted with only one daily yield per L or with age, test date, or DIM out of sequence in a L. Records from cows

with DIM interval less than 15 or greater than 75 days were also excluded. The normality of the data was also tested for yields at each DIM by L.

The Holstein data set was the largest of the three breeds. Table 1 shows the number of records available for each breed, giving an idea of relative importance in milk contributions in this region. The final data were from 15,161 Holstein, 3,049 Bruna and 660 Modicana cows. Pedigree files of sires and dams were created for each breed, which totaled 19,868 Holstein, 4,598 Bruna, and 1,037 Modicana animals, respectively.

Table 1. Number of test day milk records available before and after the editing process for Holstein, Bruna and Modicana breeds^A

Data	Holstein	Bruna	Modicana
Original	378,354	95,330	18,553
Final data	214,650	44,768	8,669
1 st Lactation	91,464	17,139	3,490
2 nd Lactation	70,708	14,769	2,767
3 rd Lactation	52,478	12,860	2,412

^ACalvings from January 1994 to December 1999.

Statistical-genetic model. The process of finding the variance components that maximized the likelihood function was based on derivative free REML methodology (Smith and Graser, 1986) that was applied to an autoregressive TD animal model. The convergence criterion was met when the variance of the simplex was less than 10^{-8} . The occurrence of local maxima was checked by two consecutive cold starts without significant change in the log-likelihood (up to 4 decimal places). The autoregressive TD animal model was as follows :

$$y_{ijklmnpqo} = \text{HTD}_i + \text{Age}_j(\mathbf{H}_k) + \text{DIM}_m(\mathbf{H}_k \mathbf{L}_l) + \mathbf{a}_n + \text{LTE}_p + \text{STE}_q + \mathbf{e}_{ijklmnpqo},$$

where, y is the TD observation, **HTD** is the fixed effect of herd-test-date, **Age(H)** is the fixed effect of the age at calving nested within herd, **DIM(H L)** is the fixed effect of DIM nested within herd and lactation, **a** is the random effect of the animal, **LTE** is the random effect of the long-term environmental effects accounting for the autocorrelations generated by the cow across repeated lactations, **STE** is the random effect of short term environmental effects accounting for the autocorrelations due to cow within each lactation, and **e** is the random residual effect that is assumed to be normally distributed.

A detailed description of the model expectations and (co)variance structure is in Carvalheira *et al.* (2001). To help ensure accuracy at least 4 observations in each contemporary group were required. Farms (herds) were grouped based in cluster analysis using the method of Ward (SAS, 1989), where phenotypic mean and standard deviation in first L defined similarity between herds. It was assumed that farms with similar phenotypic mean and standard deviation had similar management.

RESULTS AND DISCUSSION

The magnitude of variance component estimates for the STE effects (Table 2) indicated that an important part of the nongenetic variation due to the repeated effect of cow within an L was accounted by this effect. The TD records were consistently highly correlated within a lactation, ranging from 0.55 to 0.76.

Table 2. (Co)variance components and genetic parameters for daily milk yield for Holstein, Bruna and Modicana breeds

Component	Holstein	Bruna	Modicana
Genetic variance ^A	7.204	7.189	3.309
Error variance	3.901	1.511	0.801
LTE ^B variance	11.578	6.015	<0.000
LTE autocorrelation	0.215	<0.000	0.800
STE ^C variance (L1) ^D	4.792	4.599	5.552
STE autocorrelation (L1)	0.660	0.553	0.696
STE variance (L2) ^D	10.950	7.144	8.597
STE autocorrelation (L2)	0.668	0.554	0.724
STE variance (L3) ^D	14.922	9.038	11.325
STE autocorrelation (L3)	0.614	0.552	0.757
Phenotypic variance (L1)	27.474	19.314	9.662
Phenotypic variance (L2)	33.633	21.859	12.708
Phenotypic variance (L3)	37.604	23.753	15.436
Heritability (L1)	0.262	0.372	0.342
Heritability (L2)	0.214	0.329	0.260
Heritability (L3)	0.192	0.303	0.214

^AVariances are in kg².

^BLong term environmental effects.

^CShort term environmental effects.

^DL1 = 1st Lactation; L2 = 2nd Lactation; L3 = 3rd Lactation.

Persistent environmental effects did not have a major effect on milking performance of Modicana cows in this study. A small LTE variance associated with a high correlation (Table 2) may explain the small variability in cow performance between lactations for this breed, which afforded relatively little impact from events during juvenile growth and dry periods. On the other hand, differently from results obtained from US Holsteins (Carvalho *et al.*, 1998), the LTE contribution for the Holstein and Bruna breeds was an important component, although with a low correlation (Table 2). This pattern may be expected from breeds with high genetic potential, grown in relatively harsh environments (like southeastern Sicily) where events during juvenile growth and especially those occurring during the cow's productive lifetime (e.g., udder injury, infection, etc.), may have a marked effect on the expression of the trait.

Among these breeds, Modicana had the smallest additive genetic variance (Table 2). There is a scale effect in this dual purpose breed, shown by smaller phenotypic means and variances. Other reasons are more data related. The population size of this breed is small, with a relatively small distribution (few farms in a limited area), and their genes are being shared with some frequency, suggesting a restricted gene pool with a restricted genetic variance. Nevertheless, this breed presented (Table 2) medium to high heritabilities in the first three lactations, an indication of ample opportunity for genetic gain by selection. The estimated heritabilities for these breeds and lactations are within the range reported in the literature (e.g., Stanton *et al.*, 1991 ; de Alba and Kennedy, 1994 ; Reents *et al.*, 1994 ; Carvalheira *et al.*, 1998).

Autoregressive TD animal models utilize monthly milk yields to evaluate herd management effects and individual cow productivity. Estimated effects of age and lactation curves were determined from the data available for individual farms. Corresponding milk management curves indicate the within-year variation in average daily milk yield and seasonal effects on quality, availability and cost of feed. Comparing L curves is also a tool for identifying limitations in nutrition and management programs, and in helping managers and consultants with decision-making.

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