ESTIMATION OF GENETIC PARAMETERS FOR DAIRY EWES USING RANDOM REGRESSION ANIMAL MODEL

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Abstract

The objective of the study was to compare different models in the estimation of genetic parameters for test-day milk records in Churra da Terra Quente (CTQ) ewes. Data comprising 10700 test-day measurements from the first lactation of 3096 ewes were used in analysis of morning milk yield (MMY), afternoon milk yield (AMY), and daily milk yield (DMY). Records before 30 and after 150 days in milk were discharged. Average milk yield was 217.1 g, 198.3 g, and 415.4 g for MMY, AMY, and DMY, respectively. Pedigree le contained 5494 animals. Simple fixed regression animal model (FRM) and random regression animal models (RRM), where orthogonal Legendre polynomials of order 3 were used. The REML method as implemented in the VCE-5 programme was applied for estimation of (co)variance components. Statistical models contained linear regression on days in milk and number of lambs born as fixed effects, while fock-test-day, permanent environment of a ewe, and direct additive genetic effect were treated as random. Estimates of heritability from FRM were low, from 2.9% for AMY to 8.2% for MMY. Heritability estimates from RRM presented a maximum at 60 days of lactation (≥ 33.9%) and decreased to values lower than 2.5% at the end of lactation. There is a potential for using random regression to model additive genetic and permanent environmental effects for genetic evaluation in CTQ ewes, especially from the first two thirds of lactation when decision on mating has to be taken.

Key words: Genetic evaluation, covariance, heritability, ewes

INTRODUCTION

Genetic improvement of the milking ability is the first tool to improve cheese production, and consequently the income to the producers. Genetic evaluations are based on variances, covariances, heritabilities, genetic and phenotypic correlations, these parameters are also necessary to predict direct and correlated response to selection [13]. Genetic parameters are characteristics of the particular populations, and environmental conditions, and may change over time due to selection and management decisions [2]. During long time genetic evaluation of dairy traits was based on estimated complete (305-d in cows and 150-d in sheeps) lactation yield, however, this production is not real (observed) but estimated, and it is necessary to correct this trait for known environmental factors. In the last decade a new statistical methodology was developed to use the individual longitudinal test-day records, this procedure considers genetic, and environmental effects on test-day basis [9]. This methodology presents several advantages over the traditional 150-d lactation models, among these are: 1) ability to account for environmental effects of each test-day; 2) better possibility to account for heterogeneity of variation along trajectory [11]; and 3) each measurement can be adjusted more appropriately for specific conditions on the day it was taken. Various statistical methods have been used for analysis of test-day records, namely fixed regression models [8] and random regression models [6]. In fixed

regression models, it is assumed that the differences among animals are constant through lactation. However, there is evidence that individual animals show specific lactation curve, which deviates from common curve within herd or any other contemporary group [6]. The objectives of this study were: 1) to estimate genetic parameters for test-day milk records in CTQ dairy ewes; and 2) to compare FRM with RRM in the estimation of genetic parameters for test-day milk records in CTQ ewes.

MATERIAL AND METHOD

Data from test-day records for daily milk yield (DMY), morning milk yield (MMY) and afternoon milk yield (AMY) from the first lactation, collected by the CTQ breeding association, from 2000 to 2005 were used. All flocks were on the alternate a.m.-p.m. testing plan, and all ewes were milked twice a day, after one month suckling, following the ICAR [4] rules with the A_4 contrast method. Data were edited, and test-day records were removed from analysis: 1) if the first test-day record was obtained before 30 days post-partum; 2) if the first test-day record was obtained after 75 days post-partum; 3) if records occurring after 150 days post-partum; and 4) if ewes presented less than 3 test-days records. After the first test-day record, subsequent records were considered if obtained at approximately monthly intervals thereafter.

After data editing total of 10700 test-day milk records, between 30 and 150 days in milk (DIM) of 3096 ewes were used. The mean number of test-day per ewe was 3.75. For the ewes in the final data set, ancestors were traced back in the pedigree as far as parents were known. The pedigree file included 5970 animals, of which 2872 were base animals, and 3098 were non-base animals.

Simple fixed regression animal model (FRM) and random regression animal models (RRM), where orthogonal Legendre polynomials of order 3 were used. To account for the temporary environment of the test-day records within flock, contemporary groups were defined as flock test-day (FTD) as defined by Ptak and Schaeffer [9]. The FRM can be represented as:

$$y_{ijk} = \mu + BT_i + FTD_j + b_n DIM_{ijk} + pe_k + a_k + e_{ijk}$$

where:

y_{ijkl} is the test-day record for DMY, MMY or AMY; μ is the overall mean; BT_i is the fixed effect of birth type i with two levels (simple or multiple); FTD_j is the random effect flock test date j with 2393 levels; b_0 and b_1 are regression coefficients that describe the test-days milk production by DIM; pe_k is the random effect of permanent environment represented common environment for all test-days for animal k with 3098 levels; a_k is the additive random effect; e_{ijkl} is the random residual effect, assumed as normally distributed with mean zero and variance s^2_e.

The RRM can be represented as:

$$y_{ijk} = \mu + BT_i + FTD_j + b_n DIM_{ijk} + \gamma_m F_m(t) + a_m F_m(t) + e_{ijk}$$

where:

y_{ijkl} is the test-day record for DMY, MMY or AMY; μ is the overall mean; BT_i is the fixed effect of birth type (j) with two levels (simple or multiple); FTD_j is the flock test date with 2393 levels; b_0 and b_1 are regression coefficients that describes the test-day records for DIM; γ_m and a_m are the random regression coefficients to the random permanent environment and additive effects, respectively, associated to the specific polynomial coefficients (F_m, $m = 0$, p-1) with p being the polynomial order); e_{ijkl} is the random residual, assumed as normally distributed with mean zero and variance s^2_e.

REML algorithm and optimization by a quasi-Newton algorithms on the basis of analytical gradients [7] implemented in the variance components estimation package VCE [12] was used to estimate the covariance structure of the models.

RESULTS AND DISCUSSIONS

Heritability, FTD, permanent environment, and residual variance proportions estimates for FRM model are presented in Table 1. It is well know that milk yield is a trait with moderate heritability (next to 0.3), however in this study heritability estimates were lower than 0.10, and varied from a minimum of 2.9% for AMY to a maximum of 8.2% for MMY. These estimates are inferior to those attained by Baro et al. [1] and Ligda et al. [5].

However, similar values (0.10) can be found in other studies ([8], [3]). These exceptionally low results are, probably, due to the extensive production system. The low genetic progress attained in the Sarda breed as been attributed to the annual climatic variations in the semi-intensive systems [10].

Estimated (co)variance components, and ratios of phenotypic variance by random regression model (RR) for DMY, MMY, and AMY are presented in Table 2. Heritability estimates presented a maximum at 60 days of lactation (= 33.9%) and decreased to values lower than 2.5% at the end of lactation.

These results are in accordance with the expected since heritability estimates are specific of breed, and production system under consideration. The heritability estimates will increase with the improvement of the management system, as observed by Van Vleck et al. [14] for dairy cows, where heritability estimates increased with the increasing of production level, reflecting the improvement in the management system. In our study genetic links among flocks are weak because of low use of rams through artificial insemination, which contributes to the low heritabilities estimates.

Table 1 Heritability, FTD, pe and residual estimates (± standard errors) for DMY, MMY, and AMY.

Trait	h^2	FTD	pe	Residual
DMY	0.05 ± 0.063	0.40 ± 0.009	0.24 ± 0.063	0.30 ± 0.005
MMY	0.08 ± 0.068	0.39 ± 0.009	0.22 ± 0.067	0.30 ± 0.005
AMY	0.03 ± 0.060	0.43 ± 0.009	0.23 ± 0.060	0.31 ± 0.006

FTD – flock test day; pe – permanent environment; DMY - daily milk yield; MMY - morning milk yield, AMY - afternoon milk yield

Table 2 Estimated (co)variance components, and ratios of phenotypic variance in RRM with Legendre polynomials of order 3 for DMY, MMY, and AMY

DIM	Var(ph)	Var(a)	Var(pe)	e^2	h^2	pe^2	ftd^2
			DMY				
30	65448.6	19285.2	36710.5	0.051	0.295	0.561	0.094
60	30038.9	10193.2	10392.7	0.110	0.339	0.346	0.204
90	18308.7	3205.4	5650.4	0.181	0.175	0.309	0.335
120	12562.7	516.4	2593.3	0.264	0.041	0.206	0.488
150	10345.9	261.7	631.3	0.321	0.025	0.061	0.593
			MMY				
30	16845.6	5792.4	8516.2	0.054	0.344	0.506	0.097
60	8131.1	3138.3	2455.8	0.111	0.386	0.302	0.201
90	4971.5	886.7	1547.8	0.182	0.178	0.311	0.328
120	3382.3	108.4	737.0	0.267	0.032	0.218	0.483
150	2828.1	84.2	206.9	0.320	0.030	0.073	0.577
			AMY				
30	16845.6	5792.4	8516.2	0.054	0.344	0.506	0.097
60	8131.1	3138.3	2455.8	0.111	0.386	0.302	0.201
90	4971.5	886.7	1547.8	0.182	0.178	0.311	0.328
120	3382.3	108.4	737.0	0.267	0.032	0.218	0.483
150	2828.1	84.2	206.9	0.320	0.030	0.073	0.577

RRM – random regression model, pe – permanent environment; DMY - daily milk yield; MMY - morning milk yield, AMY - afternoon milk yield; DIM – days in milk;

CONCLUSIONS

There is a potential for using random regression to model additive genetic and permanent environmental effects for genetic evaluation in CTQ ewes, especially from the first two thirds of lactation when decision on mating has to be taken.

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