Genetic parameters of milk yield and days in milk of friesian cattle in Tunisia

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Introduction

Dairy production in Tunisia has benefited from the importation of cattle and semen from Europe and North America. There are approximately 120,000 purebred cows, of which 95% are Friesian-Holsteins and 4% are Brown Swiss. Tunisia is still importing cattle and semen. The national dairy herd is characterized by small farms (80%) of fewer than 20 cows and large farms with more than 100 cows (cooperatives, state and private farms). Seventeen percent are milk recorded. Milk recording was first started in 1961 and dairy records were processed by hand until 1983 when electronic data processing started. Yield and reproduction characteristics of dairy cattle under Tunisian environment were reported by Djemali and Berger (1992). The specific objective of this study was to follow up the previous study and estimate genetic parameters for milk yield and days in milk (DIM) of friesian cattle under Tunisian environmental conditions.

Materials and Methods

The data were 1370 complete first lactation records from 60 herds under the milk recording system of the Office de l'Elevage et des Pâturages. Heifers were North American Holsteins, European friesians and their progeny born and raised in Tunisia. The percentage of Holstein genes in descendants of imported cows was unknown. Only lactation records from sires with full identification and daughters in at least 10 different herds were used in this study. Twenty six sires satisfied these editing conditions. The data were from 1983 to 1989.

Milk records were adjusted for age at calving, length of lactation and season of calving based on the adjustment factors developed by Djemali and Berger (1992). Three methods were used to estimate heritabilities of milk yield and DIM:

1. The Minimum Variance Quadratic estimators (MIVQUE(0))

2. The Maximum Likelihood (ML)

3. The Restricted Maximum Likelihood (REML)

using analyses options of SAS's procedure VARCOMP. The following model was used:

$$P_{ijkl} = \mu + h_i + y_j + hy_{ij} + s_k + e_{ijkl}$$

where P_{ijkl} is milk yield or DIM; μ is the underlying mean; h_i is effect of herd $i(i=1,...,60)$; y_j is effect of year of calving $j(j=1, ...,7)$; s_k is effect of sire $k(k=1,...,26)$ and e_{ijkl} is the residual. Herd, year effects and herd by year interaction were fixed. Sire effect and the error term were random. Heritabilities were estimated by the ratio of 4 times the variance component of the sire to phenotypic variance.

Results and discussion

Means and standard deviations for first parity milk yield and DIM are in Table 1. They were slightly greater than those reported for all cows by Djemali and Berger (1992).

Heritability estimates of milk yield and DIM by the three estimation methods are in Table 2. MIVQUE(0) gave the lowest estimate for milk yield while ML and REML estimates were relatively higher. It is worth notifying that MIVQUE(0) is very often used and assumes importance through the wide exposure it receives as the default in SAS's procedure VARCOMP. William and Monahan(1984) reported, after their simulation study, that the MIVQUE(0) is a poor estimator for variance components even for only mildly unbalanced data. Compared to REML, the ML estimator is biased downward as a consequence of its failure to take account of loss of degrees of freedom associated with estimation of fixed effects. While ML estimates the variance components by those values which maximize the full likelihood function over the parameter space, REML partitions the likelihood into two pieces, one of which is free of fixed effects, and maximizes only that portion of the likelihood (Harville, 1977).

Heritability estimate of milk yield of friesian cattle under Tunisian environment is in the range of the heritability values of the temperate regions (Maïjala and Hanna, 1974). As stated by Djemali and Berger (1992), adjustment factors along with genetic parameters are needed for a given population to enhance formulation of breeding plans and increase production efficiency. Freeman (1993) reported that one of the areas where genetic gain may be made is improved modeling.

Heritability estimates of DIM, by the three methods, showed that MIVQUE(0) estimator was similar to the REML estimator while ML estimator was the lowest. William and Monahan (1984) reported that MIVQUE(0) should be used only when one is confident that the random factor variance (sire variance in our case) is close to zero. This may explains why MIVQUE(0) was similar to REML in this case. This result indicates that DIM is an environmental trait rather than a heritable one. Djemali and Berger (1992) found no significant differences among friesian strains for DIM and reported that DIM was associated with seasonal variation in available forage and extreme heat rather than a consequence of low milk yield potential.

Conclusions

1. Variance component estimators derived from MIVQUE(0) gave a poor heritability estimate of milk yield compared to ML and REML methods.

2. Days in milk seems to be an environmental trait rather than a consequence of milk yield potential.

3. Available adjustment factors for nongenetic sources of variation and genetic parameter estimates made it possible to develop and implement a BLUP repeated Animal Model for dairy cattle evaluation in Tunisia. These evaluation procedures will permit ,if accurate sire and cow identification is expanded, Tunisia improve its milk production and maintain its national purebred cattle as a source of germplasm for the native cattle population.

Acknowledgments

References

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Table 1. Means and standard deviations of first lactations

Variable	Lactations	X	SD
Milk yield, kg	1370	4600	1596
DIM	1370	298	73

Table 2. Heritability estimates of adjusted milk yield and DIM

Method	Milk yield	SE	DIM	SE
MIVQUE(0)	0.11	0.05	0.06	0.04
ML	0.22	0.07	0.04	0.03
REML	0.26	0.08	0.07	0.04