ESTIMATES OF GENETIC CHANGE IN MILK YIELD IN A GYR HERD

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SUMMARY

We evaluated genetic change in milk yield up to 305 days, lactation length and daily milk yield in Gyr cattle selected for milk production. The data were obtained from the records of a herd raised in the municipality of Cajuru, SP, Brazil. Two statistical models were utilized to estimate repeatability and genetic change. Month and year of calving, bull, within-bull cow, cow’s age at calving, and lactation length had significant effects. A total of 3997 lactations corresponding to the period from 1962 to 1987 were analysed by methods A and B. Method A is based on repeated observations of the same animal, and method B is based on the principle of the use of sires over successive years. The genetic change estimated for milk yield during the period analysed was 18.5 kg/year. When adjusted for lactation length, the estimate was 12.9 kg/year. By analysing the data containing information about the first lactation only for each cow, genetic change for milk yield was estimated by method B. The estimate thus obtained was -0.45 kg/year.

INTRODUCTION

In Brazil, a country of tropical climate, in addition to the European cattle traditionally utilized for dairy purposes, a considerable increase in the number of Zebu (Zebu-European half-bred) animals exploited for milk production has been observed. The Gyr breed is the most extensively used for milk production and, even though the number of animals of this breed has remained practically constant, over the last few years there has been a significant increase in the number of animals used for commercial milk production. Gyrs can be used both as "purebreds" in some regions of the country and for crosses with European breeds.

Milk yields obtained for Holstein and Jersey herds, as well as for other temperate climate breeds in studies of genetic change, range from 30 to 110 kg/year (Van Vleck and Henderson, 1961; Cassel et al., 1986).

In studies of genetic change in the tropics, especially in herds of Indian origin, variable results have been obtained, ranging from 7 to as much as 40 kg milk/year (Lôbo et al., 1982; Ramos et al., 1985; Ledic and Lôbo, 1987). The results obtained in Latin American studies have been quite similar to those reported for Zebu breeds by Indian investigators.

The reasons for the low-magnitude results reported are basically the lack of a selection program, the generalized use of natural mating and the use of untested bulls for most cases of Artificial Insemination (AI). This use of untested bulls is the consequence of the slow diffusion of AI which has prevented the performance of tests with a large number of animals, and to the lack of an extensive program of genetic improvement which would provide large amounts of reliable data for the evaluation of genetic gain. The objective of
The present study was to estimate genetic change in milk yield using two distinct methodologies.

**MATERIAL AND METHODS**

The data used in the present study were obtained from the records of a Gyr herd selected for dairy production and raised in the municipality of Cajuru, State of São Paulo. A total of 3987 lactations by 1272 cows sired by 78 bulls and covering the period from 1962 to 1987 were analyzed statistically. According to the Köppen classification, the climate of Cajuru, located in the northeastern region of the State of São Paulo, is subtropical. Management of the herd is semi-extensive, with the animals put out to pasture most of the day, except for the time when they are gathered in the stable for mechanical milking twice a day.

The data were analyzed using the SAEG (Genetic and Statistical Analysis System) program developed by the State University of Viçosa (1988) and the LSMLM (Least Squares and Maximum Likelihood Computer Program) of Harvey (1985).

The following linear models were used:

**Model I (Complete)**

\[
y_{ijkl} = \mu + a_i + b_{ij} + F_k + e_{ijkl},
\]

where:

- \(y_{ijkl}\) = response for each dependent variable
- \(\mu\) = overall mean
- \(a_i\) = sire effect (random)
- \(b_{ij}\) = within-sire cow effect (random)
- \(F_k\) = set of fixed effects
  - continuous [cow age (linear (L), quadratic (Q) and cubic (C) effects), and lactation length (L, Q, C)]
  - discrete (month of calving, year of calving)
- \(e_{ijkl}\) = random error for each observation.

Model I was used for the repeatability estimates and for the linear regression coefficients for milk yield over year of calving \([b_{t(y)}]\), obtained by least squares analysis of variance, which corresponds to phenotypic change. The linear regression coefficient over year of calving \([b_{t(y)}]\), which estimates environmental change, was obtained by maximum likelihood analysis of variance. Thus, genetic change is estimated as follows: \(b(y) = b_{t(y)} - b_{t(y)}\).

**Model II**

\[
y_{ijk} = \mu + s_i + A_j + e_{ijk},
\]

where:

- \(y_{ijk}\) = deviation of cow's yield in relation to contemporary mean
- \(\mu\) = overall mean
- \(s_i\) = sire effect
- \(A_j\) = year-season effect
- \(e_{ijk}\) = random error for each observation.

Model II was used to estimate intra-sire regression, which estimates \(-1/2\) genetic change (g), by \(b_{s(y-P)}\), where \(b\) is the regression coefficient, \(P-P\) is cow deviation in relation to her contemporaries, \(T\) is the time (years), \(S\) the sires used, and \(g\), the mean annual genetic change.

Two methods were used in the present study to estimate genetic change. Method A is based on the principle of repeated observations on the same animal over the years (Rendel and Robertson, 1950), and method B is based on the
repeated use of sires over successive years (Smith, 1962).

RESULTS AND DISCUSSION

The nonadjusted means and coefficients of variation (CV) for milk yield and lactation length over the study period for 1272 Gyr cows were 2359 kg (CV = 27%) and 285 days, respectively, as shown in Table 1.

Table 1: Nonadjusted Overall Means and Coefficients of Variation (CV) for Milk Yield up to 305 Days, Lactation Length, and Daily Milk Yield.

<table>
<thead>
<tr>
<th>Traits</th>
<th>No. of Observations</th>
<th>Mean</th>
<th>CV(%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lactation length (days)</td>
<td>3987</td>
<td>285</td>
<td>14</td>
</tr>
<tr>
<td>Milk yield (kg)</td>
<td>3987</td>
<td>2359</td>
<td>29</td>
</tr>
<tr>
<td>Daily milk yield (kg)</td>
<td>3987</td>
<td>8.22</td>
<td>14</td>
</tr>
</tbody>
</table>

The results of least squares analysis of variance for milk yield up to 305 days (MY305), lactation length (LL305) and daily milk yield (DY305) using model I are presented in Table 2.

Table 2: Least Squares Analysis of Variance for Milk Yield up to 305 Days, Lactation Length and Daily Milk Yield Using Model I (Complete)

<table>
<thead>
<tr>
<th>Sources of Variation</th>
<th>d.f.</th>
<th>MY305 (x10^-2)</th>
<th>DY305 (x10^-2)</th>
<th>LL305</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sire</td>
<td>77</td>
<td>917,197**</td>
<td>1,191**</td>
<td>1,981</td>
</tr>
<tr>
<td>Cow:sire</td>
<td>1,194</td>
<td>490,354**</td>
<td>612**</td>
<td>2,540**</td>
</tr>
<tr>
<td>Month of calving</td>
<td>11</td>
<td>1,454,900**</td>
<td>1,730**</td>
<td>925*</td>
</tr>
<tr>
<td>Year of calving</td>
<td>25</td>
<td>2,200,703**</td>
<td>2,631**</td>
<td>5,994**</td>
</tr>
<tr>
<td>Lactation length</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Linear effect</td>
<td>1</td>
<td>30,783,905**</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Quadratic effect</td>
<td>1</td>
<td>266,552*</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cubic effect</td>
<td>1</td>
<td>216,408*</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cow age</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Linear effect</td>
<td>1</td>
<td>127,448*</td>
<td>265*</td>
<td>2,264*</td>
</tr>
<tr>
<td>Quadratic effect</td>
<td>1</td>
<td>78,475,483**</td>
<td>91,180**</td>
<td>1,843*</td>
</tr>
<tr>
<td>Cubic effect</td>
<td>1</td>
<td>14,891,067**</td>
<td>17,731**</td>
<td>225</td>
</tr>
<tr>
<td>Error</td>
<td>2,673</td>
<td>156,176</td>
<td>195</td>
<td>979</td>
</tr>
</tbody>
</table>

d.f. = degrees of freedom; *P<0.05; **P<0.01.

All effects included in the model were significant (P<0.05) except for sire effect on lactation length.

On the basis of the solution of model I, repeatability estimates for milk yield up to 305 days, lactation length and daily milk yield were obtained by the least squares method. Repeatability estimates by intraclass correlation were used to calculate environmental change using model I and maximum likelihood procedures (Henderson et al., 1959).

Estimates of annual phenotypic (p), genetic (g) and environmental (e) changes obtained from model I using method A are presented in Table 3. Genetic change (g) was estimated by the difference between linear regression for year of calving obtained from least squares analysis of variance b(y,c) and from maximum likelihood analysis of variance b(x). For this last analysis, the
values of 0.46, 0.34, and 0.43 were used for the repeatability estimates for MY305, LL305, and DY305, respectively. The g estimate for milk yield was 18.5 kg per year. When lactation length was included in the model the estimate was 12.94 kg owing to the reduction in additive genetic variation for milk yield.

Table 3 Estimates of Annual Phenotypic (p), Genetic (g) and Environmental (e) Changes for Milk Yield, Lactation Length and Daily Milk Yield Estimated by Method A, Including or Excluding Lactation Length in the Model

<table>
<thead>
<tr>
<th>Traits</th>
<th>All lactations</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>p</td>
</tr>
<tr>
<td>Milk yield (kg)</td>
<td>17.16</td>
</tr>
<tr>
<td>Lactation length (days)</td>
<td>0.27</td>
</tr>
<tr>
<td>Daily milk yield (kg)</td>
<td>-0.52</td>
</tr>
</tbody>
</table>

Genetic change for milk yield up to 305 days for cows at first lactation (method B) was estimated by deviation regression of cow's yield in relation to the within-sire mean for her contemporaries. These results were quite different from those obtained by method A. The estimate of genetic change in milk yield up to 305 days was -0.45 kg per year for cows at first lactation. This estimate is null (P>0.05).

On the basis of method A, which considers all lactations, and of the genetic change obtained by the differences between the regression coefficients (βg-βp), taking into consideration the effects of selection and incomplete repeatability of the trait, we conclude that there was positive genetic change for milk yield in the herd studied.

The fact that there was no selection for cows at first lactation (method B) during the study period led to null genetic change estimates.

The two methods used in the present study provide genetic change estimates that cannot be compared since they are based on distinct principles and different sets of data were used for statistical analysis.

REFERENCES