Genotype by environment interaction for milk production traits in Tunisian Holstein dairy

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ABSTRACT

The data consisted of 37118 TD milk record of 5851 primiparous Holstein cows of Tunisia. Herd-years of calving means for milk production traits were clustered in three levels using the CLUSTER procedure in SAS software. Production levels included low, medium and high levels. Genotype by environment interaction were investigated by applying a sire model. Generally, the highest heritability estimates of 305-d milk production traits were found in high level rather than low level. Genetic correlation between expression in low and high level was 0.14 for milk yield, 0.22 for fat yield and 0.18 for protein yield. Low spearman correlations (ranged from 0.08 to 0.50) between estimated of the 74 common sires showed re-ranking of sires for these levels. Results from this research indicated that milk production of daughters of the same sires depends greatly on the production environment.

Key words: dairy cattle, genotype by environment interaction, genetic correlations, Cluster analysis

Introduction

Genotype x environment interaction (GxE) can be defined as different sets of genes that determine varying levels of expression in different environments (Bertrand et al., 1987). When genotypes react differently in different environments, GxE is an important parameter to consider (Falconer and Mackay, 1996). Falconer (1952) proposed to utilize genetic correlation to describe G x E by defining the same measure in two environments as distinct characters. High estimates of genetic correlations between environments (>0.80) suggest no evidence for strong G x E (Robertson 1959). Most studies of G x E for production traits in dairy cattle were developed in temperate regions and indicated that genetic correlations between environments do not deviate substantially from unity, but that variances and heritabilities differ considerably among environments (Carabaño et al., 1989, 1990; Boldman and Freeman, 1990; Stanton et al., 1991). The environments in which dairy farming is practiced in Tunisia vary in many ways, such as the average herd production, level of feeding, elevation and climate variables including temperature and humidity. The purpose of this study was to investigate the possibility that a GxE exists among different production systems in Tunisia.

Materials and Methods

Data. The data comprised 37118 TD milk record of 5851 primiparous Holstein cows of Tunisia born between 2000 and 2006 the progeny 445 sires in 30 herds. Data were provided by the Tunisian Center for Genetic Improvement of the Livestock and Pasture Office. The variables used to characterize the environment of each cow were the herd-year averages of each trait. Only herd-year subclasses with at least 4 cow records were kept. Cows were required to have a minimum of five TD records between 7 and 335 DIM. Herds with fewer than 4 cows per herd x year of calving were omitted. Further edits excluded irregular data for daily milk yield (< 2 and > 70 kg), fat content (< 1,5% and > 9%), and protein percentage (< 1% and > 7%). Three seasons were identified ((January-March, April-August, September-December). And age at calving was classified into 6 classes (< 26 mo, 26 to 27, 28 to 29, 30 to 31, 32 to 33, and > 33 mo).

Definition of Environment. At the second stage of data preparing the observations were divided into low, medium and high herd-year classes with regard to MILK, PROT and FAT herd-year averages of each trait. For the herd classes, CLUSTER procedure with Ward’s minimum variance in SAS package (9.0) was used. Cluster analysis is an exploratory technique designed to classify data into subgroups which share similar characteristics (Lin and Lin, 1994). Descriptive statistics on these management classes in addition to other characteristics of Tunisian environments are in Table 1. Once the clusters were established, at least 3 daughters of sires in each environment were required to evaluate genotype by environment interaction. To fulfill those criteria, further elimination of records was done. Only 74 of 455 Holstein sires had at least 3 daughters in three levels for MILK, PROT and FAT.
Heritability for trait in environment \( t \) (\( t = 1, 2, 3 \)) was computed as follows:

\[
y = X\beta + Za + e
\]

where \( Y = \begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} \), \( X = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \), \( Z = \begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \end{bmatrix} \), \( \alpha = \begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \alpha_3 \end{bmatrix} \), and \( e = \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix} \).

\[
\begin{bmatrix} \sigma^2_{a_1} & \sigma^2_{a_2} & \sigma^2_{a_3} \\ \sigma^2_{a_1} & \sigma^2_{a_2} & \sigma^2_{a_3} \\ \sigma^2_{a_1} & \sigma^2_{a_2} & \sigma^2_{a_3} \end{bmatrix} \times A
\]

where \( A \) is the matrix of the additive genetic relationships among animals; \( \sigma^2_{a_{i,j}} \) = additive genetic variance for the trait in groups \( i=1,2 \); \( \sigma^2_{a_{1,2}} \) = additive genetic covariance for the trait between groups 1 and 3 and \( \sigma^2_{a_{2,3}} \) = additive genetic variance for the trait between groups 2 and 3, and \( R = I - R_0 \) is the residual (co)variances.

Matrix for \( R_0 = \begin{bmatrix} \sigma^2_{e_1} & 0 & 0 \\ 0 & \sigma^2_{e_2} & 0 \\ 0 & 0 & \sigma^2_{e_3} \end{bmatrix} \)

where \( \sigma^2_{e_i} \) = residual variance for the trait in group \( i = 1, 2 \) and 3.

Heritability for trait in environment \( t \) (\( t = 1, 2, 3 \)) was computed as follows:

\[
h^2_t = \frac{4 \times \sigma^2_{a_t}}{\sigma^2_{a_t} + \sigma^2_{e_t}}
\]

**Results And Discussion**

Total herds and records and the phenotypic means and standard deviations for milk, fat and protein yield in first lactation for all environmental classifications are presented in Table 1. Results show that there exist significant differences between low, medium and high, yielding for mean of each trait. The estimated parameters (Table 2) are in agreement with the studies of Stanton et al.(1991), Cienfuegos - Rivas et al.(1999), Costa et al.(2000) and Raffrenato et al.(2003) where genetic and residual variances for milk yield traits were smaller in the low than in high production environments. The reason of this difference is the result of a better environment (Hill et al., 1983; Powell et al.,1983 and Ceron-Munoz et al., 2004). Changes in genetic, residual, and other variance components for MILK, PROT, and FAT in low high yield environment lead to higher heritability in the high environment (Table 3). Heritabilities increasing with production level estimated were also reported.
by (Gengler et al., 2005) and (Hammanmi and Croquet, 2006). Heritability of milk yield ranged from 0.11 to 0.27. Then heritability was estimated for fat yield, in a range from 0.07 to 0.18. These differences were also found by Weigel and Rekaya (2000), 0.28 to 0.37 (5 clusters); Zwald et al. (2003a), 0.24 to 0.42 (7 clusters); and Fikse (2002), 0.29 to 0.36 (3 clusters). Estimated heritabilities for protein yield ranged from 0.11 to 0.23. Large heritability estimates for milk yield in high levels reflect high genetic variation of milk production by cows in this class compared to that of their contemporaries in the low level.

Table 2. Estimates of additive genetic (\(\sigma^2_a\)), total variance (\(\sigma^2_e\)) and residual variance (\(\sigma^2_y\)) for milk yield (MILK), protein yield (PROT), and fat yield (FAT) in low, medium and high levels .

<table>
<thead>
<tr>
<th></th>
<th>Milk</th>
<th>Fat</th>
<th>Protein</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low</td>
<td>279079.13</td>
<td>5074.9</td>
<td>609.87</td>
</tr>
<tr>
<td></td>
<td>30764.4</td>
<td>466</td>
<td>68.52</td>
</tr>
<tr>
<td></td>
<td>271388.13</td>
<td>946</td>
<td>592.74</td>
</tr>
<tr>
<td>Medium</td>
<td>326753.31</td>
<td>818.9</td>
<td>372.77</td>
</tr>
<tr>
<td></td>
<td>62450.4</td>
<td>90.1</td>
<td>74.07</td>
</tr>
<tr>
<td></td>
<td>310840.71</td>
<td>796.4</td>
<td>354.25</td>
</tr>
<tr>
<td>High</td>
<td>439093.6</td>
<td>1265.9</td>
<td>686.87</td>
</tr>
<tr>
<td></td>
<td>121864.8</td>
<td>223.9</td>
<td>161.12</td>
</tr>
<tr>
<td></td>
<td>408627.4</td>
<td>1209.9</td>
<td>646.59</td>
</tr>
</tbody>
</table>

The genetic correlation between the traits was used to study possible effects of GxE. The genetic correlations between the different groups are presented in Table 3. Genetic correlation estimates among milk yields in different HM levels in Tunisia were lower than the threshold of 0.80 suggested by Robertson (1959). Generally, the lowest genetic correlations were estimated across low and high production levels that were 0.14; 0.22 and 0.18 for milk, fat and protein yield, suggesting that GxE would have an important impact on animal performance ( Robertson, 1959). Hammami et al. (2008) found low genetic correlation coefficient between herds in high and levels milk production in Tunisia (0.70). Raffrenato et al. (2003) obtained relatively low genetic correlations between low and high production environment. These authors suggested a major re-ranking of sires among the various environments. Spearman rank correlations across three production levels for 74 of common sires ranged from 0.08 to 0.50. Low genetic and spearman correlations are translated as re-ranking of sires across production levels.

Table 3. Spearman correlation coefficients for the 20 top sires (below diagonal), estimated 305-days heritabilities (on diagonals and bold) and 305-days genetic correlations (above diagonal) by production levels for milk production traits.

<table>
<thead>
<tr>
<th></th>
<th>Low</th>
<th>Medium</th>
<th>High</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk</td>
<td>0.11±0.01</td>
<td>0.23</td>
<td>0.14</td>
</tr>
<tr>
<td></td>
<td>0.10</td>
<td>0.19±0.02</td>
<td>0.21</td>
</tr>
<tr>
<td></td>
<td>0.08</td>
<td>0.20</td>
<td>0.27±0.02</td>
</tr>
<tr>
<td>Fat</td>
<td>0.07±0.005</td>
<td>0.25</td>
<td>0.22</td>
</tr>
<tr>
<td></td>
<td>0.50</td>
<td>0.11±0.007</td>
<td>0.57</td>
</tr>
<tr>
<td></td>
<td>0.30</td>
<td>0.42</td>
<td>0.18±0.006</td>
</tr>
<tr>
<td></td>
<td>0.11±0.008</td>
<td>0.18</td>
<td>0.18</td>
</tr>
<tr>
<td>Protein</td>
<td>0.19±0.01</td>
<td>0.36</td>
<td>0.23±0.01</td>
</tr>
<tr>
<td></td>
<td>0.22</td>
<td>0.32</td>
<td>0.23±0.01</td>
</tr>
</tbody>
</table>

Conclusion

The herd-grouping criteria using environment descriptor variables and cluster analysis were efficient for stratifying and characterizing production systems in Tunisia dairy herds. In general, results from this study indicate the presence of a G x E for milk production traits in Tunisian Holsteins dairy cattle. Use of this information is important for designing evaluation and selection strategies to maximize genetic response in Tunisian herd environments.

References