International Journal of Farming and Allied Sciences
Available online at www.ijfas.com
©2014 IJFAS Journal-2014-3-6/623-628/ 30 June, 2014
ISSN 2322-4134 ©2014 IJFAS

Interaction between genotype and geographic region for milk production traits in Tunisian Holstein cattle

A. Hamrouni[1], M. Djemali[1] and S. Bedhiaf[2]

1-Institut National Agronomique de Tunisie,
2-Institut National de Recherche Agronomique de Tunis

Corresponding author: **A. Hamrouni**

ABSTRACT: This study was designed to examine the existence of a genotype × region interaction on milk production traits in Holstein dairy cows in Tunisia. The data set for this study was provided by Tunisian Center for Genetic Improvement of the Livestock and Pasture Office. A total 63569 TD milk record of 6912 Holstein cows of Tunisia were used. Data were classified as belonging to three regions of the country: Northern, Central and Southern. Only data from sires with daughters in three regions were used in each analysis. Genetic parameters were estimated using residual maximum likelihood (REML). A multivariate model was applied. The estimated heritability for the milk production traits ranged between 0.11 to 0.14 for the Central region; 0.09 to 0.19 for the Northern region and 0.30 to 0.39 for the Southern region. The Pearson's correlations of the 26 sires represented in three regions were estimated. Genetic correlation estimates among milk yields traits in different regions in Tunisia were lower than the threshold of 0.80 suggested by Robertson (1959). These results indicate the existence of genotypeenvironment interaction which may have several implications for the genetic improvement of Holstein cattle in Tunisia. It also encourages further studies oriented toward the identification of specific environmental effects related to these interactions.

Keywords: dairy cattle, genotype by environment interaction, genetic correlations, Tunisia

INTRODUCTION

The genotype-environment interaction (G×E) results from the lack of adaptation of particular genotypes to specific conditions of production systems. It may alter the genetic, phenotypic and environmental variances and, consequently, modify the estimates of genetic and phenotypic parameters. The effect of G×E reduces selection responses, rendering selection programs or importation of improved germplasm economically less efficient (Dickerson, 1962; Montaldo, 2001). A useful way to quantify GxE is estimation of genetic correlation between the traits expressed in different environments (Falconer and Mackay, 1996). Correlation coefficient below 0.8 gives an indication of G×E (Robertson, 1959). Since 1960, Tunisia has imported Holstein germplasm, (mainly animals and semen) to increase productivity of its dairy cattle populations. Once genotype has been fitted to the existing environment or region, then there would be less variation for more improvement through upgrading due to stress, high temperature and the humidity index level affecting the survival of a high-milk-producing cow while the marginal improvement from improving feeding and management tended to be greater than that of genetic improvement (Tumwasorn, 2012). There are major differences when considering the production system (that is, feed and feeding, and herd management) and the study of the magnitude of genotype × region or environment interaction on milk production traits in Holstein cows across regions of Tunisia of great importance. Differentiation of environments in Tunisia is important, because Holstein herds and production level could be influenced for the environment in different magnitude. There are no studies on G×E involving estimates of genetic correlations among regions for Holstein cattle in Tunisia. Therefore, this type of studies may give some indication of what could happen when selection is performed under several environmental conditions. The objective of this study was to investigate the presence of genotype- geographical region interactions for milk production traits in Holstein cattle in Tunisia.

MATERIALS AND METHODS

Data

The data comprised 63569 records from 6912 Holstein cows that had calved at some during 2003 to 2009. The data were collected by the milk recording system of the Tunisian Genetic Improvement Center, Livestock and Pasture Office, Tunis. In this study, only records from the first 3 lactations were retained. A minimum of 5 TD records, for milk, fat, and protein yields were required for a cow observation to be included in the analysis, which excluded cows with very short lactations. Records obtained before 7 or after 335 DIM were also discarded. Herds with fewer than 4 cows per herd x year of calving were omitted. Records were classified by location of herd as Northern, Central and Southern regions. Northern region included the mediterranean states of Ariana, Ben-Arous, Bizerte, Béjà, Jendouba, Nabeul, Siliana and Zaghouan; The Central region involve semi arid and temperate states of Kairouan and Sidi-Bouzid and the Southern region included the temperate and arid states of Gabès and Sfax. For the study of G×I, sires with at least 3 daughters at different herds within each environment were chosen. Only 26 of 519 Holstein sires had at least 3 daughters in three regions. A full description of the data used is given in Table 1.

Model description and statistical analysis

The data were subjected to analysis of variance to test effect of G ×E. the general linear model analysis used the GLM procedure of the Statistical Analysis System software (SAS, 9.0). The model was established according to equation 1:

$$y_{ijk} = \mu + G_i + E_j + G \times E_{ij} + e_{ijk} \qquad (1)$$

Where Y_{ijk} is milk yield; μ is the population mean; G_i is the effect of the i^{th} sire; E_j is the effect of the j^{th} region; GE_{ij} is the interaction between the i^{th} sire and the j^{th} region and e_{ijk} is the random error.

Model for estimation of genetic parameters

Genetic parameters were estimated using residual maximum likelihood (REML) as applied in SAS, Version 9.0. Genetic correlations for milk production (r_g) were estimated using records of daughters of sires distributed in several regions. Heritability (h^2) was determined as the ratio of the additive genetic variance to the total phenotypic variance. Rank correlations were calculated using PROC CORR. 3 seasons (January-March, April-August, September- December) were identified (Djemali et Berger,1992). And age at calving was classified into 5 classes (≤30, 30-42, 42-54,54-58 et >58). The statistical model used was the same for all observations in the dataset and was expressed in matrix notation as shown in Equation:

$$y = X\beta + Za + e \qquad (2)$$

with

$$y = \begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \times \begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 \\ 0 & Z_2 & 0 \\ 0 & 0 & Z_3 \end{bmatrix} \times \begin{bmatrix} a_1 \\ a_2 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix}$$

where Y = is a vector of 305-days milk, protein or fat yield, β_i vector of fixed effects of herd-year of calving, season of calving, age of cow at calving and lactation, a_i = vector of the random additive genetic effect of sire, e_i = vector of random residual effects, X_i=incidence matrix related to the fixed effects referring to β_i and Z_i is the incidence matrix related to the random additive genetic effect of sire (a_i) in each region i = North, Central and South. The random effects were var(a) = $A\sigma_a^2$ where A is the numerator relationship matrix and var(e) = $I\sigma_e^2$ where I is the identity matrix.

Table 1. Description of data and mean of 305-d milk yield and standard deviation (in parentheses) for different regions (Northern, Southern and Central) in Tunisia

	Northern	Central	Southern
Test-day records	54 289	6335	2945
Number of cows	5760	677	475
Number of sires	519	70	159
Milk (Kg)	6125±1798	5664±1574	5946±1632
Fat (Kg)	207±63	194±57	203±62
Protein (Kg)	191±56	176±48	189±54

RESULTS AND DISCUSSION

The results of ANOVA also showed significant ($P < 0.05$) genotype × region interactions for 305 day milk yield, protein yield and fat yield all studied traits. Clearly, the presence of such sizeable G × E interactions will lead to changes in the ranking of genotypes; hence, certain genotypes exhibited their highest performance in selected regions while others showed their best performance in their respective favorite regions. presence of the G×E indicated that the phenotypic expression of one genotype might be superior to another genotype in one environment but inferior in a different environment (Falconer and Mackay, 1996). A plot of the interaction means showed trends of each genotype exposed to the 3 diverse environmental conditions (Figure 1,2 and 3).

Larger additive genetic variances was found for the Southern than for Central or Northern regions. Additive genetic variance estimated for Southern region was 1.94 and 3.55 times those for Northern and Central regions, respectively. Differences between residual variances were low (table 2). The higher standard error of heritability estimates for all the traits under study indicated that these traits were highly influenced by environmental factors and management of the herd such as feed and feeding, and health care could also contribute to the variation (Usman et al., 2012; Valencia et al.,2008 ; Endriss et al.,2013). The results revealed that the estimated Heritability for the Southern region (from 0.30 to 0.39) was higher than the value obtained for other regions in Northern (from 0.09 to 0.19) and Central (from 0.11 to 0.14). These heritability values indicates that in spite of the existence of an important additive genetic variance in all three regions which make selection potentially effective at each region, selection of sires across regions deserves further analysis. These results showed that milk yield traits is not the same trait for the 3 bioclimatical regions.

The genetic correlations, estimated for milk production traits up to 305 days are shown in table 3. The reduced value of the genetic correlation between the regions estimated in this study for milk yield, (from 0.20 to 0.48), protein yield (from 0.31 to 0.49) and fat yield (from 0.31 to 0.52) significantly less than one, indicates an important genotype-environment interaction, and therefore, a different expression of the same genes in the daughters of the same sire on each environment (Stanton, 1991; Cienfuegos,1999; Costa, 1998; Muñoz, 2001; Zwald, 2003). In other studies, authors had considered genetic correlations below 0.80, as having important negative effects in the efficiency of selection programs and reducing selection responses (Robertson, 1959; Carabaño, 1989; Cienfuegos, 1999, Muñoz, 2001). According to Robertson (1959), inferior correlation values as this, suggests that the interaction genotype environment is biologically important. Mulder (2007) concluded that when the genetic correlation is higher than 0.60, it is more appropriate to carry out a unique genetic program with progeny tests for the bulls in both environments. On the contrary, when the genetic correlation was lower or equal to 0.60 a specific genetic program was more opportune, as well as progeny tests in each environment. Large differences among regions for feeding, climate, herd size level of production and particular management in the present study, probable could explain the low value of genetic correlation estimated between Northern and Southern; Northern and Central and Southern and Central regions of this study. In Colombia, Muñoz, (2001) found evidences of G×I for milk production in Holstein cattle in a study involving four regions. They found a significantly lower than unity ($p<0.05$). Carabaño, (1989) estimated an average value of 0.81 for genetic correlations for milk production between United States and Spain. In the Holstein breed, Cerón-Muñoz, (2001) studied the dairy production up to 305 d in four regions of Colombia. They informed interaction genotypeenvironment between Cundinamarca and the other three regions, with coefficients of genetic correlation from 0.70 to 0.83. Nauta, (2006) also observed G×E when comparing the organic and traditional production systems in Holland (genetic correlation of 0.80). Valencia, (2008), in three Mexican regions,obtained values of 0.73, 0.38 and 0.93 for the correlations between North-Center, North-South and Center-South, respectively. Carneiro, (2009) referred genetic correlations from 0.09 to 0.57, when analyzing the dairy production in seven dairy regions of Paraná state, Brazil. In Cuba, Suárez, (2009) obtained an estimate of 0.49 for the genetic correlation between the genetic values of the milk production at 244 d in Siboney from Cuba, in different environments. Spearman rank correlations across three production levels for 74 of common sires ranged from 0.24 to 0.59. Low genetic and spearman correlations are translated as re-ranking of sires across production levels.

Zwald, (2003) identified factors that cause genotype by environment interactions in Holstein herds in seventeen countries with temperate climate. They used genetic correlation estimates between records classified by quintiles for all production, reproduction, climate and others evaluated traits. Variables with genetic correlations deviating the most from unity were temperature (0.84), herd size (0.79), sire PTA for milk (0.89), percent of North American Holstein genes (0.83), peak milk yield (0.84) fat:protein ratio (0.90), and standard deviation for milk yield (0.90). In this present study probably any of these factors could be causes of genotype by environment interaction. Any of these factors could be causes of genotype by environment interaction in this study. The lower values found in this study could be attributed to more extreme differences in some of these factors between regions. These may involve feeding, climate, altitude over sea level, herd size, production levels and different management practices.

Table 2. Estimates of additive genetic (σ^2_a), total variance (σ^2_y) and residual variance (σ^2_e) for milk yield (MILK), protein yield (PROT), and fat yield (FAT) in Northern, Southern and Central regions

	Milk	Fat	Protein
Northern			
σ^2_y	1819203,6	2135,26	1815,5
σ^2_a	328817,2	184,64	352,4
σ^2_e	1736999,3	2089,1	1727,4
Southern			
σ^2_y	1631673,3	2142,05	1686,75
σ^2_a	639003,6	703	514,2
σ^2_e	1471922,4	1966,3	1558,2
Central			
σ^2_y	1690257,8	2143,8	1549,89
σ^2_a	179951,6	306,8	185,56
σ^2_e	1645269,9	2067,1	1503,5

Table 3. Spearman correlation coefficients for the 26 top sires (below diagonal), estimated 305-days heritabilities (on diagonals and bold) and 305-days genetic correlations (above diagonal) by production regions for milk production traits

		Central	Northern	Southern
	Central	0,11±0,04	0,20	0,37
Milk	Northern	0,55	0,18±0,06	0,48
	Southern	0,41	0,24	0,39±0,13
	Central	0,14±0,05	0,52	0,21
Fat	Northern	0,59	0,09±0,02	0,37
	Southern	0,41	0,46	0,32±0,11
	Central	0,12±0,04	0,49	0,31
Protein	Northern	0,56	0,19±0,07	0.46
	Southern	0,38	0,33	0,30±0,10

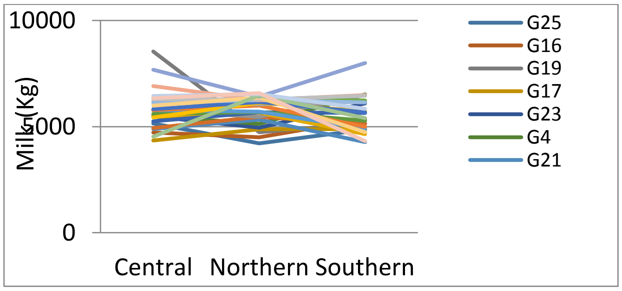

Figure 1. Least squares means of 305-day milk yield for 26 sires by region interaction

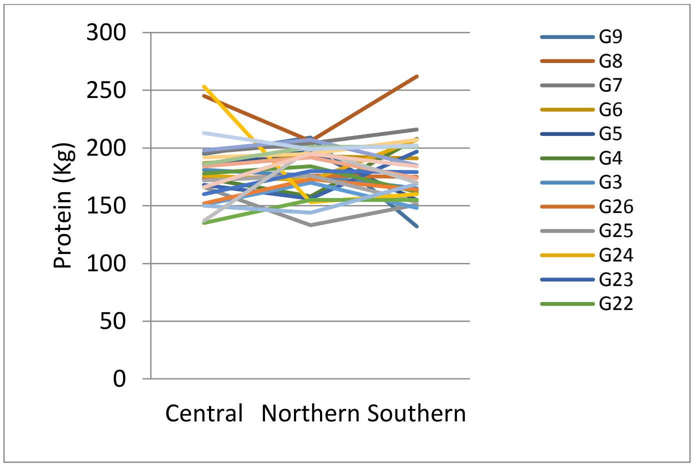

Figure 2. Least squares means of 305-day protein yield for 26 sires by region interaction

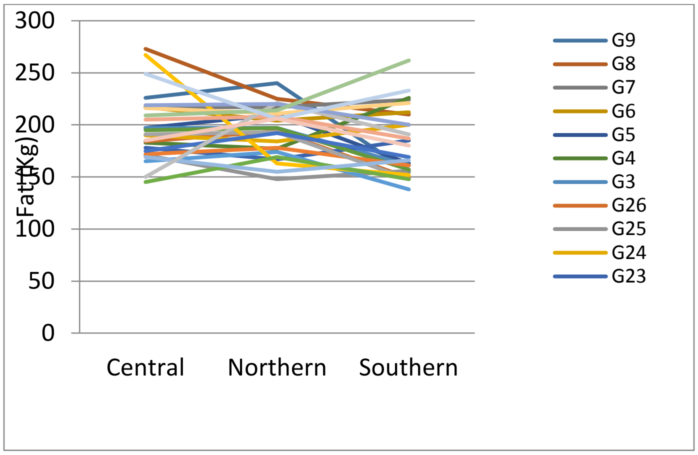

Figure 3. Least squares means of 305-day fat yield for 26 sires by region interaction

CONCLUSION

Results of this study showed that milk yield in Tunisian conditions are affected by regional differences leading to the existence of GxEI. The ANOVA results showed a significant genotype × region interaction. This interaction resulted in inconsistent performance and a ranking shift of genotypes across regions. In addition, The low value of genetic correlation estimated in the present study suggest that genotype-environmental interactions might exists for Holstein sires through regions in Tunisia. G×E reduces genetic gains and therefore reduce the economic returns from the use of selected artificial insemination sires. It is concluded that for using Tunisia sires, the environmental conditions should be considered for optimizing the genetic improvement and increase productivity.

REFERENCES

Carabaño MJ, Van Vleck D and Wiggans G. 1989. Estimation of genetic parameters for milk and fat yields of dairy cattle in Spain and the Unites States. J. Dairy Sci. 72: 3013-3018.

Carneiro de Paula M, Elias Nunes M, Campos da Silva LO, Lopes de Oliveira CA, Altair Antônio Valotto AA and Pohl Ribas N. 2009.Interação genótipo × ambiente para produção de leite de bovinos da raça Holandesa entre bacias leiteiras no estado do Paraná. Rev. Bras. Zootec. 38:467.

Cerón-Muñoz MF, Tonhati H, Costa C and Benavides F. 2001. Interacción genotipo-ambiente en ganado Holstein colombiano. Arch. Latinoam. Prod. Anim. 9:74.

Cienfuegos RE, Oltenacu PA, Blake RW, Schwager SJ, Castillo H and Ruiz F. 1999. Interaction between milk yield of Holstein cows in Mexico and the United States. J. Dairy Sci.82: 2218-2223.

Costa CN, Blake RW, Pollak EJ and Oltenacu PA. 1998. Genetic relationships for milk and fat between Holstein populations in Brazil and the United States. Proc. 6th World Congres Genet. Appl. Livest. Prod., Armidale, Australia. 23: 323-326.

Dickerson GE. 1962. Implications of geneticenvironmental interaction in animal breeding. Anim. Prod. 4: 47-63.

Djemali M, Berger PJ. 1992. Yield and reproduction Characteristics of Fresian cattle under North African conditions. J.Dairy.Sci.75:3568-3575.

Endris M, Tumwasorn S, Sopannarath P, Wongwan C and Prasanpanich S. 2012. Estimation of direct genetic effects on milk yield and lactation length in the Aownoi Dairy Cooperative. Kasetsart J. (Nat. Sci.). 46(4):546–553.

Falconer D and Mackay T.1996. Introduction to quantitative genetics. Longman Group Ltd.

Montaldo HH. 2001. Genotype by environment interactions in livestock breeding programs: a review. Interciencia. 26: 229-235.

Mulder HA. 2007. Methods to optimize livestock breeding programs with genotype by environment interaction and genetic heterogeneity of environmental variance. PhD Thesis: Wageningen University. The Netherlands

Muñoz MF, Tonhati C, Costa C and Benavides F. 2001. Interacción genotipo-ambiente en ganado Holstein colombiano. Arch. Latin. Prod.Anim. 9: 74-78.

Nauta WJ, Veerkamp RF, Brascamp EW and Bovenhuis H. 2006. Genotype by environment interaction for dairy production traits between organic and conventional dairy cattle production in The Netherlands. J. Dairy Sci. 89: 2729.

Robert C, Foulley JL and Ducrocq V. 1995. Genetic variation of traits measured in several environments. I. Estimation and testing of homogeneous genetic and intra-class correlations between environments. Genet. Sel. Evol.27: 111-123.

Robertson A. 1959. The sampling variance of the genetic correlation coefficient. Biometrics, 15: 469-485

Stanton TL, Blake RW, Quaas RL, Van Vleck D and Carabaño MJ. 1991. Genotype by environment interaction for Holstein milk yield in Colombia, Mexico, and Puerto Rico. J. Dairy Sci.74: 1700-1714.

Suárez MA, Zubizarreta I and Pérez T. 2009. Interactión genotipo ambiente en ganado bovino Siboney de Cuba. Livestock Res. Rural Develop. 21 (9).

Tumwasorn S. 2012. The optimization of environment and genotype to maximize farm income in the tropics. Khon Kaen Agr. J. 40(2): 100–103.

Usman T, Guo G, Suhail SM, Ahmed S, Qiaoxiang L, Qureshi M.S and Wang Y. 2012. Performance traits study of Holstein Friesiancattle under subtropical conditions. J. Anim.and Plant Sci. 22(2): 91–95.

Valencia M, Montaldo HH and Ruíz F. 2008. Interaction between genotype and geographic region for dairy production in Mexican Holstein cattle. Arch. Zootec. 57: 457.

Zwald NR, Weigel KA, Fikse WF and Rekaya R. 2003. Identification of factors that cause genotype by environment interaction between herds of Holstein cattle in seventeen countries. J. Dairy Sci. 86: 1009-1018.

.