Genotype-Environment Interaction Effects For Milk Production Traits For Holstein Cattle In Mexico

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Introduction

Global dairy production is increasingly based on the use of a limited number of high-performance populations selected mostly in intensive production systems in few countries. Genotype-environment interaction (GEI) studies may help in evaluating whether predicted superiority of animals under certain environmental conditions will be expressed in different environments.

Several environmental variables have been studied to evaluate their role on generating GEI for economically important traits in dairy cattle. Some of them have been country, region, herd size, average protein yield, coefficient of variation for protein yield, altitude, temperature humidity index, average temperature, milk yield, annual rainfall, peak milk yield, persistency, age at first calving, culling rate, and maximum monthly temperature (Fikse et al. (2003); Zwald et al. (2003); Bryant et al. (2007); Valencia et al. (2008); and Montaldo et al. (2009)). Previous studies on GEI in Mexican Holstein cattle involved the estimation of genetic correlations between countries and between regions for milk production (Cienfuegos-Rivas et al. (2006); Valencia et al. (2008); Montaldo et al. (2009)), but results concerning fat and protein yields and the possible influence of different herd environmental descriptors on the correlations are lacking.

The objective of this study was to determine GEI effects for milk, fat and protein yield from estimates of genetic correlations between high and low data group of several environmental descriptors in Mexico and genetic correlations between each level in Mexico with Canada and with USA data, for Holstein cattle.

Material and methods

Predicted transmitting abilities (PTA) for 305-d, mature equivalent milk (MLK), fat (FAT) and protein (PRO) yields for Mexican Holstein bulls were obtained using a repeatability model from the analysis of 65,880 to 95,155 records, obtained between 1997 and 2008 by the Mexican Holstein Association. Analyses were done using ASReml (Gilmour et al. (2006)). Fixed effects were calving season-parity and herd-year-season of calving. The pedigree file included 323,638 animals, of which 14,482 were sires and 158,363 were dams plus 150,763 cows without progeny. Data were edited to include only cows with first lactation and milk yield records, with known sires and dams; with known date of birth. Other restrictions were:

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$\geq$100 days in milk, $\geq$18 months of age at first calving, herds were required to have at least 3 records. For all the traits, extreme values more than 3 standard deviations above or below average were excluded from the analysis. Official genetic evaluations for 2008 of Holstein bulls used in the US for MLK, FAT and PRO, were obtained from the website of the Animal Improvement Laboratory, Department of Agriculture of the United States. Official genetic evaluations for 2008 of Holstein bulls used in Canada for MLK, FAT and PRO were obtained from the website of the Canadian Dairy Network.

The geographical location and altitude above sea level of each herd under study, and the historical weather records, were obtained from the nearest meteorological station to each herd, from the website of the Sistema Meteorológico Nacional (http://smn.cna.gob.mx/). The environmental herd descriptors used were: altitude above sea level (ALT), average age at first calving (AFC), calving interval (CIH), average herd size (AHS), annual maximum temperature (AMT), temperature of the warmest month of the year (TWM), annual rainfall (ARF), milk yield (MYH), fat:protein ratio (FPR), and fat plus protein yield (FPY). For all criteria, herds were grouped into two levels: high and low; above and below the herd average respectively. Genetic correlations between high and low levels in Mexico were obtained using bivariate repeatability models with similar effects to those used for obtaining the PTA. The genetic correlations between countries were obtained from the observed correlations among the PTA of each bull in two countries divided by the square root of the product of their average reliabilities (Calo et al. (1973)).

Results and discussion

Genetic correlations between high and low groups in Mexico for MLK were generally high (>0.92) for most of the environmental descriptors (Figure 1) ranging from 0.87 to 0.97. The values for FAT were generally >0.80 (Figure 2) ranging from 0.63 to 0.97. The values for PRO were generally >0.84 with a range of 0.78 to 0.98 (Figure 3). Genetic correlations between high Mexican levels and US were between 0.85 and 0.90 for MLK; 0.82 and 0.87 for FAT and, 0.88 and 0.90 for PRO. Genetic correlations between high Mexican levels and Canada were between 0.81 and 0.88 for MLK, 0.79 and 0.89 for FAT and, 0.84 and 0.92 for PRO. Genetic correlations between low Mexican levels and US were between 0.86 and 0.88 for MLK; 0.78 and 0.90 for FAT, as well as 0.82 and 0.93 for PRO. Genetic correlations between low Mexican levels and Canada were between 0.81 and 0.87 for MLK, 0.79 and 0.87 for FAT and, 0.86 and 0.91 for PRO.

Genetic correlations were generally greater between Mexican high and low level groups, than between Mexico and Canada or US, for the most of the environmental descriptors for MLK, and lower for FAT and PRO (Figures 1-3). There was a trend for higher genetic correlations between high environmental descriptor levels with US or Canadian breeding values compared with low environmental levels only for AFC, AMT and TWM for MLK, AFC and ALT for FAT and ALT and ARF for PRO.

For MLK and both, high and low groups for most environmental descriptors, the genetic correlations with US breeding values were slightly higher than for Canadian Breeding values, but for FAT and PRO, the trends are less clear.

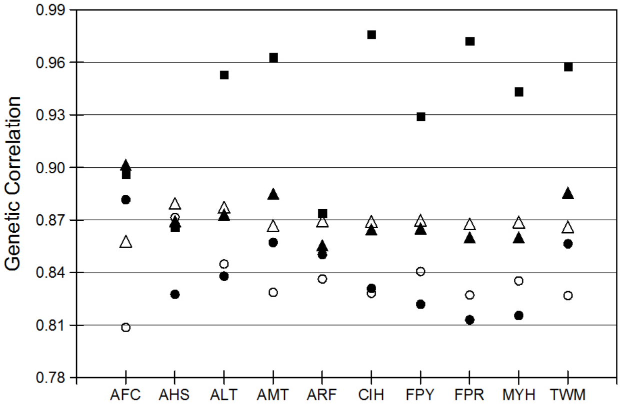

Figure 1. Genetic correlations between high and low levels for several environmental descriptors in Mexico (■), and genetic correlations between high (●) and low (○) levels in Mexico with Canadian breeding values, and high (▲) and low (△) levels in Mexico with United States breeding values for milk yield in Holstein cattle

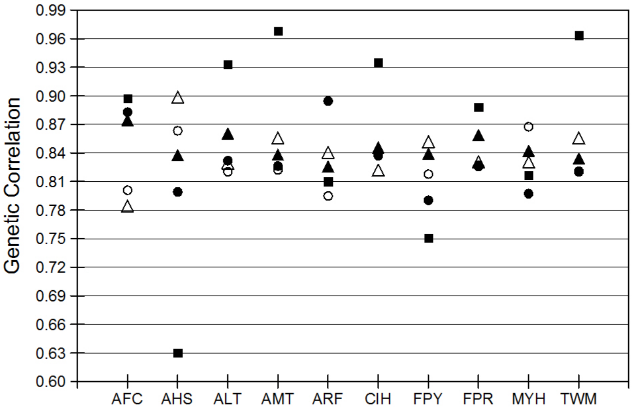

Figure 2. Genetic correlations between high and low levels for several environmental descriptors in Mexico (■), and genetic correlations between high (●) and low (○) levels in Mexico with Canadian breeding values, and high (▲) and low (△) levels in Mexico with United States breeding values for fat yield in Holstein cattle.

Environmental descriptor key

AFC=average age at first calving; AHS=average herd size; ALT=altitude above sea level; AMT=annual maximum temperature; ARF=annual rainfall; CIH=calving interval; FPY=fat plus protein yield; FPR=fat:protein ratio; MYH=milk yield; TWM=temperature of the warmest month of the year.

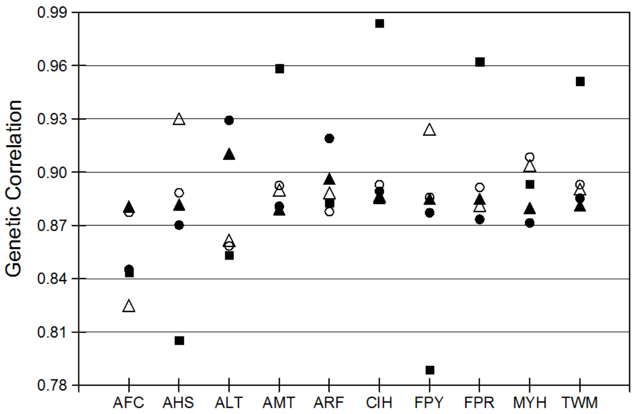

Figure 3. Genetic correlations between high and low levels for several environmental descriptors in Mexico (■), and genetic correlations between high (●) and low (○) levels in Mexico with Canadian breeding values, and high (▲) and low (△) levels in Mexico with United States breeding values for protein yield in Holstein cattle.

Conclusion

The results confirm the existence of moderate GEI effects for MLK and possibly somewhat higher GEI effects for FAT and PRO, considering both different levels for several environmental descriptors within Mexico, and between Mexico with Canada and US. Correlations related to AFC and AHS levels were in general different from those for the other descriptors.

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