

## Selection response for milk production in conventional production systems in Mexico, using genetic evaluations of Holstein sires from Canada and the United States

H. H. Montaldo,\*<sup>1</sup> S. G. Núñez-Soto,† F. J. Ruiz-López,‡ and H. Castillo-Juárez§

\*Departamento de Genética y Bioestadística, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, 04510, Distrito Federal, México

†Comité Estatal de Fomento y Protección Pecuaria de Guerrero, Servicio Nacional de Sanidad, Inocuidad y Calidad Agroalimentaria, Secretaría de Agricultura, Ganadería, Desarrollo Rural, Pesca y Alimentación, 39095, Guerrero, México

‡Centro Nacional de Investigación en Fisiología y Mejoramiento Animal, Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias; Secretaría de Agricultura, Ganadería, Desarrollo Rural, Pesca y Alimentación, 76280, Querétaro, México

§Departamento de Producción Agrícola y Animal, Universidad Autónoma Metropolitana-Xochimilco Calzada del Hueso 1100, 04960, Distrito Federal, México

### ABSTRACT

Polynomial regression models of the first, second, and third order were used to fit milk production deviations of daughters in Mexico on Canadian and US predicted transmitting ability values for 305-d mature-equivalent milk production (kg). For the pairs Canada-Mexico and Mexico-United States, 40 and 73 bulls with a minimum reliability of 0.75 were analyzed, respectively. Genetic correlations between pairs of countries were also estimated. The parameters were evaluated for all data, and for sires grouped according to the mean of the average phenotypic milk production (high and low) of their daughters' herd mates. Quadratic and cubic effects were not significant in any analysis. From linear regression models, slopes of Mexican daughter deviations on US and Canadian predicted transmitting abilities were 1.01 and 0.93, respectively. Slopes were greater but intercepts were smaller for the high versus low level of production of the sires' herd mates in Mexico. A greater difference between the genetic correlations was found for the high versus low environmental level than for the low level (0.79 vs. 0.70) for Mexico-US data compared with Canada-Mexico data (0.81 vs. 0.78). Genetic correlations between Mexico and the United States (0.74), and between Mexico and Canada (0.77), were smaller than the genetic correlation between the same Canadian and US sires (0.92), suggesting the presence of a moderate degree of genotype-environment interaction for milk production between Canada and the United States, and Mexico.

**Key words:** selection response, milk production, sire evaluation, Mexico

### INTRODUCTION

In 2005, the dairy cow population in Mexico consisted of approximately 2.2 million animals (Servicio de Información Agroalimentaria y Pesquera, Secretaría de Agricultura, Ganadería, Desarrollo Rural, Pesca y Alimentación, 2009). In 2007, the specialized dairy population consisted of approximately 0.85 million cows, and animals were raised mainly in temperate areas in the high plateaus of central Mexico and in the arid areas of northern Mexico under intensive and semi-intensive systems. This specialized dairy population, mostly Holstein, in 2007 accounted for approximately 50% of the total milk production of 10.3 million tons in the country, and that proportion is increasing (Servicio de Información Agroalimentaria y Pesquera, Secretaría de Agricultura, Ganadería, Desarrollo Rural, Pesca y Alimentación, 2009).

The number of cows in official milk recording by the Holstein Association for genetic evaluation purposes was approximately 42,000 in 2008, which was confined to registered Holsteins. Therefore, the number of recorded cows is approximately 4.9% of the number of specialized dairy cows in the country.

The development of the Holstein breed in Mexico in the last 30 yr has been based mainly on imports of live animals, semen, and embryos from the United States, Canada, and, more recently, from Europe and Oceania (Powell, 1983; Valencia et al., 1999).

Selection responses in Mexico from the use of US-selected Holstein sires, evaluated from the regression of deviations of daughters on sire PTA, have been estimated as 0.78 (Stanton et al., 1991), whereas the observed responses inside the United States have been close to 1 (Powell and Norman, 1984). These differences have been attributed both to smaller genetic variances in Latin America, which are associated with lower production levels, and to genetic correlations smaller than

Received February 19, 2009.

Accepted July 1, 2009.

<sup>1</sup>Corresponding author: montaldo@servidor.unam.mx

1 between countries (Stanton et al., 1991; Cienfuegos-Rivas et al., 1999). Cienfuegos-Rivas et al. (1999) estimated values between 0.60 and 0.93 for the genetic correlations between Mexico and the United States.

No previous studies have evaluated nonlinear relationships between selection responses in Mexico and genetic evaluation of sires from Canada and the United States. The use of these models might assess whether genes with a large positive or negative effect in a first country with a better environment would have a greater environmental sensitivity that might decrease or increase their response in a second country with a more restrictive environment.

Some authors have found nonlinear relationships between production and conformation characters in dairy cattle (Fuerst-Waltl et al., 1998). The theoretical support for such a relationship is an increasing competition for the use of the same resources once a threshold is reached (Sölkner and James, 1994). These types of effects may theoretically lead to a concave or sigmoidal relationship between evaluations and selection responses, characterized by a shift at the extremes of the distributions. Therefore, these types of interactions may lead to nonlinear relationships between genetic evaluation at a high environmental level and its genetic response at a low environmental level.

The objective of this study was to evaluate the presence of genotype  $\times$  environment interactions (**GEI**) for milk production in Holstein cattle by using linear and polynomial regression models of a second- and third-order degree to predict the contemporary deviations of daughters in Mexico from PTA of Canadian and US sires. The genetic correlations of production traits between countries were also evaluated.

## MATERIALS AND METHODS

### Data

Genetic evaluations for Mexico were obtained by the Holstein Association of Mexico for 2,502 bulls born from 1985 to 1998. The evaluations were calculated by using a single-trait repeatability animal model. Official genetic evaluations for the year 2001 in Canada were obtained from the Web site of the Canadian Dairy Network (2001) for 5,680 bulls born from 1958 to 1997. Official genetic evaluations for the year 2001 in the United States were obtained from the Web site of the Animal Improvement Programs Laboratory of the USDA (USDA-ARS, 2001) for 52,127 bulls born between 1950 and 2001. The data for bulls with evaluations in Mexico-United States and Canada-Mexico were edited in a file with a minimum reliability of 0.75. This was done to reduce the influence of random environ-

mental and genetic effects on the averages of the daughters of each bull (Montaldo, 2001). The reliability was defined as the estimated  $r_{T,PTA}^2$ , where T is the true transmitting ability of the sire.

When initially combining the files, 967 bulls had an evaluation in Mexico and the United States, whereas 382 had an evaluation in Mexico and Canada. When the data were edited to include only bulls with at least the minimum reliability, only 73 bulls had evaluations in Mexico and the United States, and only 40 had evaluations in Mexico and Canada. Among them, 40 bulls having evaluations in Canada and the United States were used as the control group. All the genetic evaluations were expressed as PTA in 305-d mature-equivalent milk production (kg). The information from 1 sire having a Studentized residual of 3.6 standard deviations in the linear regression analyses (see below) was excluded from the final data set because it had the potential to bias the estimates.

Two environmental levels were defined according to the 305-d mature-equivalent milk production average of the herd mates of the daughters of each sire in Mexico for each group of sires. Values below the general mean (10,488 kg) for the sires with information both in Mexico and the United States were classified as a low environmental level ( $n = 37$ ), and the values above the general mean ( $n = 36$ ) were considered as a high environmental level. Values below the general mean (10,585 kg) for the sires with information both in Mexico and Canada were classified as a low environmental level ( $n = 20$ ), and the values above the general mean ( $n = 20$ ) were considered as a high environmental level (Table 1).

### Analysis and Statistical Models

Polynomial regression models of a first-, second-, and third-order degree were fitted, with the contemporary deviations of the daughters in Mexico as the dependent variable and the PTA of Canada or the United States as the independent variable. The contemporary deviations of the daughters in Mexico were calculated by deregressing the Mexican PTA by dividing it by the reliability of the evaluation (Goddard, 1985).

The regression coefficients and the adjusted coefficients of determination ( $R_{adj}^2$ ) were obtained for all models with the REG procedure of the SAS program, version 8.0 (SAS Institute, Inc., Cary, NC), using ordinary least squares (Littell et al., 1991). The analyses were performed for the complete set and by environmental level. Hypothesis testing regarding the regression coefficients being lower than 1.0 and for differences between them was done by using independent *t*-tests (Gill, 1978).

Download English Version:

<https://daneshyari.com/en/article/2439380>

Download Persian Version:

<https://daneshyari.com/article/2439380>

[Daneshyari.com](https://daneshyari.com)