MODELS FOR GENETIC EVALUATIONS OF CONFORMATION, LONGEVITY AND MILK PRODUCTION TRAITS FOR HOLSTEIN CATTLE IN MEXICO

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INTRODUCTION

In earlier Mexican Holstein genetic evaluations for milk production several problems were detected : 1) the use of age-month correction factors estimated without considering differences among geographical regions and using a sire model ; 2) the possible existence of heterogeneity of variances for milk production across fixed effects was not considered ; 3) the possible existence of a genotype-environment interaction among regions was not evaluated ; and 4) the lack of genetic parameters for longevity, conformation and milk components traits limited the development of a comprehensive selection criteria for Holstein cattle in Mexico.

In this study new age-month correction factors for milk production were estimated. The existence of heterogeneity of genetic additive and residual variances was studied using different classification approaches. Also, the presence of a genotype-environment interaction was evaluated. With the aim of developing a system for Holstein cattle evaluation for Mexico, genetic and phenotypic parameters among conformation, longevity and milk production traits were estimated and some multi trait selection indexes were evaluated.

MATERIAL AND METHODS

The records used were obtained between 1970 and 1997 by the Mexican Holstein Association. Data analyzed included a file of 120 399 cows with milk production records, 10 465 cows with conformation traits and 184 269 animals in a pedigree file. Details on data and pedigree files edition can be found in Valencia *et al.* (1999), Valencia *et al.* (2000) and Valencia (2001).

Age-month correction factors (CF) for milk production were estimated for North, Central and South regions of the country, using an animal model. Additive, permanent environmental and residual variances for milk production classified by region, period and region-period were estimated as well. The same estimates were obtained for three groups (high, medium and low) of herd-years, classified according their standard deviation value.

Heritability (h^2), repeatability (r), genetic correlations (r_g) among regions, and genetic and phenotypic trends for milk production were estimated. To study genotype x environment interaction, r_g were obtained through daughters of sires distributed in several regions. A likelihood ratio test was used to evaluate if the r_g between two regions was less than one.

In addition, the h^2 for three longevity traits (total milk production until third lactation (TM3), length of productive life until third lactation (PL3) and stayability to 48 months of age (SA48), and h^2 for twelve conformation traits were estimated. The r_g and phenotypic correlations among these traits and first lactation milk production (MP1), were also estimated. All longevity traits were corrected for MP1. (Co)variances were estimated with REML procedures using an animal model with the MTDFREML program (Boldman *et al.,* 1995).

Predicted breeding values (PBV) were obtained for milk production, using the best linear unbiased predictor methodology. Expected selection response was estimated using selection index for multiple traits (Van der Werf, 2000) including MP1, SA48 and final score (FISC).

RESULTS AND DISCUSSION
CF estimated in this study were different (P < 0.05) from those currently used by the Mexican Holstein Association. Large differences between current correction factors and those estimated in this study were found for cows 18 - 40 months old, in January, and between correction factors for the North region with current correction factors for cows older than 70 months in April.

Ranges of h^2 and repeatability for milk production were 0.14 to 0.42, and of 0.36 to 0.51, respectively. All additive and residual variances, classifying the records by regions, periods and region-periods with first and all lactations were heterogeneous (P < 0.05). Even though genetic and phenotypic variances were different for herd-years classified by standard deviation level, heritabilities were similar (0.23, 0.21 and 0.24 for high medium and low level, respectively).

The r_g obtained for milk production between North and South regions (0.38), was significantly smaller than 1 (P < 0.05), indicating the presence of genotype x environment interaction.

For the genetic evaluations, averages for : number of herds where the daughters are, daughters' number, milk production of daughters, reliability (REL) and the predicted transmitting ability (PTA) for 1,790 sires, were 2.9 herds, 11.2 daughters, 9,079 kg, 49 % and 14 kg, respectively. For cows, averages were 9,566 kg, 37 % and 41 kg for first calving milk production, REL and PTA, respectively. Genetic and phenotypic trends for milk production were of 29 kg and 151 kg per year, respectively.

The h^2 for longevity traits were low (0.001 to 0.06), and those of conformation traits had values from 0.04 to 0.37. The r_g's between longevity traits were greater than 0.72, and between longevity traits and MP1 were from 0.33 to 0.64 (table 1). The r_g's between MP1 and conformation traits were from –0.27 to 0.48, and between SA48 and conformation traits from –0.30 to 0.69.

Table 1. Heritability (on diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations for longevity traits [A] and first lactation milk production (MP1)

	SA48	PL3	TM3	MP1
SA48	0.03 (0.05)[B]	0.94	0.86	0.38
PL3	0.87	0.04	0.73	0.33
TM3	0.72	0.77	0.06	0.64
MP1	0.08	0.08	0.54	0.25

[A] SA48 = stayability to 48 months of age ; PL3 = length of productive life until third lactation ; TM3 = total milk production until third lactation. [B]In parenthesis : heritability corrected to underlying Normal scale.

Expected selection responses using selection index, were obtained using different relative weights for MP1 (kg), FISC (points) and SA48 (%), the relative weights being expressed in additive standard deviation units of each trait.

Expected responses per generation giving the largest increments for SA48 (%), MP1 (kg) and FISC (points), were estimated for indices whose relationships were 3 : 2 : 0, 0 : 1 : 0, and 1 : 2 : 3, respectively. For SA48, the largest response was 0.77 %, or around 1.8 % of the average by generation, for MP1, the largest response was 742 kg, which represents an increment of 8.8 %, and for FISC the largest response was 0.97 points, or 4.9 % from the population average.

According to the results obtained in this study, some of the traits that could be incorporated into selection programs for registered Holstein cattle in Mexico are those related to mammary system, feet and legs, FISC and SA48.

Selection index results suggest that the use of an index, whose relationship was 1 : 4 : 1, can yield improvements by generation of 0.71 %, 632 kg and 0.61 points for HP48, PL1 and PUFIN, respectively, for the Holstein cow population of Mexico.

CONCLUSION

It is considered appropriate that CF estimated in this study be used in future milk production genetic evaluations in Mexico, because more appropriate predictions will be achieved.

With the procedures used to obtain PBV's in this study was possible to establish the basis for a reliable system of genetic evaluations for Holstein cattle in the country. In the future, it will be necessary to make studies to consider heterogeneity in the additive and residual variances for milk production on obtaining PBV and their unbiasedness.

Due to the negative association found between MP1 and depth of the udder, feet angle, fore udder attachment and fore teat placement, is necessary to incorporate other characteristics, as selection criteria, in the improvement programs of registered Holstein cattle in Mexico. Some of the traits that could be included, are those related to mammary system, feet and legs, FISC and SA48. It is suggested a continue emphasis to selection for milk production.

ACKNOWLEDGMENTS

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