Impact of Conformation Traits on Genetic Evaluation of Length of Productive Life of Holstein Cattle in México

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Introduction

Length of productive life (LPL) is a trait of increasing importance in cattle breeding programs. In dairying, the economic advantage of LPL lies mainly in retaining productive and healthy cows for as long as possible in the herd. LPL is influenced by different factors, *e.g.* fertility, milk yield, health, management and other reasons of voluntary culling (Ducrocq & Sölkner 1998, Weigel, Palmer & Caraviello 2003).

Many of the current genetic evaluation models for length of productive life in dairy cattle are based on survival analysis, which allows to combine data on both dead (uncensored) and alive (censored) individuals, enables a proper statistical treatment of censored records and accounts for nonlinear characteristics of LPL data. Survival Analysis also allows the estimation of random effects using the covariance structure among observations based on genetic relationships and the calculation of animal culling risks with a mixed model (Ducrocq & Sölkner 1998, Caraviello, Weigel & Gianola 2004). Different traits have been used in order to increase the reliability of the prediction of length of productive life of cattle. For many years, conformation traits have been used as indirect selection criteria for herd life since they can be measured early in productive life (usually during the first lactation) and have reasonable moderate genetic correlations with longevity (Short & Lawlor 1992). In México, Holstein Association scores 24 conformation traits describing udder, feet and legs, rump and body structure. The objective of this study was to investigate the impact of conformation traits on the genetic evaluation of LPL of Mexican Holstein Cattle and to review genetic trends of sires used in this population.

Material and methods

Data. The data set obtained from the Mexican Holstein Association consisted of 10,066 lifetime records of Holstein cows calving for the first time from January 2000 to December 2008. Data files had corrected ME 305 d milk yield with an average ± std of 24,755±13,229 kg, age at first calving, censure indicator (34% of right censured records), length of productive life adjusted to 305 days in each lactation, identification of the sire and maternal grandsire and information of 24 conformation traits: height to the withers (HW) ,stature(ST), size (SI), chest width (CW), body depth (BD), rump angle (RA), rump width (RW), loin strength (LO), foot angle (FA), claw uniformity (UN), heel depth (DH), bone quality (BQ), rear leg side view (RSV), rear leg rear view (RLW), fore udder attachment (FUA), front teat placement (FTP),

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teat length (TL) , median suspensory ligament (MSL), udder texture (TE), rear udder height (RUH), rear udder width (RUW), rear teat placement(RTP), udder depth (UD), angularity (AG). Classes of conformation traits with less than 50 records were added to the immediate superior or inferior class; therefore, eventhough all classes were measured in a 1 to 9 scale, some conformation traits have different number of classes. ME Milk yields were grouped in 10 production levels within herd-year of calving.

Model. The estimation of the parameters of the Weibull distribution and the prediction of sire genetic values was performed using the program Survival Kit V3.12 (Ducrocq & Sölkner 1998; Ducrocq 1994), using a sire-maternal grandsire model. The hazard function h (t) for a particular cow at time t was modeled as follows:

$$h(t)= h_0(t)* exp\{ HA(t)_i + EP_j + NP(t)_k + FL(t)_l + CM_m + S_q + A_r \}$$

where: h(t) = Probability of an animal of being culled at day t after the fist calving, $h_0(t)$ = baseline hazard function, assumed to follow a Weibull distribution with the parameters ρ (fixed=2) and λ. Time dependent variables were $HA(t)_i$ = Effect of herd-year of calving, where i=1 to 926, $NP(t)_K$ = Effect of level production in herd-year of calving; where k=1 to 10, and $FL(t)_l$ = Effect of lactation phase with changes at the 29, 249 and 305 days in each lactation, where l=1 to 12. Time independent variables used were: EP_j = Effect of age at first calving in months, where j=1 to 14, CM_m = Score of conformation traits where m=1 to 9, S_q =Random effect of sire q, where q=1 to 1,710, A_r = Random effect of maternal grandsire r, where r=1 to 1484.

Results and discussion

The plot of ln (-ln $\hat{S}$) against ln t (graph no shown) gave a straight line with a slope equal to ρ and intercept equal to ρ ln λ which indicates that a Weibull model could be applied for the data. The heritabilities for LPL were estimated as 0.09 and 0.12 in logarithmic and real scales, respectively.

Effects of herd-year of calving, age at first calving, production level within herd-year of calving, lactation phase, and some conformation traits: RW, HW, CW, LO, SI, FA, UN, RSV, DH, RLW, TE, FUA, RUH, RTP,FTP, and AG were statistically significant ($p<0.001$; figure 1). These results are similar to those of Caraviello, Weigel and Gianola (2004) who concluded that rear legs' are traits that describe closely LPL and those of Chirinos, Hernández and Carabaño (2005) and Dadpasand *et al.* (2008) who concluded that mammary system traits have a strong relationship with functional longevity. Nevertheless, our results show that mammary system characteristics did not have the strongest relationship with length of productive life, the exception being AG.

Similarly to the findings of Chirinos, Hernandez and Carabaño (2005), animals with low milk production are at a higher risk of being culled. In the Mexican Holstein population higher relative risks of culling were associated with low production classes until class 6, after which the risk levels out (figure 2).

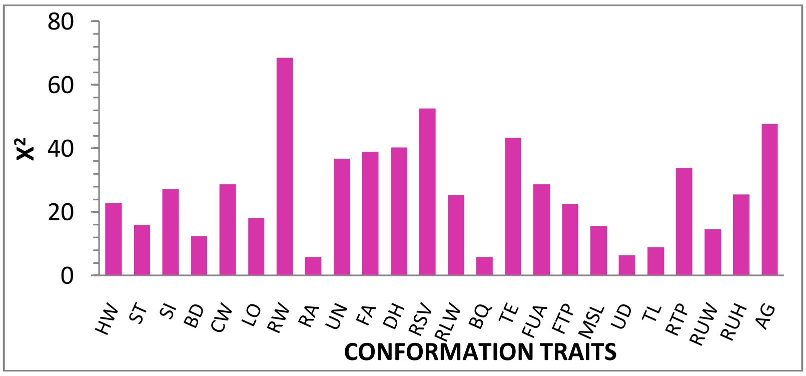

Figure 1: Contribution to the likelihood (X2) of adjusted phenotype for different conformation traits on length of productive life for Holstein cattle in Mexico. For explanation of trait abbreviations see text.

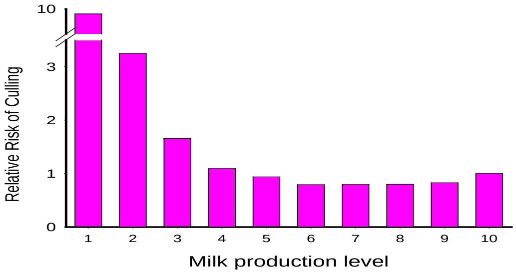

Figure 2: Relative culling risks associated to milk production levels of Holstein cattle in Mexico.

The relative risk of culling per lactation (1, 2, 3 and ≥ 4 , each one with three phases: 0-29, 30-249 and 250-305 days) changed in each phase within lactation. As expected, relative risks in lactation 1 are slightly higher than for the other lactations and the last phase of each lactation is associated with higher risks reflecting the delaying of culling cows until the lactation is finished (figure 3). These results are similar to Chirinos, Hernandez and Carabaño (2005) who conclude that relative risk is higher in days of first lactation and then decrease in later lactations.

Genetic trend for LPL of sires born from 1990 to 2002 indicate that sires' relative risk of culling were increasing slightly from 1990 to 2000 but in the last two years the risk of culling has increased significantly (figure 4). This increase of relative risk could be explained by the lack of attention of Mexican breeders to this trait possibly due to the need of increasing milk yields in difficult economic times.

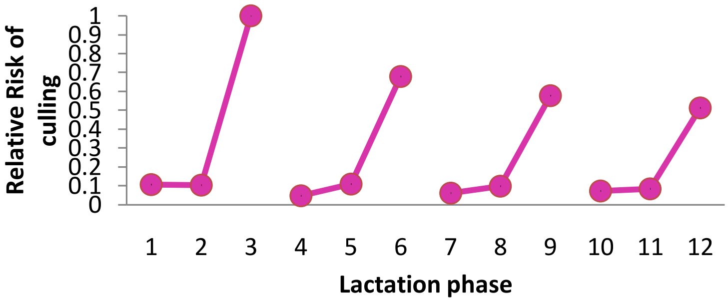

Figure 3: Relative culling risk for lactation phase of Holstein cattle in Mexico

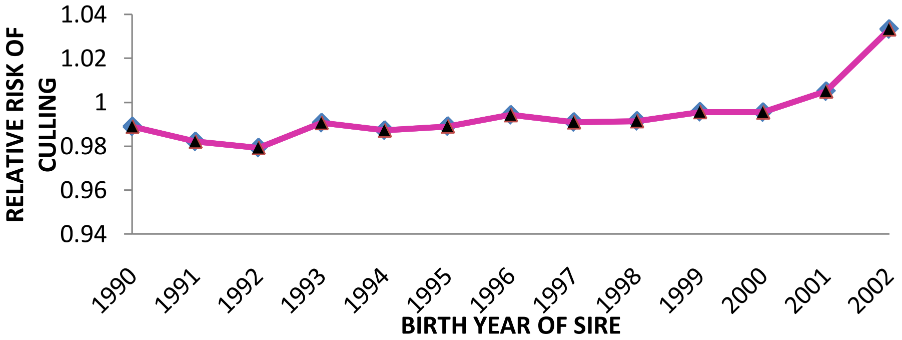

Figure 4: Genetic trend of sires for LPL (birth years from 1990 to 2002)

Conclusions

Two thirds of the conformation traits (16 of 24) scored in the Mexican Holstein population were statistically significant in order to predict breeding values for length of productive life; therefore the genetic evaluation for LPL should include these traits as indirect predictors of longevity. In addition, an improvement in LPL is expected if the trait is included in genetic selection programs.

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