

RELATIONSHIP BETWEEN TRANSMITTING ABILITY FOR MILK PREDICTED IN THE COUNTRY OF ORIGIN OF THE SIRE AND LENGTH OF PRODUCTIVE LIFE OF ITS DAUGHTERS IN MEXICO

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INTRODUCTION

Length of productive life (LPL) has been long recognized as a trait of economic importance, not only because of increased replacement costs but also because the loss of milk production incurred when the cows can not reach their full production potential (Allaire and Cunningham, 1980).

In countries where cows in dairy herd improvement programs (DHI) are in limited numbers, genetic evaluations usually involve the use of few records. When evaluating foreign sires, it is common that the number of daughters in the importing country are far less than the ones evaluated in the exporting country. This is particularly important when evaluating low heritability traits like LPL. Time from first parturition to culling is not only far from normal distributed, but it presents the added problem of a high incidence of incomplete records (those for which only part of the LPL is known, for example either because the cow is still in the herd or because the cow left the herd to continue its productive life in some other herd). Survival analysis methodology (Kalbfleish and Prentice, 1980) is well suited to handle the above mentioned cases because it can accommodate incomplete records.

Ducrocq *et al.* (1988) studied the use of a Weibull regression model to describe LPL of US dairy cows. The utilization of Weibull regression models and other survival analysis techniques allow the use of incomplete records in the analysis. Cows with culling dates on record are considered as complete records (also known as failures), while cows still in production or cows for which the data is no longer available at the time of study are considered censored records.

Ruiz (1991) used a Weibull regression model to study the effect of sire's country of origin, within herd-year standardized milk production level and herd-year on Mexican dairy cattle LPL finding a significant contribution of origin of sire group to the explanation of LPL variation. Ruiz and Trejo (1993) examined the need of an additional random term in the model to better describe the data using a frailty test and concluded that the sire effect was enough to describe the whole behavior of LPL although they never included the genetic relationships among sires or estimated the trait's heritability.

The objectives of this paper were then, to investigate if the genetic evaluation of a sire in its country of origin could be related to the LPL of its daughters in an importing country and to estimate the dispersion parameter for the sire effect under a log-gamma assumption in a Weibull model.

MATERIAL AND METHODS

Length of productive life (LPL) records of 38 797 cows, obtained between 1970 and 2001 from the Mexican Holstein Association DHI were used. LPL was defined as the time from first calving to culling. If a herd left the DHI program or a cow was sold for further production, the

record was considered as censored. Predicted transmitting abilities (PTA) for US and Canadian sires were obtained for the November 2001 genetic evaluation from the Animal Improvement Programs Laboratory-ARS-USDA and from the Canadian Dairy Network, respectively. Pedigree information was obtained for 302 sires and their ancestors (651 animals in total) from the Mexican Holstein Association.

Milk yield PTA's were standardized within country to account for differences in variation between countries. A Weibull regression model that included the fixed effects of herd-year of first calving, and linear and quadratic effects of standardized PTA and the random effect of sire was used. A log-gamma distribution was assumed for the sire random effect. Estimates of the Weibull parameters and regression coefficients were obtained through the use of The Survival Kit V3.12 (Ducrocq and Solkner, 1988). The basis of the program and the use of survival analysis in animal breeding were extensively described in Ducrocq and Casella (1996).

RESULTS AND DISCUSSION

From the total records used 8.6 % were considered censored. This was lower than the 15 % found by Ruiz (1991) because a different definition of censoring was used in that paper. Average LPL for uncensored records was 741 days while average censoring time was 360 days. The records came from 1 018 different herd-years of first parity.

Survivor Functions

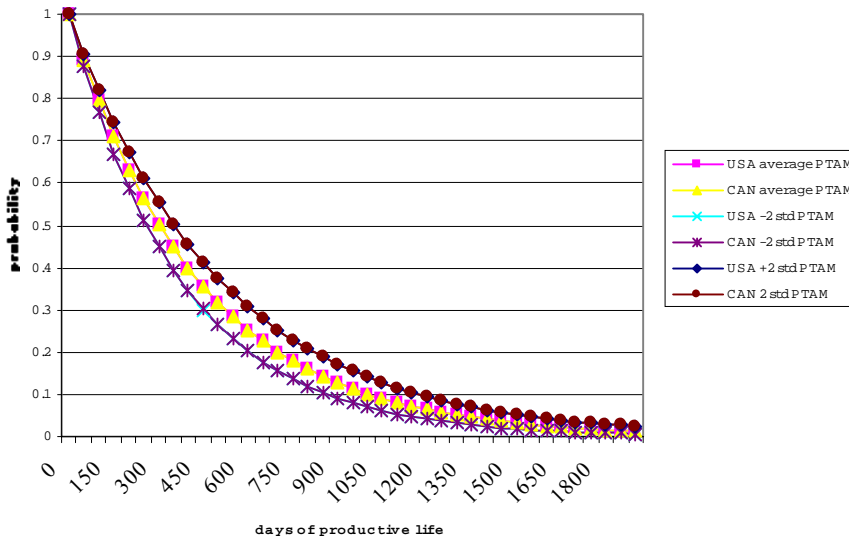


Figure 1. Survivor functions for daughters of average sires, high predicted transmitting ability for milk (PTAM) sires (+2 std) and low predicted transmitting ability for milk sires (-2 std)

Since the effects of standardized PTA squared were found not important ($P > 0.05$) the model was fitted again including the linear effects only. The estimates of the Weibull model were : $\rho = 1.86$ (s. e. 0.0078) and $\lambda = 0.001$.

The variance parameter for the assumed log-gamma distribution of the sire effect was estimated at 52.37, which in turn yielded a heritability estimate on the logarithmic scale of 0.05, very much in tune with previous estimates for longevity traits heritabilities (Valencia *et al.*, 2001)

Regression coefficients for standardized PTAs were -0.0765 (s. e. -0.0168) and -0.0761 (s. e. -0.0289) for US and Canadian sires, respectively. Average effect for US sires was -0.008 with a minimum of -0.329 and a maximum of 0.513. Similar results for Canadian sires were 0.003, -0.227 and 0.291, respectively. Average effect of herd year was zero. The survivor curve for these equations is presented in figure 1.

The survivor curves for US and Canadian sires were quite similar and no difference was found between them.

In general, the results found in this work warrant the use of foreign data in the genetic evaluation of LPL for Mexican Holstein cattle.

CONCLUSION

There is an effect of sire's PTA for milk predicted in its country of origin on the LPL of their daughters in Mexico, although no difference was found between countries.

Approximate heritability for LPL was estimated at 0.05, which is fairly close to what has been reported for this population using linear mixed models.

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