

VARIANCE COMPONENTS ESTIMATION FOR STATURE IN CHILEAN BLACK AND WHITE FRISON DAIRY CATTLE USING RANDOM REGRESSION AND BAYESIAN INFERENCE

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INTRODUCTION

Phenotypic expression of type traits changes over span life and may be regulated by different set of genes ; if this were the case type traits genetic evaluation should consider the age when different observations in the same animal are recorded. Milk production in south of Chile is mainly based on grazing, therefore concern exists because Holstein genetic introduced in the country may not fit local grazing conditions. Taller cows raised and performance tested in especially designed dairy barns may not have the required walking ability to produce on grazing conditions. Soil compaction produced for heavier cows is also an issue to be considered. Dairy cattle in Chile are not genetically evaluated for type traits, breeding stock genetic merit is erroneously extrapolated from foreign dairy sire catalogues available from frozen semen companies. Genetic evaluation of conformation traits like stature, that changes with age, requires that cows be measured several times across their life, therefore a method that account for changes as an animal becomes older should be used to obtain closer estimation of the animal's breeding value.

Analysis of observations taken across time on the same subject can be accomplished using random regression (Henderson, 1982). In dairy cattle, where there are several controls within lactation, random regression methodology was implemented by Jamrozik and Schaeffer (1997). Schaeffer and Dekkers (1994) proposed a random regression framework to analyze type traits within a BLUP context. American Holstein type traits using field data and random regression were analyzed by Uribe *et al.* (2000). Conventional linear regression models assume that regression coefficient are fixed and equal to each subject in the data set, however if the observations are taken on a random cow population it is licit to assume that regression coefficient can be split in two parts : a fixed portion common to all animal and a random part which can be associated to genetic effects of a particular animal (Henderson Jr., 1982 ; Schaeffer and Dekkers, 1994). The random part of the regression coefficient accounts for the deviation of each animal from the fixed curve at a given age.

The objective of this work was to estimate stature variance components in Chilean Black and White Frison dairy cattle using random regression and Bayesian inference within BLUP framework.

MATERIAL AND METHOD

Data. Data were obtained from 10 commercial dairy farms of the Tenth Region in south Chile during a period of 6 months. The data set had observations on 1170 Chilean Black and White Frison heifers born between June 1997 and October 1998 ; withers height was measured every two months. After data editing there were 3140 observations on 1136 heifers. Through

pedigree files 1212 ancestor without observations were also included in the analysis.

Model. by plotting stature phenotypic means against age it was observed that the dependent variable could be explained as linear and quadratic functions of age. Although a phenotypic association between withers height and age does not necessarily indicate a genetic relationship this can be used as starting point to model the genetic component of the trait. The statistical model was : $Y_{ijklm} = GC_i + MN_j + (\beta_0 + \beta_1 Age + \beta_2 Age^2)_k + a + \lambda_1 Age + \lambda_2 Age + P_{kl} + e_{ijklm}$. Where : GC_i = fixed effect of the i^{th} contemporary group, MN_j = fixed effect of the j^{th} month of birth, β_0 is the mean nested in the k^{th} year of birth ($k=1,2$), β_1 and β_2 are fixed regression coefficients of height score on age and age squared, nested in the k^{th} year of birth, Age is age in months at measurement, α , λ_1 and λ_2 are the random genetic regression coefficients, relating height of the l^{th} cow to an intercept, age and age squared respectively, P_{kl} is the permanent environmental effect of the l^{th} cow, e_{ijklm} is the random error term. It was assumed that random factors in the model followed a normal distribution with mean equal zero and a structure of the (co) variance matrix as follows :

$$Var \begin{pmatrix} a \\ \lambda_1 \\ \lambda_2 \\ pe \\ e \end{pmatrix} = \begin{pmatrix} Ag_{aa} & Ag_{a\lambda_1} & Ag_{a\lambda_2} & 0 & 0 \\ Ag_{a\lambda_1} & Ag_{\lambda_1\lambda_1} & Ag_{\lambda_1\lambda_2} & 0 & 0 \\ Ag_{a\lambda_2} & Ag_{\lambda_1\lambda_2} & Ag_{\lambda_2\lambda_2} & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_e^2 \end{pmatrix}$$

where : \mathbf{A} is the additive genetic relationship matrix, g_{ij} are the genetic (co)variance among random animal regression coefficients, \mathbf{I} is an identity matrix. (Co)variance components estimation was done using Bayesian

inference. Flat priors were given for the fixed factors of the model, while random factors were assumed to follow a multivariate normal distribution. Priors for residual and permanent environment variance were scaled inverted Chi-squared distributions. Prior distribution of the (co) variance matrix, containing α , λ_1 and λ_2 , was proportional to an inverted Wishart distribution. As analytical integration of the marginal posterior distributions is not feasible, it was approximated through Gibbs sampling as described by Jamrozik and Schaeffer (1997). The Gibbs run had 100 000 samples ; the first 40 000 were considered as the 'burn in' period and were not used in final estimation of parameters. The remaining samples were used to estimate the mean of the marginal posterior distributions of the (co)variances. Geyer (1992) indicated that uncorrelated samples of the Gibbs chain are not needed to estimate the first moment of the posterior distribution, therefore no attempts to quantify the number of independent samples of the Gibbs run were made. Estimates of genetic (co)variances at a given age were obtained as described by Uribe *et al.* (2000).

RESULTS AND DISCUSSION

The data set analyzed had 28 contemporary groups ; each included all cows measured in a given visit by the same person. The means and standard deviations of posterior distributions corresponding to parameter estimates are given in table 1. Residual and permanent

environmental variances were 1.88 and 5.78 cm², respectively. Genetic variances and corresponding heritability estimates at 5, 10, 15 and 20 months of age are given in Table 2. Heritability estimates for stature in Chilean Black and White Frison heifers varied from 0.49 to 0.55 at 5 and 20 months of age, respectively. The lowest heritability estimate (.32) was found at 9 months of age.

The ranges of ages (5 to 20 months), cattle breed and height measurement units used in this work are different than those of Uribe *et al.* (2000) however the methodology used in both studies is similar. Heritability estimates for stature were slightly higher in this study as compared to those of Uribe *et al.* (2000). The data set used in this research was much smaller than that of Uribe *et al.* (2000), however, bias due to culling was minimal because almost all heifers had the opportunity to have all possible records during the study period. A shortcoming of random regression methodology, as applied here, is that heritability estimates are not independent of age and are forced by the regression function chosen ; extrapolation of age would force heritability toward zero or unity, which is meaningless. The definition of heritability in a random regression analysis is model dependant, which conflicts with the classical definition of this parameter. Regression theory does not permit inferences outside of the range of the data, if heritability estimation is done within the limits supported by the data, the estimates should be reasonable. Permanent environmental effects in type traits might also change as age progresses therefore a more correct approach would result by modeling these effects with random regressors similar to animal additive effects. If this were the case the denominator of the heritability formula could increase with age making the heritability estimates more stable or even decrease over time. Meyer and Hill (1997) showed the equivalence between random regression models and covariance functions. Covariance functions (Kirpatrick *et al.*, 1994) can be seen as matrices for traits with many records, from this perspective the covariances among records are defined as a function of time.

Table 1. Means and standard deviations of posterior distributions

Parameter	Mean	S. Deviation
g_{aa}	39.062	6.500
g_{a_1}	-5.797	1.004
g_{a_2}	0.169	0.038
g_{λ_1}	1.011	0.170
g_{λ_2}	-0.033	0.006
g_{λ_2}	0.001	0.0002
σ_{ep}^2	5.783	0.934
σ_e^2	1.88	0.086

CONCLUSION

Results of this work showed that genetic variation for stature changes across age, which is consistent with a previous study on American Holsteins. This variation is not currently being exploited by type traits breeding programs. Chilean dairy producers could obtain an advantage

if genetic evaluation is done in their own environment because predicted genetic merit for stature, as well as other type traits, would be more pertinent. Unfortunately the implementation of such a genetic evaluation program, exploiting random regression methodology, would require animals measured several times in life which may be unfeasible from an economic standpoint.

Table 2. Genetic variances and heritabilities at different ages for stature

Age (months)	Genetic Variance	Heritability
5	7.30	0.49
10	3.89	0.34
15	6.15	0.45
20	9.32	0.55

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