Longevity in genetic evaluation of Holstein cows in Uruguay

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Abstract

The objective of this study was to estimate variance components and to analyze the possibility of carrying out a genetic evaluation of the longevity trait in animals of the Uruguayan dairy production system of the Holstein breed. Longevity was defined as a binary trait with values of 1 and 0 whether or not the cow survived a lactation, respectively. For the analysis of the variance components, programs of the Blupf90 package were used, using the REML methodology and the Bayesian methodology. Heritability (with values between 0.03 to 0.13) was increasing according to the lactation. These results of the present study shows that even though it has a high influence of environmental factors, there is additive genetic variance available and therefore there is the possibility of inclusion of longevity in the genetic evaluation of Holstein cows in Uruguay

Introduction

Stayability, is defined as the probability of a female to remain in production at a specific age, given that she had the opportunity to reach this age (Hudson and Van Vleck 1981). Therefore, the selection for longevity has the objective of identifying those individuals with the greatest capacity to remain productive, that is, with the greatest probability of survival due to voluntary and involuntary culling within the herd.

With the increase in the lifespan of the cow, it is possible to achieve a greater dilution of the maintenance and replacement costs of females, as demonstrated by Gabler, Tozer, and Heinrichs (2000). They showed that the highest lactation yield occurs after the third parturition, so keeping the animal in the system for a longer time will result in an increase in the dairy production of the establishment.

For the evaluation of longevity, different ways to define the trait to be included were proposed (Imbayarwo-Chikosi et al. 2015). The chosen form and the statistical model used depend on different factors related to the final objective of the analysis and the data available.

The objective of this study was to estimate variance components and analyze the possibility of carrying out a genetic evaluation of the longevity trait in animals of the Uruguayan dairy production system of the Holstein breed.

Materials & Methods

Data. Records were available from the 'Instituto Nacional para el Control y Mejoramiento Lechero' (MU). The database was composed of milking cow's historical information, including reproduction, milk production and disposal information. Genealogical data was available from the 'Asociacion Rural del Uruguay' (ARU).

For variance components analyses, animals were required to have a known sire and dam and with the year of first calving between 1990 and 2014, giving the cow the possibility of completing at least five lactations. After editing the final dataset include records of 828,246 animals.

Trait definition. Longevity was defined as a binary trait with values of one and zero whether or not the cow survived the lactation, respectively. Thus, analyzing the probability that the animal remains in the dairy during the first five lactations.

Statistical model. Variance components analyses were performed using programs from the BLUPF90 package (Misztal et al., 2002), using the REML methodology (REMLF90 and AIREMLF90) and the Bayesian analysis methodology through Gibbs sampling (GIBBS2F90, THRGIBBS1F90 and POSTGIBBSF90). Multiple trait linear models and non-linear models were analyzed for the binary longevity traits at different lactations.

The following multi-trait model used was:

$$\mathbf{y = Xb + Zu + Zp + e}$$

Where y is the survival observation vector (1/0), X the incidence matrix that links the observations with the fixed effects, b the fixed effects vector (contemporary group effect, composed of herd-year of first calving and age at first calving), incidence matrix Z for the animal additive genetic effect, $u = N(0,G_0 \otimes A)$ with genetic covariance matrix (G_0) and additive genetic relationship matrix (A), p = vector corresponding to the permanent environment effect and the residual effect, $e = N(0,R_0 \otimes I)$, with a residual covariance matrix (R_0).

Breeding values were estimated for the linear and non-linear models in order to establish the correlations between the predictions and to asses the re-ranking of the animals according to the methodology used.

Results and discussion

Variance component analysis. The results of the variance components performed by the linear model (REML and Bayesian methodology) and nonlinear (Bayesian) are shown in Tables 1, 2 and 3, respectively. The estimates of additive genetic variance for the first five lactations are highlighted, confirming that there is genetic variability for longevity, allowing genetic improvement for the trait.

Table 1 Additive genetic variance, heritability and genetic correlations for the first five lactations - linear (REML)

Additive genetic variance / genetic correlation[1]					Heritability
0.004	0.004	0.005	0.006	0.007	0.03
0.97	**0.004**	0.005	0.007	0.008	0.03
0.86	0.94	**0.007**	0.009	0.012	0.04
0.87	0.93	0.98	**0.011**	0.015	0.05
0.82	0.01	0.96	0.97	**0.020**	0.08

[1] Upper triangle: additive genetic variance; lower triangle: genetic correlation between the first 5 lactations.

Table 2 Additive genetic variance, heritability and correlations for the first 5 lactations - linear (Gibbs sampling)

Additive genetic variance / genetic correlations[1]					Heritability
0.004	0.004	0.006	0.009	0.012	0.03
0.93	**0.005**	0.008	0.011	0.015	0.03
0.89	0.94	**0.012**	0.017	0.023	0.06
0.86	0.89	0.96	**0.027**	0.034	0.09
0.87	0.90	0.95	0.93	**0.049**	0.13

[1] Upper triangle: additive genetic variance; lower triangle: genetic correlation between the first 5 lactations.

Table 3 Additive genetic variance, heritability and correlation for the first 5 lactations - nonlinear

Additive genetic variance / genetic correlations[1]					Heritability
0.313	0.225	0.188	0.225	0.245	0.06
0.92	**0.197**	0.153	0.198	0.220	0.06
0.88	0.89	**0.152**	0.199	0.199	0.07
0.78	0.85	0.94	**0.298**	0.282	0.08
0.77	0.85	0.86	0.88	**0.341**	0.09

[1] Upper triangle: additive genetic variance; lower triangle: genetic correlation between the first 5 lactations.

Heritability increased according to the lactation analyzed, showing that the survival of the cow at a greater number of lactations depends more on genetic components. The methodologies present similar values for heritability and high genetic correlation values between the lactations.

The estimated values for heritability by the different models were similar to previous studies that showed values between 0.03 and 0.25 (Essl and Voith 2002; Jamrozik, Fatehi, and Schaeffer 2008; Sewalem et al. 2005).

The correlations obtained in the present study were similar with the previous studies for dairy cattle from Germany and Canada, (Heise et al. 2016 and Sewalem et al. 2007, respectively) , finding a high correlation between the different lactations.

The high correlation between traits will allow prediction of longevity at later ages from analysis carried out using the first lactations.

Correlations of the breeding values. The breeding values for the linear and non-linear model were estimated using BLUPF90 and THR1GIBBSF90 respectively, using the estimated variance components. Reliabilities were calculated using prediction error variance from the inverse of the mixed model (linear model) and from the posterior standard deviation of breeding values (non-linear models).

The correlation between the breeding values obtained through the linear model and the non-linear model for the first five lactations were greater than 0.98, which will not cause re-ranking of animals from the alternative genetic evaluation models. The correlation of the reliabilities between linear and non-linear models were greater than 0.99. No difference was found between the use of statistical analysis by direct analysis (blup) and analysis by Gibbs sampling (Bayesian).

Considering the computational cost and the greater complexity of performing a non-linear model and considering the correlation between the different models, the linear model can be used to estimate genetic values.

These results of the present study shows that even though it has a high influence of environmental factors, there is additive genetic variance available and therefore there is the possibility of inclusion of longevity in the genetic evaluation of Holstein cows in Uruguay.

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