



Genetic parameters and correlations between days open and production traits across lactations in pasture based dairy production systems



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ABSTRACT

The aim of this study was to estimate the additive genetic correlations, heritabilities and repeatabilities of days open (DO), milk (MY), fat (FY) and protein yields (PY), using data from pasture based dairy systems of Uruguay, and to explore whether DO should be interpreted as a different trait across lactations or as a trait with repeated measures. The database contained 500, 412 and 294 thousand records of first, second and third lactation, respectively. Cows were offspring of 7747 sires. Fertility records lower and upper limits were 42 and 250 days, respectively. In a first approach (Mdiff) we estimated variance components and covariances over lactations, assuming that the traits were different at each lactation. In a second approach (Mrep) estimations were carried out considering each trait as a repeated measure along lactations. In Mdiff, DO with a production trait was analyzed considering each lactation as a different trait. Three six-variate linear models were analyzed (DO-MY, DO-FY, DO-PY, and lactations first to third). In the Mrep procedure, DO, MY, FY and PY were analyzed together with a multiple trait repeatability model. For all models, the fixed effects were herd-year-season and lactation-age classes. Animal and the permanent environment effect were included as random effects. The additive genetic correlations between DO and yield traits by Mdiff were between +0.39 and +0.78; by Mrep, they ranged from +0.44 to +0.55. Heritabilities of DO by Mdiff were between 0.04 and 0.06 and 0.05 by Mrep. The additive genetic correlations of DO between lactations ranged from +0.76 to +0.91. Heritabilities of MY, FY and PY were 0.23, 0.21 and 0.21, respectively. Repeatabilities obtained were 0.10, 0.49, 0.47 and 0.49 for DO, MY, FY and PY, respectively. We concluded that the heritability of DO was low but enough to consider the trait in selection programs. We confirmed unfavorable additive genetic correlations between DO and yield traits for the Uruguayan pasture systems, which supports the importance of considering fertility in selection programs to reduce or avoid a decline in reproduction. The additive genetic correlations of DO between lactations were high, suggesting that a plausible model should consider DO records of a given animal as repeated measures.

1. Introduction

Selection in favor of production traits, e.g. milk yield (MY), has often resulted in a decline of functional traits such as the reproductive ones (Berger et al., 1981; Rauw et al., 1998; Roxström et al., 2001; Sewalem et al., 2010). Unfavorable genetic associations between production and reproductive traits come mostly from confinement production systems. Pasture-based systems, such as those predominating in Uruguay, represent a different environment, where additive genetic associations between production and reproduction might differ from those estimated in North America and Europe.

For the American and Canadian Holstein populations, the reports of

additive genetic correlations between production and reproduction traits have been unfavorable (Dematawewa and Berger, 1998; Abdallah and McDaniel, 2000; Sewalem et al., 2010). Dematawewa and Berger (1998) estimated additive genetic correlations of + 0.63, + 0.58 and + 0.57 between days open (DO) - MY, DO - protein (PY) and DO - fat yield (FY), respectively, in American Holstein. In Canada, Sewalem et al. (2010) reported a genetic correlation of + 0.29 between MY and calving - first service. Abdallah and McDaniel (2000) estimated an additive genetic correlation of +0.62 between DO and fat corrected milk.

Similar results have been found in Europe. For Spain, González-Recio et al. (2006) reported additive genetic correlations of + 0.63, +

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0.75 and + 0.76 between DO - MY, DO - FY and DO - PY, respectively. For Norwegian red cattle, Andersen-Ranberg et al. (2005) estimated an additive genetic correlation of + 0.47 between PY and calving - first service interval.

Additive genetic correlations are population parameters, affected by several factors, therefore estimates differ between countries or populations, yet unfavorable between production and reproduction. In addition, environmental and management factors have high impact on reproduction performance (Walsh et al., 2011), which explains that reproductive heritabilities are frequently below 0.10 (Dematawewa and Berger, 1998; González-Recio and Alenda, 2005; Chang et al., 2007).

Uruguay represents a different scenario, where additive genetic associations between production and reproduction might differ from those estimated in North America and Europe. In Uruguay, pastures represent approximately 55% of the dry matter intake (Rovere, 2010); these systems are possibly comparable with the Irish systems, where the additive genetic correlation between calving interval and milk production along the first three lactations ranged between 0.45 and 0.66 (Olori et al., 2003). In other pasture systems, like New Zealand, the additive genetic correlation between milk and conception rate at 42 days from first to third lactation ranged from -0.013 to -0.008 (Harris et al., 2006). Pasture systems of Uruguay have been described by Lizarralde et al. (2014). Briefly, cows normally graze year-round on grass-clover pastures lasting three to four years and annual grass pastures, and varying amounts of on-farm conserved forage (maize/sorghum and grass silage) are used to complement grazing. Concentrates are strategically used during lactation to meet the nutrient requirements of their expected production level. Holstein is the predominant breed, with an average mature cow weight of 550 kg and a milk production mean of 5300 kg. Cows mostly calve in autumn and spring, to avoid calving during summer. Heifers typically calve at 27 months of age.

Two different approaches have been considered for the analysis of dairy traits, (i) as a repeated measure trait or (ii) as different traits at each lactation. The second approach assumes that changes in the regulation and/or expression of the responsible genes may arise along cows' life (Jamrozik et al., 2005; Miglior et al., 2005; González-Recio et al., 2006; Tiezzi et al., 2012).

This study aims to fill a gap in the reports of additive genetic correlations between production and reproduction. The objectives were (i) to estimate the additive genetic and phenotypic correlations between DO - MY, DO - FY and DO - PY at first, second and third lactation under grazing conditions, using data from the Holstein population of Uruguay; (ii) to estimate the heritabilities and repeatabilities of each trait, and (iii) to examine whether DO should be considered as a different trait over lactations or as a repeated measure.

2. Materials and methods

2.1. Data and editing criteria

Dairy production and pedigree records of 415,530 cows born between 1986 and 2009 of 1138 herds were analyzed. Production and calving information was recorded between 1990 and 2013, and 1990 and 2011, respectively. The numbers of records per lactation order are presented in Table 1. Cows were sired by 7747 bulls, with an average of 61 progenies per sire. There were 343,198 cows with both parents identified, whilst 385,429 and 399,767 animals had only sire or dam identified, respectively. The database was provided by the Instituto Nacional para el Mejoramiento y Control Lechero Uruguayo, which is the official milk recording institution of the country.

The variable DO was calculated as the calving interval minus a gestation length of 280 days (Knott, 1932; VanRaden et al., 2004). MY, FY and PY are the yield of milk, fat and protein adjusted to 305 days.

Lactations in the database were edited in order to discard erroneous and/or outlier records. Animals in a given lactation were required to

have records in all the previous lactations. Observations of DO of 42–350 days' range were included in the analysis. Records of DO at 250 days were considered complete, according to VanRaden et al. (2004). For production traits values within 1500–12,500 kg for MY and 50 and 350 kg for PY and FY were considered in the analysis. Additionally, observations of MY, PY or FY above or below ± 1.5 standard deviations within contemporary groups were considered outliers and deleted. Contemporary groups required a minimum of 5 observations.

2.2. Statistical analysis

Variables were modeled by two approaches. Firstly, each trait was considered independently at each lactation (Mdiff). Secondly, traits were considered as repeated measures across lactations (Mrep).

The Mdiff model was:

$$Y = Xb + Za + e$$

Where Y are the vectors of observations for linear variables (DO and MY or PY or FY) at first, second and third lactation, respectively; b is the vector of fixed effects (herd-year-season and lactation-age class); a is the vector of random animal effects; e is the random residual effect; X and Z are incidence matrices relating records to fixed and random animal effects.

The Mrep model was:

$$Y = Xb + Za + Wp + e$$

Where Y is the vector of observations for linear variables (DO, MY, PY and FY); b is the vector of fixed effects (herd-year-season and lactation-age class); a is the vector of random animal effects; p is the vector of permanent environmental effects and non-additive genetic effects; e is the random residual effect; X , Z and W are incidence matrices relating records to fixed, animal and permanent environmental effects, respectively.

For both models, it was assumed that random and residual effects are independently distributed with mean zero and variance σ_e^2 , σ_a^2 , respectively. In the repeatability model, it was also assumed that permanent environmental effects are independently distributed with mean zero and variance σ_p^2 . Therefore: $\text{var}(a) = A\sigma_a^2$; $\text{var}(p) = I\sigma_p^2$; $\text{var}(e) = Ie_e^2 = R$.

Analyses were performed in a Bayesian framework, using the software Gibbs2f90 (Misztal et al., 2002).

With Mdiff, a single chain of 500,000 samples after discarding the first 300,000 samples was analyzed. The sampling interval was 100, leaving 5000 samples to estimate the parameters from the posterior distributions.

With Mrep, the chain analyzed was 200,000 samples long, after discarding the first 100,000 samples. The sampling interval was 10, leaving 20,000 samples to estimate the parameters from the posterior distributions.

Convergence diagnostic and statistical analysis of the Markov Chain Monte Carlo sampling output were performed with CODA package (Plummer et al., 2006) of the R language/environment (R Core Team, 2014).

In the Mdiff approach heritabilities (h^2) were estimated as:

$$h^2 = \sigma_a^2 / (\sigma_a^2 + \sigma_e^2)$$

Otherwise, heritabilities (h^2) were estimated as:

$$h^2 = \sigma_a^2 / (\sigma_a^2 + \sigma_p^2 + \sigma_e^2)$$

Repeatabilities (R) were estimated as:

$$R = (\sigma_a^2 + \sigma_p^2) / (\sigma_a^2 + \sigma_p^2 + \sigma_e^2)$$

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