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Reaction norm of fertility traits adjusted for protein and fat production level across lactations in Holstein cattle

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ABSTRACT

A total of 304,001 artificial insemination outcomes in up to 7 lactations from 142.389 Holstein cows, daughters of 5,349 sires and 101,433 dams, calving between January 1995 and December 2007 in 1,347 herds were studied by a reaction norm model. The (co)variance components for days to first service (DFS), days open, nonreturn rate in the first service (NRFS), and number of services per conception were estimated by 6 models: 3 Legendre polynomial degrees for the genetic effects and adjustment or not for the level of fat plus protein (FP) production recorded at day closest to DFS. For all traits and type of FP adjustment, a second degree polynomial showed the best fit. The use of the adjusted FP model did not increase the level of genetic (co)variance components except for DFS. The heritability for each of the traits was low in general (0.03-0.10) and increased from the first to fourth calving, nevertheless a very important variability was found for the estimated breeding value (EBV) of the sires. The genetic correlations (\mathbf{r}_{σ}) were close to unity between adjacent calvings, but decreased for most distant parities, ranging from $r_g = 0.36$ (for DFS) to $r_g = 0.63$ (for NRFS), confirming the existence of heterogeneous genetic (co)variance components and EBV across lactations. The results of the eigendecomposition of r_g shows that the first eigenvalue explained between 82 to 92% and the second between 8 to 14% of the genetic variance for all traits; therefore, a deformation of the overall mean trajectory for reproductive performance across the trajectory of the different calving could be expected if selection favored these eigenfunctions. The results of EBV for the 50 best sires showed a substantial reranking and variation in the shape of response across lactations. The more important aspect to highlight, however, is the difference between the EBV of the same sizes in

which is particularly important for DFS and NRFS. This component of fertility adds another dimension to selection for fertility that can be used to change the negative genetic progress of reproductive performance presented in this population of Holstein cows. The use of a reaction norm model should allow producers to obtain more robust cows for maintenance of fertility levels along the whole productive life of the cows. **Key words:** Holstein reproduction trait, genetic parameter, reaction norm model, plasticity

different calvings, a characteristic known as plasticity,

INTRODUCTION

Maintaining profitability on dairy farms largely relies on attaining high levels of production per cow (Van-Raden, 2003; González-Recio et al., 2004; Miglior et al., 2005). Therefore, production (milk, fat, protein, and components paid for) is the trait that receives the largest selection pressure in most dairy cattle populations (Shook, 2006; Interbull, 2012). However, high-yielding cows are prone to show a negative energy balance around the peak of production, which interferes with their ability to become pregnant, given that the time of first insemination and the negative energy balance period coincide (Veerkamp et al., 2008). Therefore, future sustainability of intensive production systems for dairy cattle will largely rely on the ability to select animals that can cope with increasing levels of milk production while avoiding undesired culling for reproductive failure. Given that the production level increases from the first to the following lactations, energy balance of cows in second and subsequent lactations can increasingly deteriorate if the cow is not able to recover its body condition before the next calving. Up to now, fertility of lactating cows has been evaluated using a variety of traits (Jorjani, 2007) and, generally, the models used consider reproductive traits along successive parities as repeated measures of the same trait. However, the use of this approach has some drawbacks. First, genetic evaluations may be biased if the underlying assump-

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tions of constant genetic (co)variances, breeding values across lactations, and unity correlations between lactations do not hold. Second, and more importantly in the context of selection for robustness in high-yielding cows, eventual differences in the genetic ability to maintain initial reproductive performance along parities cannot be detected.

The analysis of traits measured at different time points in the animal's productive life has been undertaken from different perspectives. First, as function valued traits characters (Pletcher and Geyer, 1999), that is, traits that change as a function of some independent and continuous variable (e.g., a time scale measured as parity number), using covariance functions (Kirkpatrick et al., 1990), or, equivalently, random regression models (**RRM**; Schaeffer and Dekkers, 1994). Alternatively, observed phenotypes taken in the same individual along time can be viewed as a set of responses to environmental variation at different time points (e.g., reproductive response to changes in production level and associated body condition along successive lactations) in the context of reaction norm models (Gomulkiewicz and Kirkpatrick, 1992). Reaction norm models can also be viewed as a special case of RRM (Kolmodin et al., 2002). Fertility traits fall into the function valued traits category or can also be viewed as reactions to changing conditions along parities and could be properly analyzed by using RRM (Schaeffer, 2004). Reaction norm models to study the sensitivity of production traits to different environments or plasticity of production have been previously used in several studies (de Jong, 1995; Kolmodin et al., 2002; Calus and Veerkamp, 2003). However, bibliographical references about this type of analysis for fertility traits across parities are very scarce.

The objective of this study was to estimate genetic (co)variance components and breeding values for changes in reproductive performance across parities. The reaction norm models used accounted or not for fat plus protein production at the closest day to first service. This type of model provides a way of measuring both the level and persistency of reproductive performance, which might help in selecting more robust and profitable cows.

MATERIALS AND METHODS

Data

Records from the official milk and reproductive recording program in the Basque country, Girona and Navarre in Spain, were used in this study. The overall reproductive file contained 316,565 AI records from up to 7 parities of Holstein cows calving between January 1995 and December 2007 in 1,347 herds. Test-day yields closest to the insemination date for the cows with reproductive information were extracted from an overall file with 3,201,353 milk, fat, and protein test-day records collected on a monthly basis. A maximum absolute distance of 31 d between the day of first service and the closest (preceding or subsequent) milk test day was required. After editing and merging both data files, 304,001 AI outcomes in up to 7 lactations from 142,389 Holstein cows were included in the subsequent analyses. These cows were daughters of 5,349 sires and 101,433 dams (56,090 of these dams were themselves present in the data). The pedigree file contained a total of 223,711 individuals.

Reproductive performance was measured by 4 traits: interval (days) from calving to first service (**DFS**), days open (**DO**), nonreturn rate in the first service (**NRFS**), and number of services per conception (**NSC**). The editing process for these 4 characters followed the same restriction as in González-Recio et al. (2004). Fat plus protein yield (**FP**) in the test day closest to the day of first service was used to adjust for level of production.

Statistical Analyses

Single trait models for each fertility trait were used. The following general model formulation applied for all traits:

$$y_{ijklmn\tau\lambda} = \operatorname{RYS}_{i} + \sum_{r=0}^{r=2} \alpha_{rj} \Phi_{r}(\tau) + \sum_{r=0}^{r=2} \beta_{rj} \Phi_{r}(\lambda) + \sum_{r=0}^{r=0,1,2} a_{rk} \Phi_{r}(j) + p_{l} + h_{m} + e_{ijklmn\tau\lambda},$$

where $y_{ijklmn\tau\lambda}$ is the fertility trait observation (DFS, DO, NRFS, NSC); RYS_i is the *i*th combination of region, year, and season of calving $(i = 1, \ldots, 114)$; α_{ri} is the rth fixed regression coefficient on months of age at calving (τ) , nested to the *j*th level of parity (j =1,..., 7); β_{ri} is the *r*th fixed regression coefficient on kilograms of FP (λ), nested to the *j*th parity; a_{rk} is the rth random additive genetic regression coefficient on lactation number (j) for animal $k \ (k = 1, \dots, 223, 711)$; Φ_r is the *r*th term of the Legendre polynomial where the time variable was alternatively age at calving (τ) , FP yield (λ) , or the lactation number (j); the order of fit was r = 2 (intercept, linear, and quadratic terms) for the fixed Legendre polynomials, but r = 0.1,2 for the random animal genetic effect, leading to 3 different models for each order of fit; p_l is the random permanent environmental effect for cow l $(l = 1, ..., 142, 389); h_m$ is the random effect of herd m (m = 1, ..., 1, 122); and $e_{ijklmn\tau\lambda}$ is the residual term.

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