Genotype by environment interaction for activity-based estrus traits in relation to production level for Danish Holstein

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ABSTRACT

The objective of this study was to investigate whether genotype by environment interaction exists for female fertility traits and production of energy-corrected milk at 70 d in milk (ECM70). Fertility traits considered were the activity-based estrus traits interval from calving to first high activity (CFHA), duration of high activity episode (DHA), as an indicator for first estrus duration, and strength of high activity episode (SHA), as an indicator for first estrus strength. The physical activity traits were derived from electronic activity tags for 11,522 first-parity cows housed in 125 commercial dairy herds. Data were analyzed using a univariate random regression animal model (URRM), by regressing the phenotypic performance on the average herd ECM70 as an environmental gradient. Furthermore, the genetic correlations between CFHA and ECM70 as a function of production level were estimated using a bivariate random regression animal model (BRRM). For all traits, heterogeneity of additive genetic variances and heritability estimates was observed. The heritability estimate for CFHA decreased from 0.25 to 0.10 with increasing production level and the heritability estimate for ECM70 decreased from 0.35 to 0.15 with increasing production level using URRM. The genetic correlation of the same trait in low and high production levels was around 0.74 for CFHA and 0.80 for ECM70 using URRM, but when data were analyzed using the multiple-trait analysis (MT), genetic correlation estimates between low and high production levels were not significantly different from unity. Furthermore, the genetic correlation of SHA between low and high production level was 0.22 using URRM, but the corresponding correlation estimate had large standard error when data were analyzed using MT. The genetic correlation between CFHA and ECM70 as a function of production environment was weak but unfavorable and decreased slightly from 0.09 to 0.04 with increasing production level using BRRM. Moreover, the same trend was observed when the data were analyzed using MT where the genetic correlation between CFHA and ECM70 in the low production environment was 0.29 compared with −0.13 in the high production environment, but these estimates had large standard errors. In conclusion, regardless of the trait used, in relation to average herd ECM70 production, the results indicated no clear evidence of strong genotype by environment interaction that would cause significant re-ranking of sires between low and high production environments.
Key words: activity-based estrus traits, female fertility, genotype by environment interaction, random regression model

INTRODUCTION

Dairy cow fertility is becoming increasingly important throughout the world because it has a substantial effect on the overall profitability of dairy cattle. For that reason, selection indices worldwide have changed from the previous focus on yield to a more balanced breeding approach that includes longevity, udder health, and fertility (Miglior et al., 2005). An increasing number of countries are performing genetic evaluations for female fertility, and in August 2015, 21 countries were included in the international genetic evaluation for female fertility (Interbull, 2015). This wide range of environments increases the concerns of possible genotype by environment interaction ($\mathbf{G} \times \mathbf{E}$), which might lead to a change in the performance of animals and their offspring between the environments where they are selected and where they are used (Falconer and Mackay, 1996).

Genotype by environment interaction exists when the ability to alter the phenotype in response to changes in the environment differs among animals (Falconer and Mackay, 1996). Recently, reaction norm models have been used to describe effects that change gradually over a continuous scale (de Jong, 1995; Falconer and Mackay, 1996) where the genotype effect is modeled as a function of a continuous environmental scale, which results in heterogeneous variance components and heritabilities that change with the environmental gradient (Kolmodin et al., 2002; Ravagnolo and Misztal, 2002b; Strandberg et al., 2009). The reaction norm model is similar to the random regression test day models used in dairy cattle breeding (Schaeffer, 2004), but the covariate used is the environmental gradients instead of DIM.

Although the previous studies indicated that expression of fertility is sensitive to environmental components such as seasons and climatic factors (Ravagnolo and Misztal, 2002b; Oseni et al., 2004; Boonkum et al., 2011; Ismael et al., 2016) and milk production level (Ravagnolo and Misztal, 2002a), few studies have been performed on G × E for female fertility within a country, and these studies found little evidence of G × E as most of the genetic correlations between environments were close to unity. Kolmodin et al. (2002) used a random regression model to study G × E for days open in Nordic Red dairy breeds where the environmental scale was defined as herd year average of protein yield, and they found a large heterogeneity of genetic variance. Furthermore, the heritability estimates of days open increased as herd year average protein increased and ranged from 0 to 0.35. Strandberg et al. (2009) used the herd average production to study G × E for the interval from calving to first insemination (**CFI**) and calving interval in UK Holstein cows and found a slightly higher heritability for both traits at low production level compared with high production level. Haile-Mariam et al. (2008) used average herd lactation milk yield as the continuous environmental descriptor to study G × E in Holstein cows in Australia and found that heritability of CFI decreased with increasing production—heritability of CFI in low production environment was higher than the heritability in high production environment. On the other hand, heritability estimates for calving interval and first service nonreturn rate were homogeneous across production environments. Furthermore, the low genetic correlations found between low and high production environments were associated with large standard errors and thus there was no conclusive evidence of the existence of significant G × E, causing re-ranking of bulls across production environments for both traits.

One of the main problems hindering the genetic improvement for better fertility in dairy cattle is the antagonistic genetic correlation between production and fertility traits, indicating that selection for increased production reduces reproductive efficiency (Berry et al., 2003; König et al., 2008; Sewalem et al., 2010). However, the unfavorable genetic correlation between yield and fertility was not constant across different environments. For example, Kolmodin et al. (2002) used a multiple-trait random regression model to investigate the heterogeneity of the genetic correlation between days open and protein yield, using the average herd protein production as environmental descriptor. They found a decrease in the genetic correlation with increasing protein production. This implies that the unfavorable genetic correlation between production and fertility can be alleviated by improving the production environment. However, in contradiction, Haile-Mariam et al. (2008) found that the genetic correlation between CFI and milk yield increased with increasing production environment, using the average milk yield as an environmental descriptor.

The previous studies on G × E for fertility traits were performed based on AI data, and the decision of when and how many times to inseminate cows is done by the farmer. This decision could be influenced by factors that vary from cow to cow (e.g., based on the cow's milk yield). This may influence the genetic parameters such as heritability of fertility traits and the genetic correlations between yield and fertility traits. However, the development of some new technologies makes it possible to record new fertility traits that are free from farmer interventions. This may alleviate human bias on all estimates of genetic parameters and may thus provide higher heritability estimates than the traditional measures. For example, CFI is the traditional measure of the return to cyclic estrus after calving and the heritability estimate of this trait in Holstein cows in Nordic countries is only 0.05 (SEGES, 2015). On the other hand, the interval from calving to first high activity episode (**CFHA**) is an objective measure of return to cyclicity after calving and it can be measured by activity tags. This trait has heritability estimates of 0.12 to 0.18 (Løvendahl and Chagunda, 2009; Ismael et al., 2015), which is higher than CFI. In addition, these devices are found to be useful to measure other estrus-related traits [e.g., strength of first high activity episode (**SHA**) and duration of high activity episode (**DHA**) as an indicator of estrus strength and estrus duration, respectively (Løvendahl and Chagunda, 2009; Ismael et al., 2015)]. These traits are not routinely recorded in most current breeding programs, but could be useful for improving the ability to detect cows display-