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Genotype by environment interaction for production, somatic cell score, workability, and conformation traits in Dutch Holstein-Friesian cows between farms with or without grazing

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ABSTRACT

In this study, genotype by environment interaction was investigated for production traits, somatic cell score (SCS), workability traits, and conformation traits for Holstein-Friesian cows producing on farms with or without grazing in the Netherlands. Additionally, heritabilities and repeatabilities were estimated in both farm systems. Data were available for 1,019 Dutch farms, and farm type was known for those farms, 142 farms without grazing and 877 farms with grazing. The data set consisted of 428,600 test-day records for production from 49,412 cows, and from this data set a subset for SCS was created, consisting of 374,734 test-day records from 45,955 cows. For workability and conformation traits, the data set consisted of 30,180 cows. Bivariate mixed models with multiple fixed effects and random sire and random permanent environment effects were applied. The majority of sires had daughters in both farm types. The heritabilities for milk yield (0.27), fat yield (0.19), and protein yield (0.20) were higher in farms with grazing than in farms without grazing with heritabilities of 0.24 for milk yield, 0.18 for fat yield, and 0.18 for protein yield. Repeatability was lower in the grazing farms for milk yield, fat yield, and protein yield, probably because of alternating quality of dry matter intake during grazing. Genetic correlations between grazing and no grazing were 0.99, 0.98, 0.97, and 1.00 for milk yield, fat yield, protein yield, and SCS, respectively. Genetic correlations for workability traits and conformation traits between grazing and no grazing varied between 0.93 and 1.00. For all traits, genetic correlations were close to unity, indicating no genotype by environment interaction between farms with or without grazing for production traits, SCS, workability traits, and conformation traits in Dutch Holstein-Friesians. Therefore, the same sires can be used for both farms with grazing and without grazing.

Key words: genotype by environment interaction, grazing, milk production, conformation

INTRODUCTION

The percentage of dairy cows kept on Dutch farms with year-round confinement increased from 10% in 2000 to 30% in 2013 (CBS, 2014). In the Netherlands, milk yield is higher in farms without grazing compared with farms with the traditional full grazing system (Reijs et al., 2013). Farms without grazing also showed higher BCS and higher BW in the United States (Washburn et al., 2002), and an increase in lameness and frequency of knee and hock swellings in Great Britain (Haskell et al., 2006). Better locomotion scores, straighter rear leg side view, steeper foot angle, and better legs and feet were observed on farms with grazing compared with farms without grazing in Great Britain (Onyiro and Brotherstone, 2008).

The question arises whether a genotype by environment interaction (**G × E**) occurs between the 2 environments. The G × E is a phenomenon where the performance of different genotypes is not equally affected by the different environments (Falconer, 1989). As a result, genotypes that are performing well in one environment might be less successful in another environment. If G × E occurs, it can result in (1) a scaling effect, where the differences between sires in different environments are unequal but the ranking of sires is the same, or (2) reranking, a change in the ranking of sires across environments. With reranking, the genetic basis for the trait is different for each environment (Lynch and Walsh, 1998). In current breeding value estimation, the heterogeneity of variances is corrected for (Meuwissen et al., 1996), but possible reranking of sires in different environments is not taken into account (Calus et al., 2002). If sires with daughters in one environment are genetically evaluated and G × E occurs, the results

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might not be adequate predictors for offspring in other environments, thereby reducing the efficiency of genetic improvement programs (Boettcher et al., 2003; Mulder and Bijma, 2005; Mulder et al., 2006; Hammami et al., 2009). To avoid this problem, it would be better that selection of sires is performed in the environments in which daughters are expected to perform (Falconer, 1952).

Numerous studies investigated the possible existence of G × E in dairy cattle. The G × E was observed between climatic environments in the United States and Mexico (Cienfuegos-Rivas et al., 1999). Mulder et al. (2004) observed small reranking between farms with automatic and farms with conventional milking systems. Boettcher et al. (2003) and Kearney et al. (2004a,b) studied G × E between farms with grazing and no grazing in Canada and the United States, respectively, and genetic correlations ranged between 0.88 and 0.96 for production traits, and between 0.90 to 0.97 for conformation traits. In most G × E studies, reranking of sires did sometimes occur for a particular trait, but the differences between environments were not so large that separate genetic evaluations for each environment were advised (Boettcher et al., 2003; Mulder et al., 2004; Kearney et al., 2004a,b). In the Netherlands, it is unknown whether G × E exists between farms with grazing and no grazing.

The aim of this study was, therefore, to investigate the existence of G × E for milk yield, fat yield, protein yield, SCS, workability traits, and conformation traits between Holstein-Friesian cows producing in farms with or without grazing in the Netherlands.

MATERIALS AND METHODS

Data

Records of Dutch Holstein-Friesian cows were provided by CRV (Arnhem, the Netherlands). Farmers provided the grazing status to the database of CRV voluntarily. Selection of herds was done by CRV by selecting herds with a known grazing status (grazing or no grazing) for dairy cows in the years 2010, 2011, and 2012. Only herds that did not change their grazing system within these years and where at least 98% of the cows were Holstein Friesian were selected. The initial data set contained information from 1,019 herds, 142 herds without grazing and 877 herds with grazing. At farms with grazing, cows were grazing on average 10.9 h/d and 161.1 d/yr.

Data sets for (1) production traits, (2) SCS, and (3) workability traits and conformation traits were created. The data sets were edited to conform to the standards used by CRV for breeding value estimation (CRV, 2013, 2014). Data editing was done using R software (R Core Team, 2014). All cows in the data sets were at least 7/8 Holstein-Friesian and herd-book registered. Data set 1 contained 2,032,064 test-day records from 133,127 cows and contained information about first parity test-day milk samples from 5 to 335 d in milk. For every record, information about birth date, calving date, milk yield, protein yield, and fat yield was provided. From cows moving to a different herd, only records from the first herd were left in the data set. At least 5 daughters per sire, 5 cows per herd test date and 5 records per cow were required in the data set, resulting in 428,600 test-day records from 49,412 cows. In data set 1, 773 sires had daughters in both farm types. Cows in data set 2 were selected in the same way as cows were in data set 1. However, the number of records was reduced because SCC was not measured at every test-day. The SCC is not normally distributed; therefore, SCC was transformed into SCS and was calculated by SCS = 100 × [$\log_2$(SCC)], which was slightly different from the equation used by CRV for breeding value estimation (CRV, 2014). The same edits were applied as in data set 1. After editing, data set 2 contained 374,734 records from 45,955 cows. In data set 2, 729 sires had daughters in both farm types. Data set 3 contained 75,188 records from cows that were scored for 23 conformation traits and 2 workability traits (milking speed and temperament during milking) by a classifier on a certain date. Only records that were scored in 2010, 2011, or 2012 were kept in the data set. At least 5 cows per classification date per farm, 5 cows per combined variable of classifier and half year period of classification date and classification standard (Black-and-White and Red-and-White), 5 cows per age class (18 mo classes: <25 mo, 25–40 mo, a separate class for each month, >40 mo), and 5 cows per lactation class (13 classes: each for 1 month of lactation and with the thirteenth category for 13 and more months of lactation) were required, remaining 28,694 cows in data set 3. In data set 3, 512 sires had daughters in both farm types. Details about the data sets are in Table 1.

The pedigree file contained pedigree information for all the cows in the data sets. The pedigree was trimmed with the “pedigree” package in R (Coster, 2012), and included the sire of the cow, the parents of the sire, and the grandparents of the sire.

Statistical Analysis

As was suggested by Falconer (1952), the same trait measured in farms with or without grazing was treated as 2 separate traits. The genetic correlation r_g between