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Interaction between genotype and geographical region for milk production traits of Iranian Holstein dairy cattle

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ABSTRACT

In order to investigate the presence of genotype by environment (G × E) interactions, first lactation milk production traits of Iranian Holstein cows were used. The data were collected by the National Animal Breeding Center of Iran, Karaj. The records were classified by herds in cold, semi-cold, moderate or warm regions based on climatic data of weather stations. The edited data that were collected between 2004 and 2010, included 618,343, 472,597 and 243,792 test day records for milk, fat and protein yields, respectively. Variance components were estimated using Bayesian's Gibbs sampling method in a random regression model (RRM). For all traits, after examining models according to DIC, better fitting RRM was the model with heterogeneous residual variances. Genetic parameters estimate for milk production traits were different in the four regions. The highest genetic variances were obtained for cold climate regions; and the highest residual variances across the lactation were obtained for warm climate. Genetic variances and heritability estimates revealed unequal genetic expression of Holstein genes under different climates. Generally, for fat and protein yields, the genetic correlation between different regions was lower than that for milk yield, especially for genetic correlations of protein yield between cold and warm regions (ranged from 0.22 to 0.48). The lower correlations between warm and other regions, especially at the beginning and the end of lactation, showed that a trait in different environments was genetically different traits. For milk and fat yields, the high genetic correlations for 305-d yield (>0.84) between cold, semi-cold and moderate regions indicated a few rank changes of animals over these climates. The results indicated that superior sires in one of regions have their genetic expression for yield limited under other climate conditions and indicated the existence of G × E interaction which may have several implications for the genetic improvement of Holstein cows in Iran.

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1. Introduction

Use of artificial insemination in dairy industries across regions and countries raises questions about the use of records from daughters located in subpopulations and select sires for other subpopulations; and animal breeders are more concerned about re-ranking of animals than about differences in scale between environments because differences in scale do not affect the ranking of the animals for the considered trait. Therefore, an important parameter to consider is the magnitude of genotype by environment (G × E) interaction, which occurs when different genotypes react differently in different environments (Falconer and

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MacKay, 1996); and this interaction can cause re-ranking of animals across environments (Lynch and Walsh, 1998). Therefore, when genotypes have significant differences between the quantitative measures of the phenotypic plasticity, then there is a G × E interaction.

Plastic genotypes are known by highly variable phenotypes across environments, whereas stable genotypes are known by relatively constant phenotypes across environments. Differences in the phenotypic plasticity could be explained by the fact that some alleles may only be expressed in some specific environment due to change in some gene regulations depending on the environment; favorable genes in some environments may become unfavorable under other environmental conditions (Falconer and MacKay, 1996).

Countries in the tropics often rely on exotic germplasm for breeding purposes. They, however, have climatic conditions, production systems and markets that are different from those where animals were evaluated. Consequently, the G × E interaction can cause reduced efficiency of their genetic improvement programs (Banos and Smith, 1991).

When the interest is in discrete environments; for example, geographic regions, multi-trait approach is the logical option (Windig et al., 2011). The studies on the multi-trait approach assumed treated performance in different countries or regions as separate, though correlated traits (Ceron-Munoz et al., 2004; Nauta et al., 2006; Hammami et al., 2008; Santana et al., 2012). Hammami et al. (2008) demonstrated that the genetic parameters of lactation curves revealed differences in gene expressions between Luxembourg and Tunisian Holsteins; and also low genetic correlations across regions in Mexico indicate re-ranking of sires (Valencia et al., 2008). Nauta et al. (2006) reported that the magnitude of G × E interaction between conventional and organic milk, fat and protein yields is importance and comparable with G × E interaction between a grass-based system as in New Zealand and high-input systems as in North America or Western Europe. According to Santana et al. (2012) on birth and weaning weights of composite beef cattle, the low genetic correlations among the most studied regions to suggest that a separate genetic evaluation for some regions should be undertaken.

An improved type of models is a random regression model (RRM) that allows defining individual TD (test day) variation in the shape of the trajectory with a set of random regression coefficients. RRMs that consider heterogeneous residual variances are more suitable for fitting the data than are models that consider the residual variance as being homogeneous (Jamrozik and Schaeffer, 1997). Therefore, authors found it important to model the heterogeneity of residual variance across the lactations (Jaffrézic et al., 2000; Zavadilová et al., 2005).

Current practices ignore genotype by environment interactions in Iran as large country; and all herds in different regions are assumed to have the same condition (Bohlouli et al., 2013). In fact, herds in the hot, dry climate of the southern provinces are under much different climate and management conditions than herds in a cool, wet climate such as the northern provinces of Iran. Therefore, the aim of this study was to determine the genotype by environment interaction of milk production traits of Holstein cattle in different geographical regions of Iran using multi-trait random regression model.

2. Material and methods

2.1. Data

Test day records of milk production traits of primiparous Iranian Holstein dairy cows collected between April 2004 and March 2010 were used. Records of dairy cattle were provided by the National Animal Breeding Center of Iran, Karaj. The majority of the Iranian dairy cattle population consists of several native breeds and their crosses with Holsteins. Approximately 800,000 animals are purebred Holsteins. These are either descendants of the cows originally imported from North America and Europe or Holstein upgrades of domestic breeds over 50 yr. The herds are under official performance and pedigree recording. Artificial insemination is used almost exclusively; and 60–80% of semen is from US and Canadian sires (Ghavi Hossein-Zadeh et al., 2009).

Daily records for milk, fat and protein yields ranged from 1.5 to 70 kg, from 0.03 to 5.56 kg and from 0.03 to 3.09 kg, respectively. Lactation records were required to have only 2 or 3 milking per day and at least five test days between 5 and 305 days in milk (DIM), and cows were excluded if their first reported test date occurred after 75 DIM. The cows with calving age between 21 and 46 months were considered in the analyses; and only herd-year of calving subclasses with at least four recorded cows were kept.

Records were classified by herds in cold, semi-cold, moderate or warm regions based on climatic data of weather stations (Mirzamohamadi and Rashidi, 2013). Descriptive characteristics of climatic data are given in Table 1.

We selected common sires with at least five recorded daughters in each climatic condition to create genetic connectedness between the different environmental groups. Finally, the data included 618,343, 472,597 and 243,792 first-lactation TD records of 72,108, 57,415 and 29,475 cows and 229, 216 and 103 common sires for milk, fat and protein yields, respectively. The number of TD records for each trait based on different classes of DIM is shown in Fig. 1. Pedigree was traced back as far as possible to increase across-region connections. Summary of data set used for estimation of variance components are given in Table 2.

2.2. Statistical models

The choice of fixed effects to be considered was made after testing whether the effects were statistically significant with GLM procedure of SAS (Statistical Analysis System (SAS), 2003). The following multiple-trait RRM, which considered the performance of daughters in the four regions as different correlated traits, was fitted to estimate variance components:

$$y_{tijklm} = \mathrm{HTD}_{ti} + \mathrm{MF}_{tj} + \sum_{n=1}^{q} \alpha_{tkn} z_n(d) + \sum_{n=1}^{q} \beta_{t\ln} z_n(d) + \sum_{n=1}^{q} \gamma_{t\ln} z_n(d) + e_{tijklm}$$

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