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Genetic parameters for major milk proteins in Dutch Holstein-Friesians

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ABSTRACT

The objective of this study was to estimate genetic parameters for major milk proteins. One morning milk sample was collected from 1,940 first-parity Holstein-Friesian cows in February or March 2005. Each sample was analyzed with capillary zone electrophoresis to determine the relative concentrations of the 6 major milk proteins. The results show that there is considerable genetic variation in milk protein composition. The intraherd heritabilities for the relative protein concentrations were high and ranged from 0.25 for β-casein to 0.80 for β-lactoglobulin. The intraherd heritability for the summed whey fractions (0.71) was higher than that for the summed casein fractions (0.41). Further, there was relatively more variation in the summed whey fraction (coefficient of variation was 11% and standard deviation was 1.23) compared with the summed casein fraction (coefficient of variation was 2% and standard deviation was 1.72). For the caseins and α-lactalbumin, the proportion of phenotypic variation explained by herd was approximately 14%. For β-lactoglobulin, the proportion of phenotypic variation explained by herd was considerably lower (5%). Eighty percent of the genetic correlations among the relative contributions of the major milk proteins were between −0.38 and +0.45. The genetic correlations suggest that it is possible to change the relative proportion of caseins in milk. Strong negative genetic correlations were found for β-lactoglobulin with the summed casein fractions (−0.76), and for β-lactoglobulin with casein index (−0.98). This study suggests that there are opportunities to change the milk protein composition in the cow's milk using selective breeding.
Key words: protein composition, heritability, genetic correlation, Dutch Holstein-Friesian

INTRODUCTION

Bovine milk represents a unique source of bioactive components and nutrients, which include proteins. The major milk proteins are α_{S1}-CN, α_{S2}-CN, β-CN, κ-CN, α-LA, and β-LG. The protein composition of milk plays an important role in the profitability of the dairy industry. Specific proteins contribute to the production of specific milk products. Caseins, for example, are important for cheese yield, milk coagulation time, and curd firmness (Wedholm et al., 2006), whereas β-LG is important for the heat stability of milk (Feagan, 1979). To explore the possibilities of altering milk protein composition by selective breeding, genetic parameters such as heritability and genetic covariance are needed. Although many studies have reported the genetic variation for protein percentages and protein yields (Hayes et al., 1984; Bobe et al., 1999; Ikonen et al., 2004), only a few studies have estimated the magnitude of the genetic variation of milk proteins (Renner and Kosmack, 1975; Kroeker et al., 1985; Ikonen et al., 1997; Bobe et al., 1999; Graml and Pirchner, 2003). Furthermore, these studies estimated the heritability of the major milk proteins, but no studies have reported genetic correlations among the major milk proteins. The limited number of studies is a reflection of the technological difficulties of quantifying the 6 major bovine milk proteins simultaneously on a large number of cows and daughters of bulls, which is a prerequisite for estimating their genetic parameters.

In the present study, capillary zone electrophoresis (**CZE**) was used to separate the major milk proteins. This technique provides rapid separation of the proteins, high resolution, and is reproducible (Heck et al., 2008). Heck et al. (2008) showed that the protein composition of milk varies substantially among cows at the phenotypic level. However, it is not known to what extent this variation arises from genetic factors.

The objective of this study was to estimate the heritability of milk protein composition and to estimate the genetic and phenotypic correlations among the major milk proteins and of milk protein composition with milk production traits in a population of 1,940 Dutch Holstein-Friesian cows.

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MATERIALS AND METHODS

Animals

As part of the Dutch Milk Genomics Initiative, information was collected on 1,940 first-parity cows, distributed over 398 commercial herds throughout the Netherlands. At least 3 cows were selected per herd, and each cow was at least 87.5% Holstein-Friesian. The cows descended from 1 of 5 proven bulls (899 cows), from 1 of 50 test bulls (849 cows), or from 1 of 15 other proven bulls (192 cows). The last group of cows ensured sampling of at least 3 cows per herd. The pedigree of the cows was supplied by the CRV (Arnhem, the Netherlands). The cows were milked twice daily; and each cow was between d 63 and 282 of lactation at the time of sampling. Almost all animals have also been used in previous studies for the genetic analysis of urea (Stoop et al., 2007) and milk fatty acid composition (Schennink et al., 2007; Stoop et al., 2008). A morning milk sample was collected from each cow during February and March 2005, which is the winter period, to be used in the analysis of the major milk proteins.

Phenotypes

Observations of the test-day morning milk yield were obtained from the CRV. True protein, fat, and lactose percentages were determined by infrared spectroscopy using a Fourier-transformed interferogram (MilkoScan FT 6000, Foss Electric, Hillerød, Denmark) at the milk control station laboratory (Zutphen, the Netherlands). Protein, fat, and lactose yields were calculated by multiplying the respective percentages by the observed milk yield. Morning milk yields were missing for 147 cows; therefore, only 1,793 records were analyzed for protein, fat, and lactose yields.

The relative concentrations of the 6 major milk proteins were determined by CZE, which is a technique used to separate proteins based on differences in size and charge. Using this method, we quantified α_{S1}-CN, α_{S2}-CN, β-CN, κ-CN, α-LA, and β-LG. They were expressed as a percentage of the total protein fraction. Heck et al. (2008) provides a detailed description of the CZE technique used in this study.

The milk protein κ-CN, as determined in our study, consisted only of κ-CN-1P (nonglycosylated, monophosphorylated state; Heck et al., 2008). Sum casein (**Σcasein**) was defined as the sum of the percentages of α_{S1}-CN, α_{S2}-CN, β-CN, and κ-CN. Sum whey (**Σwhey**) was calculated by adding the percentages of α-LA and β-LG. Furthermore, casein yield was calculated by multiplying Σcasein by total protein yield. The casein index was calculated as

$$\text{casein index} = \frac{\Sigma\text{casein}}{\Sigma\text{casein} + \Sigma\text{whey}} \times 100.$$

Genotypes

Blood samples of cows for DNA isolation were collected. Genotypes for the κ-CN C5309T, κ-CN A5345C, and κ-CN A5365G (the latter 3 to enable genotyping of κ-CN variants A, B, and E) polymorphisms had been genotyped using a SNaPshot assay (Applied Biosystems, Foster City, CA; Schennink et al., 2008; Heck et al., 2009). Genotypes for κ-CN were missing for 208 cows because no DNA sample was available or the DNA sample could not be genotyped unambiguously. The β-CN and β-LG genotypes were determined by CZE and confirmed by genotyping 2 β-CN polymorphisms and 1 β-LG polymorphism for 849 genotyped cows by the Illumina Golden Gate assay (Illumina, San Diego, CA; Heck et al., 2009).

Statistical Analysis

To estimate the genetic parameters and variance components, ASReml was used (Gilmour et al., 2002). The following animal model was used in the analyses:

$$\begin{aligned} y_{ijklmn} = \mu &+ b_1 \times \text{lactst}_i + b_2 \times e^{-0.05 \times \text{lactst}_i} \\ &+ b_3 \times ca_j + b_4 \times ca_j^2 + \text{season}_k + \text{scode}_l \\ &+ \text{animal}_m + \text{herd}_n + e_{ijklmn}, \end{aligned} \quad [1]$$

where y_{ijklmn} was the observation for animal m in herd n with sire-code l, season k, calving age j, and lactation day i for the trait of interest. The overall mean of the trait was μ, lactst_i was a covariate describing the effect of day i of lactation, ca_j was a covariate describing the effect of age at first calving in j days, season_k was the fixed effect of the kth class of calving season [3 classes: summer (June–August 2004), autumn (September–November 2004), and winter (December 2004-February 2005)], scode_l was the fixed effect of the lth class of the 3 different sire groups, animal_m was the random additive genetic effect of animal m, herd_n was a random herd effect of the nth herd, and e_{ijklmn} was the random residual effect. Effects of the β-CN, κ-CN, and β-LG polymorphisms were estimated using the same animal model as described above and including a milk protein genotype as a fixed effect in the animal model. Ungenotyped animals were included as a separate class.

The variance-covariance structure of the additive genetic effects was $\text{Var}(\text{animal}) = A\sigma_a^2$, where A was a matrix of additive genetic relationships among indi-