Estimation of Genetic Parameters for the Protein Profile in Danish Holstein Milk

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ABSTRACT: Seven protein traits were measured in bovine milk by LC-MS using samples from 370 animals: Protein%, casein (CN)%, κ-CN%, α_{S1}-CN%, α_{S2}-CN%, β-CN%, β-lactoglobulin (βLG%) and α-lactalbumin (αLA%). A genomic relationship matrix calculated based on the HD SNP information of these animals was used in the univariate and bivariate analysis of the protein traits. Hertitabilities were ranging from 0.77 for κ-CN% to 0 for α_{S1}-CN% (SE: 0.13-0.21). The genetic correlation between β-CN and κ-CN was low (0.01 ± 0.53) whereas the genetic correlation of α_{s2}-CN with both β-CN and κ-CN was high (< -0.90). Furthermore αLA% and βLG% were highly correlated (0.71 ± 0.14) and had a low correlation to CN% (0.08 ± 0.25; -0.08 ± 0.30, respectively). In this study κ-CN% and the whey proteins showed a high heritability whereas α_{S1}-CN%, α_{S2}-CN% and β-CN% showed a low heritability in Danish Holstein cattle.

Keywords: Dairy cattle, Protein profile, Genetic parameters

Introduction

Whole bovine milk protein consists of approximately 80% of caseins whereas the other 20% consists of whey proteins, mainly β-lactoglobulin (β-LG) and α-lactalbumin (α-LA) (Farrell et al. 2004). The four caseins (α_{s1}-, α_{s2}-, β-, and κ-CN) are encoded by four genes tightly linked in a 250-kb cluster mapped to BTA6 (Hayes and Petit, 1993). Recently, we have shown that there is a difference between breeds in the protein profile and that the CN genes play a role in explaining the difference between breeds (Gustavsson et al. 2014).

The protein profile of milk plays an important role for the technological properties of milk, like e.g. the coagulation of milk during cheese making. Changes in relative concentrations of individual milk proteins have a major effect on milk coagulation properties and cheese production (Bonfatti et al. 2010; Bonfatti et al. 2011a; Wedholm et al. 2006). To explore the possibilities to change the protein profile by selective breeding we estimated the heritability and genetic correlations of the protein profile of Danish Holstein milk.

Materials and Methods

Data. Morning milk samples were collected of 456 Danish Holstein cows in the period from October to December 2009 (winter period). The animals were distributed over 20 different commercial herds in Denmark in such a way that most sires (200 sires in total) from the Danish Holstein cattle population were represented. All cows were in mid-lactation (d 129 to 228 of lactation) and within parity 1 to 3. A detailed protein profile (α_{s1}-, α_{s2}-, β-, and κ-CN, β-LG, α-LA) of the milk was determined in duplo using the LC/electrospray ionization-mass spectrometry (LC/ESI-MS) procedure as described in detail by Jensen et al. (2012). The phenotypes are expressed as a percentage of the total protein fraction.

Genotypes. In total 371 cows were genotyped using the bovine HD SNP array. The genomic DNA was extracted from ear tissue. The Illumina® Infinium II Multisample assay was used in combination with the Beadstudio software to analyze the samples. Minimum call rates of 80% for individuals and 95% for loci were set as quality parameters. Marker loci with minor allele frequencies (MAFs) below 1% were excluded.

Calculation of the G-matrix. The genomic relationship matrix (GRM) was calculated for each chromosome separately as described by the first method presented in VanRaden et al. (2008). In total 588,528 SNP markers were included to calculate the G-matrix.

Estimation of genetic parameters. To estimate the genetic parameters and variance components the REML approach in DMU was used (Madsen and Jensen, 2007). The analysis was based on the following model:

$$Y_{ijk} = \mu + herd_i + parity_j + animal_k + e_{ijk} \qquad (1)$$

Where Y_{ijk} is the phenotype of individual k in herd i and lactation j, μ is the fixed mean effect, herd is a fixed effect (i = 1, 2, …, 19), parity is a fixed effect (j = 1,2,3), and animal is the random additive genetic effect based on **G** of animal k.

To estimate the heritability univariate analyses were performed. The heritability was defined as:

$$h^2 = \sigma^2_a / (\sigma^2_a + \sigma^2_e) \qquad (2)$$

where σ^2_a was the genetic variation and σ^2_e was the residual variation.

Genetic and environmental correlations were studied by fitting a series of bivariate analyses with a REML approach in the R version of DMU (Madsen and Jensen, 2007).

Results and Discussion

The heritabilities for the different proteins in the Danish Holstein milk samples are presented in Table 1. For the caseins the highest heritability was found for κ-CN% (0.77) followed by $α_{s2}$-CN%, β-CN% and $α_{s1}$-CN%. The order of the proteins according to their heritability is in line with the results found by Schopen et al. (2009). However, the magnitude of the hertibilities found in the Dutch study was higher compared to our results. This was also observed for α-LA% and β-LG%, where, in our study, the heritabilities were 0.43 and 0.58, respectively, while the heritabilities found by Schopen et al. (2009) were 0.55 and 0.80, respectively. Bonfatti et al. (2011b) showed a lower hertibility for κ-CN% and β-LG% (0.63 and 0.34 respectively) compared to our estimates which were 0.77 and 0.58 for κ-CN% and β-LG%, respectively. The heritability for $α_{s1}$-CN% was much higher in the studies of Schopen et al. (2009) and Bonfatti et al. (2011b) (0.47 and 0.68, respectively compared to our results (0). A possible explanation for the low heritability in our study for $α_{s1}$-CN% could be the fact that there is low genetic variation in the $α_{s1}$-CN gene in the Danish Holstein (Poulsen et al. 2013). All 371 animals included in this analysis had genotype BB for the $α_{s1}$-CN gene.

Table 1. Estimates of heritability, phenotypic mean, standard deviation and genetic variances for the relative protein profile in Danish Holstein milk.

Trait	h^2	SE	Mean	SD	V_g	SE_g
Prot%	0.47	0.19	3.43	0.26	$2.80e^{-2}$	0.17
CN%	0.58	0.21	0.87	0.02	$3.23e^{-4}$	$1.8e^{-2}$
κ_CN%	0.77	0.21	0.06	0.01	$6.71e^{-5}$	$8.2e^{-3}$
$α_{S2}$_CN%	0.14	0.15	0.05	0.01	$1.43e^{-5}$	$3.8e^{-3}$
$α_{S1}$_CN%	$9.0e^{-5}$	0.12	0.27	0.03	$6.50e^{-8}$	$2.6e^{-4}$
β_CN%	0.05	0.13	0.36	0.03	$3.68e^{-5}$	$6.0e^{-3}$
β-LG%	0.58	0.20	0.08	0.02	$1.30e^{-4}$	$1.2e^{-2}$
α-LA%	0.40	0.19	0.03	0.01	$1.56e^{-5}$	$3.9e^{-3}$

h^2: heritability; SE: Standard error of the heritability; Mean: phenotypic mean of the trait. SD: phenotypic standard deviation of the trait; V_g: genomic variance of the trait. SE_g: Standard error of the genomic variance of the trait

The genetic correlation between β-CN and κ-CN was low (0.01 ± 0.53), whereas the genetic correlations of $α_{s2}$-CN with β-CN and κ-CN were high (< -0.90). The genetic correlations showed that the whey proteins (αLA%, and β-LG%) were highly correlated (0.71 ± 0.14). Both α-LA%, and β-LG% had a very low correlation to CN% (0.08 ± 0.25; -0.08 ± 0.30, respectively). The high genetic correlation between the whey proteins and the low correlation of the whey proteins to the CN% may reflect that the casein:whey ratio is rather constant. This is in contrast to the results of Schopen et al. (2009) where they presented a negative correlation between the whey proteins (-0.34) and a strong negative correlation between the CN and whey proteins (-0.76). Bonfatti et al. (2011b) showed a genetic correlation of 0.10 between αLA%, and β-LG%, and showed a positive correlation between the total CN and total whey proteins (0.42).

The differences in both heritability estimates and genetic correlations between our study, Schopen et al. (2009) and Bonfatti et al. (2011b) could be explained by differences in the sampling populations with regard to breed, analytic method applied and set-up and size of the population. It is likely that there are differences in genotype frequencies of the CN and whey genes between Holstein (our study and Schopen et al (2009)) and Simmental cattle (Bonfatti et al. (2011b). Furthermore, the population size used in our study was 370 compared to 1,940 animals used in Schopen et al. (2009). This is also reflected in the relative high SE in our study.

Conclusion

In this study, we have shown that there is genetic variation for some of the specific CN and whey proteins in the Danish Holstein population. Furthermore genetic correlations indicated that there was a low correlation between β-CN% and κ-CN% and that the whey proteins were highly correlated to each other but showed low genetic correlation to CN%. These results show that κ-CN% and the whey proteins have a high heritability and that $α_{S1}$-CN%, $α_{S2}$-CN% and β-CN% have a low heritability in Danish Holstein cattle.

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