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Short communication

Genetics of milk fatty acid groups predicted during routine data recording in Holstein dairy cattle

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ABSTRACT

The aim of this paper was to estimate genetic parameters for groups of milk fatty acids (FA), namely saturated (SFA), unsaturated (UFA), monounsaturated (MUFA) and polyunsaturated (PUFA), in Holstein cows. Mid-infrared spectroscopy (MIRS) was used to predict FA groups (g/100 g of milk) of 72,848 samples recorded on 17,873 cows between September 2011 and November 2012. Univariate and multivariate models were implemented in a Bayesian framework to estimate (co)variance components for SFA, UFA, MUFA, PUFA, daily milk yield, milk fat and milk protein. Statistical models included fixed effect of parity by stage of lactation, and random effects of herd-test-date, cow permanent environmental, animal additive genetic and residual. Posterior means of heritability estimates for SFA, UFA, MUFA and PUFA were 0.246, 0.069, 0.082 and 0.078, respectively. Estimates of genetic correlations between FA groups ranged from 0.405 (SFA and PUFA) to 0.952 (MUFA and UFA). The increase of fat content led to an increase of all groups of FA, in particular SFA, with undesirable effects on the healthy quality of the product. The study highlighted the existence of exploitable additive genetic variation for groups of FA routinely predicted by MIRS and thus there is potential to address the selection to healthy milk FA composition.

1. Introduction

The saturated fatty acids (SFA) increase blood cholesterol, which in turn is associated with increased blood pressure, risk of cardiovascular diseases, obesity, and insulin resistance (Mensink et al., 2003; Rasmussen et al., 2006; Sacks and Katan, 2002; Vessby et al., 2001). This has often led to the "demonization" of bovine milk fat (MF), as it typically contains 70% SFA, 25% monounsaturated FA (MUFA), and 5% polyunsaturated FA (PUFA).

Fat composition of cow milk is influenced by metabolic status and stage of lactation of the animal, as negative energy balance directly impacts the presence of unsaturated FA (UFA). The mobilization of fat reserves has been found to increase the content of UFA in milk (Gross et al., 2011; Samková et al., 2012), whereas contents of SFA decrease rapidly till the peak of lactation and then increase weakly (Soyeurt et al., 2008). Stoop et al. (2009) found similar results, showing that proportions of SFA, in particular C6:0–C14:0, peaked around the third month of lactation. Seasonality is another factor which determines milk FA composition, with a decrease of SFA content and

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an increase of UFA and trans-FA in grazing season (Heck et al., 2009; Jahreis et al., 1996). Heck et al. (2009) reported that FA synthesized *de novo* had a minimum in summer, whereas blood-derived FA had a minimum in winter. Moreover, the effect of animal nutrition on FA composition has been widely studied because feeding supplementation is an efficient way to modify FA composition of milk (Palmquist et al., 1993). The interest on FA profile of animal products, including milk, is also relevant for the new labeling procedures required by European Union with regulation No. 1169/2011 (http://ec.europa.eu/food/food/labellingnutrition/foodlabelling/proposed_legislation_en.htm) which is mandatory from December 2014. The regulation establishes that energy level and amount of fat (particularly SFA) of products destined to human consumption must be reported on their label.

Differences in FA profile of milk among dairy cattle breeds have been highlighted either in The Netherlands (Maurice-Van Eijndhoven et al., 2013) and in the Walloon region of Belgium (Soyeurt et al., 2006). Moreover, several studies have estimated genetic parameters for major FA groups in Holstein populations (e.g., Gion et al., 2011; Mele et al., 2009; Soyeurt et al., 2007; Tullo et al., 2014). Recently, genetic evaluation for FA composition has been developed in the Walloon region of Belgium, and it was suggested to evaluate animals on the basis of a Nutritional Quality Index (Gengler et al., 2012). The major constraint for the implementation of genetic evaluations for milk FA profile is the reference analysis (gas-chromatography), which is costly and time-consuming. The use of mid-infrared spectroscopy (MIRS) has revealed great potentiality for the genetic analysis of FA at population level, as recently reviewed by De Marchi et al. (2014). The aim of this work was to estimate genetic parameters for groups of FA predicted by MIRS in milk of Italian Holstein-Friesian cows collected during routine test-day milk recording.

2. Materials and methods

2.1. Data

Starting September 2011, the assessment of FA groups has been routinely implemented in milk recording system of Veneto region (northeast Italy), along with milk coagulation properties (De Marchi et al., 2012; Tiezzi et al., 2013). Models for the prediction of FA content (g/100 g of milk) have been developed and commercialized by FOSS (Hillerød, Denmark), and installed on Milko-Scan FT6000 (FOSS) in the laboratory of the Breeders Association of Veneto region (Padova, Italy).

A total of 91,218 morning milk samples from 25,317 cows were collected between September 2011 and November 2012. Somatic cell count (SCC) was assessed by Cell Fossomatic 250 (FOSS), and MF, milk protein (MP), SFA, MUFA and PUFA by Milko-Scan FT6000. Unsaturated FA were not directly predicted by MIRS and they were calculated from MF and SFA as: (% MF * 0.95) - % SFA. Records on studied traits were retained if they deviated less than 3.5 standard deviations from the respective mean. Moreover, records from cows with known sire and dam, in parity 1–5, between 5 and 365 days in milk and with at least 2 observations in a given lactation were retained in the dataset. Sires of cows were considered if they had at least 3 daughters in 3 herds. Cows were required to have recorded performance in a single lactation and at least 3 animals were required to be controlled on each herd-test-date (HTD). After editing of the data as above, 72,848 records from 17,873 cows were available for statistical analysis. Animals were sampled in 347 herds and were daughters of 1235 sires. Sires were born between 1988 and 2008, with the majority ($n=728$) born between 2004 and 2007.

2.2. Statistical analyses

The following linear animal model was used to analyze the data:

$$y = Xb + Z_h h + Z_p p + Z_a a + e,$$

where y is the vector of phenotypic values for the analyzed trait, b is the vector of fixed effect of parity by stage of lactation (three classes of parity, with the last including parities 3–5, and twelve monthly classes of days in milk, 6–35 days, 36–65 days, 66–95 days, 96–125 days, 126–155 days, 156–185 days, 186–215 days, 216–245 days, 246–275 days, 276–305 days, 306–335 days, and 336–365 days), h is the vector of solutions for HTD random effect, p is the vector of solutions for cow permanent environmental effect, a is the vector of solutions for cow additive genetic effect and e is the vector of random residuals. Vectors h, p, a and e were assumed normally distributed with mean 0 and variance estimated from the data (σ^2_h, σ^2_p, σ^2_a, and σ^2_e, respectively). $\boldsymbol{X}$, $\boldsymbol{Z_h}$, $\boldsymbol{Z_p}$ and $\boldsymbol{Z_a}$ are the respective incidence matrices of appropriate order.

Univariate analyses were performed to estimate variance components and sets of 4-trait analyses including milk yield (MY), MF, MP and one of the four groups of FA were performed to estimate genetic correlations. A 4-trait analysis was used to estimate the correlations between groups of FA.

Models were implemented in a Bayesian framework using the software GIBBS3F90 (Misztal, available at: http://nce.ads.uga.edu/%7Eignacy/programs.html). For univariate models, 150,000 iterations were run discarding the first 50,000 samples as burn-in and storing samples every 10 iterations, and for the 4-trait multivariate analyses, chains included 600,000 iterations with the first 100,000 samples discarded as burn-in and a thinning interval of 50 iterations.

Heritability (h^2), intra-herd heritability (h^2_{IH}), repeatability (rep), and genetic correlation (r_{gen}) were defined as:

$$h^2 = \frac{\sigma^2_a}{\sigma^2_a + \sigma^2_p + \sigma^2_h + \sigma^2_e}$$

$$h^2_{IH} = \frac{\sigma^2_a}{\sigma^2_a + \sigma^2_p + \sigma^2_e}$$

$$rep = \frac{\sigma^2_a + \sigma^2_p}{\sigma^2_a + \sigma^2_p + \sigma^2_h + \sigma^2_e}$$

$$r_{gen} = \frac{\mathrm{cov}_a}{\sqrt{\sigma^2_{x,a} * \sigma^2_{y,a}}}$$

where σ^2_a is the additive genetic variance, σ^2_p is the cow permanent environmental variance, σ^2_h is the HTD variance, σ^2_e is the residual variance and cov_a is the additive genetic covariance. The posterior means of the marginal