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Genetic and nongenetic factors associated with milk color in dairy cows

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ABSTRACT

Milk color is one of the sensory properties that can influence consumer choice of one product over another and it influences the quality of processed dairy products. This study aims to quantify the cow-level genetic and nongenetic factors associated with bovine milk color traits. A total of 136,807 spectra from Irish commercial and research herds (with multiple breeds and crosses) were used. Milk lightness ($\hat{L}$*), red-green index (â*), and yellow-blue index ($\hat{b}$*) were predicted for individual milk samples using only the mid-infrared spectrum of the milk sample. Factors associated with milk color were breed, stage of lactation, parity, milking-time, udder health status, pasture grazing, and seasonal calving. (Co)variance components for $\hat{L}$*, â*, and $\hat{b}$* were estimated using random regressions on the additive genetic and within-lactation permanent environmental effects. Greater $\hat{b}$* value (i.e., more yellow color) was evident in milk from Jersey cows. Milk $\hat{L}$* increased consistently with stage of lactation, whereas â* increased until mid lactation to subsequently plateau. Milk $\hat{b}$* deteriorated until 31 to 60 DIM, but then improved thereafter until the end of lactation. Relative to multiparous cows, milk yielded by primiparae was, on average, lighter (i.e., greater $\hat{L}$*), more red (i.e., greater â*), and less yellow (i.e., lower $\hat{b}$*). Milk from the morning milk session had lower $\hat{L}$*, â*, and $\hat{b}$*. Heritability estimates (±SE) for milk color varied between 0.15 ± 0.02 (30 DIM) and 0.46 ± 0.02 (210 DIM) for $\hat{L}$*, between 0.09 ± 0.01 (30 DIM) and 0.15 ± 0.02 (305 DIM) for â*, and between 0.18 ± 0.02 (21 DIM) and 0.56 ± 0.03 (305 DIM) for $\hat{b}$*. For all the 3 milk color features, the within-trait genetic correlations approached unity as the time intervals compared shortened and were generally <0.40 between the peripheries of the lactation. Strong positive genetic correlations existed between $\hat{b}$* value and milk fat concentration, ranging from 0.82 ± 0.19 at 5 DIM to 0.96 ± 0.01 at 305 DIM and confirming the observed phenotypic correlation (0.64, SE = 0.01). Results of the present study suggest that breeding strategies for the enhancement of milk color traits could be implemented for dairy cattle populations. Such strategies, coupled with the knowledge of milk color traits variation due to nongenetic factors, may represent a tool for the dairy processors to reduce, if not eliminate, the use of artificial pigments during milk manufacturing.

Key words: milk color, mid-infrared spectroscopy, genetic parameter, dairy industry, Commission Internationale d'Eclairage L*a*b*

INTRODUCTION

Food color is known to affect food choice (Clydesdale, 1993). The sensory properties of milk (i.e., appearance, color, flavor, aroma, and texture) are also important because of their close relationship with product quality (Wadhwani and McMahon, 2012) and consumer acceptance (Phillips et al., 1995). The yellow color of butter and many cheeses is influenced by milk fat carotenoid content (Descalzo et al., 2012), and market preferences for milk fat color varies across the world (Berry et al., 2009). For example, the yellow color of dairy products is sometimes said to be associated with a more green image by consumers, because of its association with grazing animals (Descalzo et al., 2012). In direct contrast, however, in New Zealand the yellow color of milk and its associated products is considered an unfavorable attribute in the opinion of many consumers (Morris et al., 2002).

Milk color is known to be affected by many factors including animal genetic merit and breed (Winkelman et al., 1999; Noziere et al., 2006; Berry et al., 2009), stage of lactation and parity (Calderón et al., 2007; Jadhav et al., 2008), time of milking (Quist et al., 2008), udder health status (Espada and Vijverberg, 2002), as well as herd-level factors such as pasture grazing and seasonal calving (Agabriel et al., 2007; Solah et al., 2007; Walker et al., 2013).

To our knowledge no study has attempted to quantify the contribution of genetics to variability in milk color

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in terms of lightness (**L***), red-green (**a***), and yellow-blue (**b***) values. Winkelman et al. (1999) estimated genetic and phenotypic correlations of milk color traits (in terms of milk color, fat color, and β-carotene yield) with each other and with milk production traits (milk, fat, and protein yields). Milk color, in this case, was determined by extraction from milk of the nonsaponifiable compounds. Because several studies that investigated food color used the Commission Internationale d'Eclairage L*a*b* method as color measurement, especially on meat color (Fletcher, 1999, on broiler meat; Liu et al., 2003, on beef; Zhang et al., 2007, on pork meat), in the present study this method was used to investigate milk color.

Recently mid-infrared spectroscopy (**MIRS**) has been demonstrated to be a useful low-cost and rapid screening tool (De Marchi et al., 2014) to acquire and predict innovative milk technological phenotypes (Visentin et al., 2015, 2016) and determine the L*, a*, and b* color value of milk (McDermott et al., 2016). Prediction equations developed using MIRS can be used to quantify the milk color of individual animal samples during routine milk recording as well as more frequently available bulk tank milk samples. Therefore, MIRS is useful to collate large numbers of unbiased records of milk color throughout lactation which can be used to estimate animal breeding values.

Thus, the objective of the present study was to quantify the contribution of cow-level genetic and nongenetic factors to variability in milk color as described by L*, a*, and b* indices predicted using MIRS equations.

MATERIALS AND METHODS

Milk Sample Collection

A total of 174,062 milk samples were collected between January 2013 and December 2015 from 10,394 dairy cows of 5 different breeds (Holstein, Friesian, Jersey, Montbeliarde, and Norwegian Red) and crosses. Of these, 129,086 samples were from 1,661 research cows from 7 research farms operated by the Teagasc Animal and Grassland Research and Innovation Centre (Moorepark, Fermoy, Co. Cork, Ireland). Cows in the research herds participated in a series of experimental treatments based on different feeding strategies, stocking rates, calving periods, and length of grazing period. A small proportion of dairy cows in the research herds (90 individuals per year) belonged to the top 1% genetic merit, as ranked based on the national selection index. The remaining 44,976 samples were collected from 8,733 cows from 69 different commercial Irish farms located in southwest Ireland. Cows in research and commercial herds were fed a basal grazed-pasture diet, but at times cows in the research farms were supplemented with a small quantity of concentrates (depending on the experimental treatment). All cows were milked twice daily and sampled based on test-day recording system. The average monthly test-day records per cow and lactation were 17 and 10, respectively. Coefficients of general heterosis and recombination loss were calculated for each cow as heterosis $= 1 - \sum_{i=1}^{n} \text{sire}_i \times \text{dam}_i$, and recombination loss $= 1 - \sum_{i=1}^{n} \frac{\text{sire}_i^2 + \text{dam}_i^2}{2}$, where sire_i and dam_i are the proportion of genes of the breed i in the sire and the dam, respectively (VanRaden and Sanders, 2003). The pedigree of all animals was traced back at least 4 generations, and comprised a total of 41,232 animals.

For the research data, milk samples were separately collected on consecutive PM and AM milkings once weekly. For commercial herds, a single milk sample was taken during the milk recording day and these samples were collected occasionally (approximately 1,249 spectra/mo) and sent for analysis as part of a related research study. Once collected, all samples were analyzed within 24 h (for research samples) or 5 d (for commercial samples) in the laboratory of Teagasc Animal and Grassland Research and Innovation Center (Moorepark, Fermoy, Co. Cork, Ireland). Milk chemical composition (concentrations of protein, fat, lactose, urea, casein, and TS) was predicted using a MilkoScan FT6000 (Foss Electronic A/S, Hillerød, Denmark) and mid-infrared spectra (wavelengths from 900 to 5,000 cm^{-1}) were stored. Somatic cell count was determined by Fossomatic (Foss Electronic A/S) and normalized by taking the $\log_{10}$ of SCC/1,000 ($\log_{10}$SCC).

Gold Standard Analysis and Prediction Model Development

Milk color was measured on a selection of samples for the development of MIR prediction equations using a Chroma Meter CR400 (Konica Minolts Sensing Europe, Nieuweigein, the Netherlands, with viewing geometry d/0) with a closed cone, set on the L*, a* and b* system. The selection of samples was discussed in detail by McDermott et al. (2016). The Chroma Meter CR was calibrated on a white tile. Sub-samples of 10-mL were measured in a cuvette and results were expressed in Commission Internationale d'Eclairage L*a*b* uniform color space. This method is a 3-dimensional opponent color system that represents L*, a*, and b* values on 3 axes. The central vertical axis represents the L* in-