



J. Dairy Sci. 98:1–14
<http://dx.doi.org/10.3168/jds.2014-8599>
 © American Dairy Science Association®, 2015.

Genetic parameters of cheese yield and curd nutrient recovery or whey loss traits predicted using Fourier-transform infrared spectroscopy of samples collected during milk recording on Holstein, Brown Swiss, and Simmental dairy cows

A. Cecchinato,¹ A. Albera, C. Cipolat-Gotet, A. Ferragina, and G. Bittante

Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro, Italy

ABSTRACT

Cheese yield is the most important technological parameter in the dairy industry in many countries. The aim of this study was to infer (co)variance components for cheese yields (CY) and nutrient recoveries in curd (REC) predicted using Fourier-transform infrared (FTIR) spectroscopy of samples collected during milk recording on Holstein, Brown Swiss, and Simmental dairy cows. A total of 311,354 FTIR spectra representing the test-day records of 29,208 dairy cows (Holstein, Brown Swiss, and Simmental) from 654 herds, collected over a 3-yr period, were available for the study. The traits of interest for each cow consisted of 3 cheese yield traits (%CY: fresh curd, curd total solids, and curd water as a percent of the weight of the processed milk), 4 curd nutrient recovery traits (REC: fat, protein, total solids, and the energy of the curd as a percent of the same nutrient in the processed milk), and 3 daily cheese production traits (daily fresh curd, total solids, and the water of the curd per cow). Calibration equations were used to predict individual test-day observations for these traits. The (co)variance components were estimated for the CY, REC, milk production, and milk composition traits via a set of 4-trait analyses within each breed. All analyses were performed using REML and linear animal models. The heritabilities of the %CY were always higher for Holstein and Brown Swiss cows (0.22 to 0.33) compared with Simmental cows (0.14 to 0.18). In general, the fresh cheese yield (%CY_{CURD}) showed genetic variation and heritability estimates that were slightly higher than those of its components, %CY_{SOLIDS} and %CY_{WATER}. The parameter REC_{PROTEIN} was the most heritable trait in all the 3 breeds, with values ranging from 0.32 to 0.41. Our estimation of the genetic relationships of the CY and REC with milk

production and composition revealed that the current selection strategies used in dairy cattle are expected to exert only limited effects on the REC traits. Instead, breeders may be able to exploit genetic variations in the %CY, particularly REC_{FAT} and REC_{PROTEIN}. This last component is not explained by the milk protein content, suggesting that its direct selection could be beneficial for cheese production aptitude. Collectively, our findings indicate that breeding strategies aimed at enhancing CY and REC could be easily and rapidly implemented for dairy cattle populations in which FTIR spectra are routinely acquired from individual milk samples.

Key words: genetic parameter, mid-infrared spectroscopy, cheese yield, whey loss, dairy breed

INTRODUCTION

The amount of milk used for cheese production is growing in many countries (International Dairy Federation, 2013), increasing the importance of the milk technological parameters that are related to dairy processing. Cheese yield (CY), which is the percentage ratio between the curd weight and the milk weight, is the most important parameter for the dairy industry and affects milk value (Emmons, 1993). Protein and fat, together with water, are the most important milk components retained in the curd, and CY is usually predicted from the milk protein and fat contents (Emmons et al., 1990; Verdier-Metz et al., 2001). This assumes that there is a linear relationship and constant recovery (REC) for milk nutrients in the curd (i.e., the percentage of a given milk nutrient that is retained in the curd).

In current dairy cattle breeding programs, the aptitude of milk for cheese production is improved via changes in milk composition, indirectly exploiting the favorable phenotypic relationships of the milk protein and fat contents with CY. Individual variations in the recoveries of protein (REC_{PROTEIN}) and fat (REC_{FAT}) are not considered. In a study on individual model

Received July 10, 2014.

Accepted March 27, 2015.

¹Corresponding author: alessio.cecchinato@unipd.it

cheeses fabricated from the milk of individual Brown Swiss cows, however, Bittante et al. (2013) showed that CY has genetic variability and a moderate heritability. Those authors also found that, although the genetic correlations of the milk fat and protein contents with CY were positive and high, the milk composition did not explain all of the genetic variation observed in CY. Othmane et al., (2002a) used a very simplified procedure in which 10 mL of milk was heated, rennet was added, milk was centrifuged after 1 hr, then drained and weighed (Othmane et al., 2002b); they estimated that CY of ovine milk is characterized by a rather low heritability (about one-half that of milk yield and one-third that of protein content).

The recoveries of protein and fat in the curd are genetically controlled traits, with high and moderate heritability values, respectively (Bittante et al., 2013). Their genetic relationships with the corresponding nutrient contents in the milk are low, whereas they show positive and consistent genetic correlations with CY (Bittante et al., 2013). Hence, breeders could perhaps more effectively improve the aptitude of milk for cheese production if they selected directly for technological parameters rather than for milk composition. However, such selection has been limited by the relative lack of phenotypic data; a routine genetic evaluation would require population-level data for individual CY or REC traits, but such work is clearly infeasible for both operative and economic reasons.

Infrared optical technologies, such as Fourier-transform infrared (FTIR) spectroscopy, have proven to be efficient in predicting a variety of chemical bonds (Brandt et al., 2010; Karoui et al., 2010) and can be used to predict milk characteristics (Rutten et al., 2009; Karoui et al., 2011; Rutten et al., 2011). Indeed, within current milk-recording schemes, milk samples are routinely analyzed for their protein and fat contents using FTIR (ICAR, 2012). As FTIR spectra are now obtained for every milk sample collected during milk recording activities, we speculated that the use of appropriate calibration equations could enable the inexpensive large-scale analysis of multiple new phenotypes that might be incorporated into the current breeding programs.

In the FTIR spectra of milk, the transmittance of many individual waves in the range from wavenumber $5.000 \times \text{cm}^{-1}$ (in the near-infrared interval) to $930 \times \text{cm}^{-1}$ (in the mid-infrared interval) was found to be heritable (Bittante and Cecchinato, 2013), as were the principal components obtained from the milk spectra (Soyeurt et al., 2010; Dagnachew et al., 2013). Bittante and Cecchinato (2013) also showed that the many heritable individual waves of the milk spectra included some whose transmittances are typically linked to the chemi-

cal bonds that characterize important components of milk. These findings provided the biological basis for using FTIR-based predictions for the selection of dairy species. Recent studies have examined the possible use of population-level FTIR predictions for the genetic improvement of milk characteristics, including the milk FA profile (Soyeurt et al., 2007b; Arnould et al., 2010; Bastin et al., 2011) and protein content (Soyeurt et al., 2007a; Arnould et al., 2009).

Cecchinato et al. (2009) showed that mid-infrared-based predictions of milk coagulation properties could be used for genetic improvement even when the predictive values of the calibration equations were moderate, as these traits were heritable and displayed genetic correlations that were much higher than the phenotypic correlations with the corresponding measured traits. Similar results were found by Rutten et al. (2010) for the milk FA profile and by Cecchinato et al. (2011a) for beef quality traits.

Ferragina et al. (2013) used FTIR spectroscopy to predict different measures of the CY and REC traits in Brown Swiss cows and obtained moderate to highly accurate predictions for most of them, except for REC-FAT, for which the coefficient of determination between the predicted and measured values in cross-validation was equal to 0.41. In an external validation study, Bittante et al. (2014) compared the genetic parameters of FTIR predictions with those of the observed measures for CY and REC traits in Brown Swiss cows. For all of the considered traits, the heritabilities of the FTIR predictions were similar to or higher than those of the measured traits; furthermore, the genetic correlations between the predicted and observed measures were very high for all the traits. These results suggest that it may be possible to consider the FTIR predictions as potential indicators traits for enhancing CY and REC traits at genetic level and, as a consequence, to apply a population-level selection scheme aimed at improving the CY-related traits in dairy cattle. However, this would require specific knowledge of the (co)variance components and heritabilities of the predicted traits in different dairy breeds. Therefore, the objective of our study was to estimate the genetic parameters for the FTIR predictions of various CY and REC traits at the population level (as obtained during routine milk recording data collection) and examine their genetic relationships with milk production and composition traits in Holstein, Brown Swiss, and Simmental cows.

MATERIALS AND METHODS

Data and Records

The data for our study were provided by the Breeders Federation of Trento Province (in the northeast

Download English Version:

<https://daneshyari.com/en/article/10975327>

Download Persian Version:

<https://daneshyari.com/article/10975327>

[Daneshyari.com](https://daneshyari.com)