



## Comparison between genetic parameters of cheese yield and nutrient recovery or whey loss traits measured from individual model cheese-making methods or predicted from unprocessed bovine milk samples using Fourier-transform infrared spectroscopy

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### ABSTRACT

Cheese yield is an important technological trait in the dairy industry. The aim of this study was to infer the genetic parameters of some cheese yield-related traits predicted using Fourier-transform infrared (FTIR) spectral analysis and compare the results with those obtained using an individual model cheese-producing procedure. A total of 1,264 model cheeses were produced using 1,500-mL milk samples collected from individual Brown Swiss cows, and individual measurements were taken for 10 traits: 3 cheese yield traits (fresh curd, curd total solids, and curd water as a percent of the weight of the processed milk), 4 milk nutrient recovery traits (fat, protein, total solids, and energy of the curd as a percent of the same nutrient in the processed milk), and 3 daily cheese production traits per cow (fresh curd, total solids, and water weight of the curd). Each unprocessed milk sample was analyzed using a MilkoScan FT6000 (Foss, Hillerød, Denmark) over the spectral range, from 5,000 to 900 wavenumber  $\times$  cm<sup>-1</sup>. The FTIR spectrum-based prediction models for the previously mentioned traits were developed using modified partial least-square regression. Cross-validation of the whole data set yielded coefficients of determination between the predicted and measured values in cross-validation of 0.65 to 0.95 for all traits, except for the recovery of fat (0.41). A 3-fold external validation was also used, in which the available data were partitioned into 2 subsets: a training set (one-third of the herds) and a testing set (two-thirds). The training set was used to develop calibration equations, whereas the testing subsets were used for external validation of the calibration equations and to estimate the heritabilities

and genetic correlations of the measured and FTIR-predicted phenotypes. The coefficients of determination between the predicted and measured values in cross-validation results obtained from the training sets were very similar to those obtained from the whole data set, but the coefficient of determination of validation values for the external validation sets were much lower for all traits (0.30 to 0.73), and particularly for fat recovery (0.05 to 0.18), for the training sets compared with the full data set. For each testing subset, the (co)variance components for the measured and FTIR-predicted phenotypes were estimated using bivariate Bayesian analyses and linear models. The intraherd heritabilities for the predicted traits obtained from our internal cross-validation using the whole data set ranged from 0.085 for daily yield of curd solids to 0.576 for protein recovery, and were similar to those obtained from the measured traits (0.079 to 0.586, respectively). The heritabilities estimated from the testing data set used for external validation were more variable but similar (on average) to the corresponding values obtained from the whole data set. Moreover, the genetic correlations between the predicted and measured traits were high in general (0.791 to 0.996), and they were always higher than the corresponding phenotypic correlations (0.383 to 0.995), especially for the external validation subset. In conclusion, we herein report that application of the cross-validation technique to the whole data set tended to overestimate the predictive ability of FTIR spectra, give more precise phenotypic predictions than the calibrations obtained using smaller data sets, and yield genetic correlations similar to those obtained from the measured traits. Collectively, our findings indicate that FTIR predictions have the potential to be used as indicator traits for the rapid and inexpensive selection of dairy populations for improvement of cheese yield, milk nutrient recovery in curd, and daily cheese production per cow.

**Key words:** genetic parameter, mid-infrared spectroscopy, cheese yield, whey loss, cross-validation

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## INTRODUCTION

Several traits are very important for the dairy industry in relation to cheese-making processes, including the cheese yield and the proportion of various milk nutrients that are retained in the curd or lost in whey. Cipolat-Gotet et al. (2013) used a model cheese-making procedure on a large number of individual samples and found that the cheese yield and nutrient recovery or whey loss traits were heavily affected by the herd (and thus by environmental, nutritional, and management factors) and individual factors (e.g., parity, stage of lactation, and milk yield of cows). Even after accounting for these factors, however, a large proportion of the individual variability remained unexplained. Using the same large data set, Bittante et al. (2013) found that all of these traits were characterized by heritability coefficients similar to or higher than those of milk yield and the fat and protein contents of the milk. The genetic correlations between cheese yields and milk composition were found to be high, but far from unity, and those between curd recovery or whey loss traits and milk composition were rather low. The authors concluded that the inclusion of milk fat and protein contents in the selection indices is an effective tool when seeking to indirectly select for cheese yield, but it cannot explain all of the genetic variability in these traits. Although such traits were much less useful for the indirect selection of nutrient recoveries in curd or losses in whey, the authors concluded that selection for these traits could contribute to increasing profitability in the milk production or cheese-making chain.

Unfortunately, although the evaluation of cheese yield traits through model cheese production is repeatable, it is also expensive and very time-consuming. Thus, these traits cannot be routinely measured on a large scale for direct genetic improvement at the population level. Similar problems in assessing other traits have been addressed by using predictions obtained from specific calibrations based on Fourier transform infrared (FTIR) spectrometry. The transmittance or absorbance of milk samples at individual wavelengths in the medium infrared and near infrared (NIR) regions of the electromagnetic spectrum are demonstrably associated with many chemical bonds (Barbano and Lynch, 2006; Brandt et al., 2010; Karoui et al., 2010) and are often heritable (Soyeurt et al., 2010; Bittante and Cecchinato, 2013; Dagnachew et al., 2013). The FTIR spectrometer-based predictions of milk fat, protein, casein, and lactose contents (Hewavitharana and van Brakel, 1997; Etzion et al., 2004; Kaylegian et al., 2006) have become routine in laboratories that analyze milk samples for the milk recording of dairy cows and other ruminants (ICAR, 2012). The FTIR spectroscopy has also been proposed

as a means to predict other interesting milk traits for which genetic parameters have been estimated, including FA profiles (Soyeurt et al., 2007b; Rutten et al., 2010; Bastin et al., 2011), detailed protein compositions (Arnould et al., 2009), milk coagulation traits (Bittante et al., 2012), and mineral profiles (Soyeurt et al., 2009). However, only one previous report compared the genetic parameters of measured and predicted traits (Cecchinato et al., 2009). Moreover, those authors emphasized the importance of estimating the genetic correlations between measured and predicted traits to correctly evaluate the effectiveness of using predicted traits for the indirect selection of desired traits.

Ferragina et al. (2013) recently reported FTIR calibrations for the major traits related to cheese yield and nutrient recovery in curd or loss in whey. Similar to the majority of studies on other milk traits, these authors calibrated the whole data set using the technique of cross-validation. In contrast, the study of Cecchinato et al. (2009) used a small subset for calibration and the rest of the data set for their validation and genetic analysis. The aims of the present study were (1) to compare the use of internal cross-validation versus external validation techniques when using FTIR spectrum-based calibrations to predict several traits related to cheese yield and nutrient recovery in milk or losses in whey; (2) to estimate the genetic parameters of the predicted cheese yield and nutrient recovery traits; (3) to compare these genetic parameters with those estimated for the corresponding traits measured following individual model cheese fabrication; (4) to estimate the genetic correlations between corresponding predicted and measured traits and consider using the former as indicator traits for the indirect selection of dairy populations; and (5) to compare the use of internal cross-validation versus external validation techniques on the genetic parameters of predicted traits and the genetic correlations between the predicted and measured traits.

## MATERIALS AND METHODS

### *Field Data*

The present study is part of the Cowplus Project. The production environment, which was previously described in Sturaro et al. (2013), represented the variety of dairy systems in the Alps, from small traditional farms to large modern systems. A total of 1,264 Brown Swiss cows from 85 herds located in Trento Province (Italy) were sampled once during evening milking (15 cows were sampled per herd, with a few exceptions, and 1 herd was sampled per day). The cows represented different parities (1 to 5), DIM (5 to 449), and production levels ( $24.3 \pm 7.9 \text{ kg} \times \text{d}^{-1}$ ). The sampling procedure

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