J. Dairy Sci. 97:1171–1186
http://dx.doi.org/10.3168/jds.2013-6799

Invited review: Mid-infrared spectroscopy as phenotyping tool for milk traits[1]

M. De Marchi,[2] V. Toffanin, M. Cassandro, and M. Penasa
Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

ABSTRACT

Interest in methods that routinely and accurately measure and predict animal characteristics is growing in importance, both for quality characterization of livestock products and for genetic purposes. Mid-infrared spectroscopy (MIRS) is a rapid and cost-effective tool for recording phenotypes at the population level. Mid-infrared spectroscopy is based on crossing matter by electromagnetic radiation and on the subsequent measure of energy absorption, and it is commonly used to determine traditional milk quality traits in official milk laboratories. The aim of this review was to focus on the use of MIRS to predict new milk phenotypes of economic relevance such as fatty acid and protein composition, coagulation properties, acidity, mineral composition, ketone bodies, body energy status, and methane emissions. Analysis of the literature demonstrated the feasibility of MIRS to predict these traits, with different accuracies and with margins of improvement of prediction equations. In general, the reviewed papers underlined the influence of data variability, reference method, and unit of measurement on the development of robust models. A crucial point in favor of the application of MIRS is to stimulate the exchange of data among countries to develop equations that take into account the biological variability of the studied traits under different conditions. Due to the large variability of reference methods used for MIRS calibration, it is essential to standardize the methods used within and across countries.
Key words: mid-infrared spectroscopy, phenotyping, quality trait, dairy cattle

INTRODUCTION

In the genomic era, phenomics is becoming a compulsory research field. This new science is concerned with the acquisition of phenotypic data on a large scale (Houle et al., 2010) and the phenotype can be described as the outcome of the interacting development between the genotype of an individual and its specific environment throughout life (Bowman, 1974). The interest in methods that routinely and accurately measure and predict animal characteristics (i.e., phenotypes) is rapidly growing. Accurate phenotypes and efficient phenotyping tools are the key ingredients, especially for genomic selection of livestock animals, which is expected to increase the genetic gain of the selected traits (Pryce et al., 2010; Lillehammer et al., 2011; Mc Hugh et al., 2011).

Furthermore, in recent years, consumers and the dairy industry have shifted the concept of quality in relation to market requirements: for example, milk coagulation traits have been studied to improve cheese production and FA composition to enrich the nutritional value of milk for human health. Breeding goals have followed these changes: if phenotypes are accurately and cheaply measured at the population level and integrated in the national milk recording systems, it may be possible to enhance the traits using genetic or genomic tools.

The need for fast, cheap, and high-throughput methods of chemical analysis has also led to the application of infrared spectroscopy in both the livestock and food sectors. The spectroscopic technique is based on the study of the interaction between matter and electromagnetic waves. Electromagnetic radiation comprises different regions according to the following wavelengths: the x-ray region (0.5–10 nm), UV region (10–350 nm), visible region (350–800 nm), near-infrared region (800–2,500 nm), mid-infrared region (2,500–25,000 nm), microwave region (100 μm–1 cm), and radio frequency region (1 cm–1 m).

One of the most important historical events for the spectroscopic technique was the development of the Fourier transform in the 1700s; in later years, this mathematical transform was improved with the use of the interferometer. In 1969, Digilab Inc. (Marlborough, MA) put the first Fourier-transform infrared spectro-

Received March 13, 2013.
Accepted November 8, 2013.
[1]M. De Marchi designed and wrote the first draft of the manuscript and V. Toffanin, M. Penasa, and M. Cassandro were involved in drafting the paper. All authors contributed to the discussion of the review.
[2]Corresponding author: massimo.demarchi@unipd.it

photometer with a dedicated minicomputer on the market, which was later refined in 1983 by the same company (Spectra-Tech Inc., Oak Ridge, TN). From the 1980s, Fourier-transform infrared spectrophotometers were combined with personal computers and this method of analysis became widely used due to its versatility and cost effectiveness. Since then, many studies have investigated the relationships between spectra wavelengths and several quality traits through the explanation of chemical bond variations.

Mid-infrared spectroscopy (**MIRS**) has been evaluated as a potential tool to collect data at the population level for phenotypic and genetic purposes, and it is becoming one of the major topics in dairy science. In the mid-infrared region, when matter is crossed by electromagnetic radiation, the bonds of the molecules make movements (e.g., vibration and rotation), which involve a more or less marked absorption of the provided energy. On the basis of supplied energy and the amount absorbed by the irradiated sample, and using spectra mathematical pretreatments, it is possible to determine the sample's chemical composition and correlated compounds (Figure 1).

The present review summarizes papers that have investigated the use of MIRS to predict milk quality traits. Furthermore, studies that adopted this technique to predict nutritional, technological, and other traits of economic relevance are also reviewed.

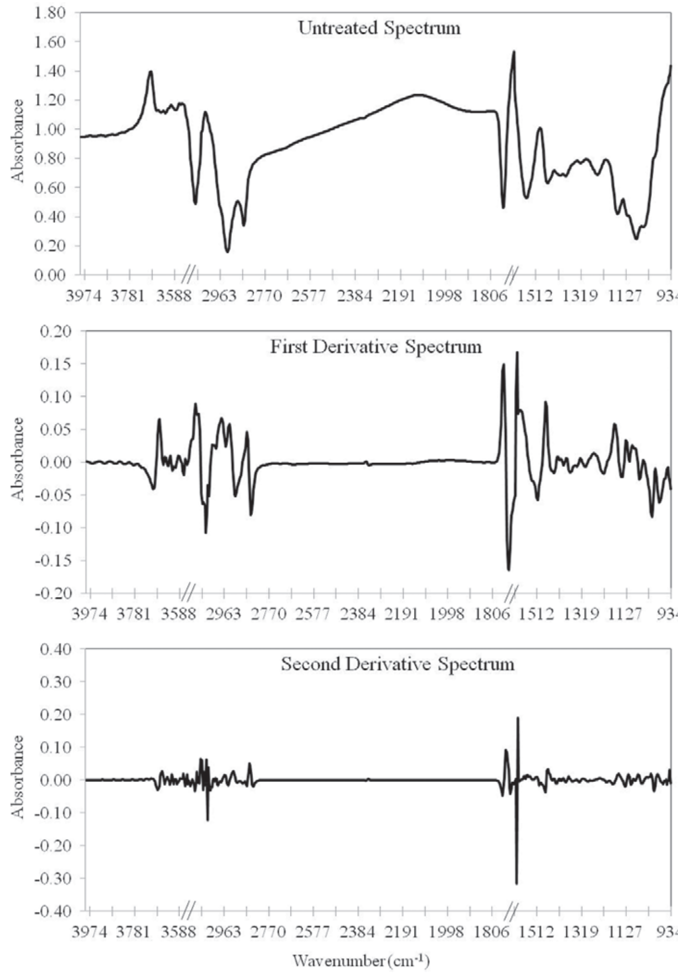

Figure 1. Examples of untreated, first-derivative, and second-derivative spectra.

PHENOTYPING OF MILK BY MIRS

Studies that aimed at investigating the effectiveness of MIRS to predict phenotypes for dairy industry applications or for genetic purposes have markedly increased over the years. Figure 2 depicts the trend in the number of papers published from 2001 to 2013 on the application of MIRS to milk, highlighting a growing interest for the topic, particularly in the last 3 yr. This is confirmed also by large international research projects that aimed at predicting new traits in the dairy industry (e.g., OptiMIR, 2012; RobustMilk, 2012). In animal science, phenomics is mainly related to the study of phenotypes of an individual. A phenotype should be routinely, cheaply, and easily measurable, should show good to optimal accuracy of prediction, depending on its use, and should exhibit genetic variation or, if it is a predictor of the real phenotype of interest, high genetic correlation with the trait of interest (Berry et al., 2012).

Currently, MIRS is used to determine quality traits in bulk and individual milk samples. In particular, most countries use MIRS in official milk-recording schemes to predict protein, casein, fat, lactose, and urea contents. Besides these traditional traits, MIRS has been used to predict other milk characteristics: FA composition (Soyeurt et al., 2006, 2008, 2011; Rutten et al., 2009; De Marchi et al., 2011; Ferrand et al., 2011; Maurice-Van Eijndhoven et al., 2013), milk protein composition (Luginbühl, 2002; Sørensen et al., 2003; Etzion et al., 2004; De Marchi et al., 2009a; Bonfatti et al., 2011; Rutten et al., 2011), milk coagulation properties (**MCP**; Dal Zotto et al., 2008; De Marchi et al., 2009b, 2013), milk acidity (De Marchi et al., 2009b), mineral composition (Soyeurt et al., 2009), melamine content (Balabin and Smirnov, 2011), ketone bodies (Heuer et al., 2001; de Roos et al., 2007; van Knegsel et al., 2010; van der Drift et al., 2012), body energy status (McParland et al., 2011), and methane emissions (Dehareng et al., 2012).

In addition, several laboratories involved in routine milk-recording systems have been storing spectral data to predict a posteriori several phenotypes; this approach is very interesting for genetic purposes.