

Breeding and Genetics Symposium: Joint Interbull/JAM Session: Milk spectral data—Cost-effective information to improve expensive and limited traits in dairy cattle breeding

10 Capitalizing on fine milk composition for breeding and management of dairy cows. Nicolas Gengler^{*1}, H el ene Soyeurt¹, Fr ed eric Dehareng², Catherine Bastin¹, Fr ed eric Colinet¹, Hedi Hammami¹, and Pierre Dardenne², ¹*University of Li ge-GxABT, Gembloux, Belgium*, ²*Walloon Agricultural Research Center, Gembloux, Belgium*.

Management and breeding of dairy cows face the challenge of permanently adapting to changing production circumstances under socio-economic constraints. If management and breeding addresses different timeframes of action, both need relevant phenotypes that allow for precise monitoring of the status of the cows, their products (i.e., milk and subsequently dairy products), their behavior and their environmental impact. Milk composition has been identified as an important source of information since it could reflect, at least partially, all these elements. Major milk components such as fat, protein, urea, and lactose contents are routinely predicted by mid-infrared (MIR) spectrometry and have been widely used for these purposes. But, milk composition is much more complex and other components might be informative. Such new milk-based phenotypes should be considered given that they are cheap, rapidly obtained, usable on a large scale, robust and reliable. In a first approach, new phenotypes can be predicted from MIR spectra using classical prediction equation based techniques. This method was used successfully for many novel traits (e.g., fatty acids, lactoferrin, minerals, milk technological properties, citrate), that can then be useful for management and breeding purposes. An innovation was to consider the longitudinal nature of the relationship between the trait of interest and the MIR spectra (e.g., to predict methane from MIR). By avoiding intermediate steps, prediction errors can be minimized when traits of interest (e.g., ketosis) are predicted directly from MIR spectra. In a second approach, in an innovative manner, patterns detected by comparing observed from expected MIR spectra can be used directly. All these traits can then be used to define best practices, adjust feeding and health management, improve animal welfare, improve milk quality and limit environmental impact. Under the condition that MIR data are available on a large scale, phenotypes for these traits will allow genetic and genomic evaluations. Introduction of novel traits into the breeding objectives will need additional research to clarify socio-economic weights and genetic correlation with other traits of interest.

Key Words: milk, spectra, novel traits

11 Applications of milk spectroscopy data to select for feed efficiency and reduced methane emissions in dairy breeding programs. Sinead McParland^{*1} and Frederic Dehareng², ¹*Animal and Grassland Research & Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork, Ireland*, ²*Walloon Agricultural Research Centre, Gembloux, Belgium*.

Feed efficiency (FE), the difference between energy intake and the energy demanded and supplied by various reservoirs and sinks, is of increasing importance. One such energy sink is methane emissions (ME); ME also have repercussions on climate change. Collection of the necessary data for the computation of genetic evaluations for both FE and ME are, however, laborious and expensive. Mid-infrared spectrometry (MIRS) offers a solution to routinely collect data on milk recorded

animals at no additional cost to milk recording. The use of MIRS to accurately predict animal and milk traits, including energy balance (EB) and milk fatty acids (FA) has recently been shown and validated. When changes in body mass are zero, EB is mathematically identical to residual feed intake (RFI), a measure commonly used to depict FE. The relationship between ME and milk FA has also been reported. Therefore, it was recently hypothesized that both RFI and ME could also be predicted from milk. Two separate studies were conducted using 1,270 records of RFI from Irish Holstein-Friesians, and 77 records of ME from Belgian Holstein cows. Accuracy (i.e., correlation) of predicting RFI and ME using partial least squares regression on the MIR spectral data was 0.62 and 0.87, respectively, in cross validation. Both studies were limited by small numbers, and have yet to be independently validated. The heritability of MIR-predicted RFI was 0.06, and was lower than the heritability of measured RFI using the same data set (0.10), however the genetic correlation between MIR-predicted and measured RFI was 0.78 using the limited data set. Furthermore, when prediction equations were applied to larger data sets of MIR spectral data, the lactation profile for RFI was in line with expectations based on profiles estimated from measured RFI. The shape of the lactation profile of predicted ME was, however, dependent on stage of lactation. The major limitation precluding FE and ME from breeding programs in the past can be resolved through the use of MIRS on milk recorded animals.

Key Words: feed efficiency, methane, mid infrared spectrum

12 Using milk spectroscopy phenotypes in genetic selection programs to improve the nutraceutical value of milk in dairy cows. Henk Bovenhuis^{*}, *Animal Breeding and Genomics Centre, Wageningen University, Wageningen, the Netherlands*.

Milk is a unique product that is specifically suited to nourish the offspring and because initially milk is the young's only food it has to contain all essential ingredients. However, several studies have indicated that in modern human diets, a high intake of saturated fatty acids is a risk factor for cardiovascular diseases. Milk and dairy products are major sources of these fatty acids. Milk fat composition is strongly affected by genetic factors, which suggests that there are opportunities to change milk fat composition by means of selective breeding. A crucial factor in successful selection strategies is the availability of phenotypes. Milk fat composition can be accurately determined based on gas chromatography (GC); however, this analytical method is expensive and relatively time consuming. Alternatively, fatty acids can be predicted based on infrared spectra. Infrared prediction of unsaturated fatty acids might be based on indirect relations or on a direct relationship between infrared frequencies and the double bond within the fatty acid chain. Distinguishing direct and indirect relations is relevant as it might have consequences for the range of conditions under which prediction equations are valid. Bouwman (2014) compared genome-wide associations for GC-based fatty acids with infrared-predicted fatty acids and found considerable differences. A typical example was the region on BTA26 containing the SCD1 polymorphism. More recently, we studied the effect of the SCD1 polymorphism on all 1,060 individual infrared wavelengths (Wang et al., 2015). No wavelengths were significantly affected by the SCD1 polymorphism whereas the SCD1 polymorphism has been shown to have significant effects on the content of C10:0, C14:0, C18:0, C10:1, C12:1,

C14:1, and C16:1 (Duchemin et al., 2012). This suggests that infrared spectra contain little direct information on the content of these fatty acids. This confirms results by Eskildsen et al. (2014), who concluded that prediction of individual fatty acids relies on correlations with fat content rather than on direct relations with specific Infrared frequencies.

Key Words: infrared, prediction, milk fatty acids

13 Do milk spectroscopy phenotypes have a role to play in dairy fertility and health breeding programs? Catherine Bastin*¹, Léonard Théron², Aurélie Lainé¹, and Nicolas Gengler¹, ¹*University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium*, ²*Faculty of Veterinary Medicine, Clinical Department of Production Animals, University of Liège, Liège, Belgium*.

Genetic selection allows for permanent improvement of dairy cow fertility and health. However, these traits are generally complex, difficult to record, and lowly heritable (<0.10). Hence, indicators have been proven as useful in the prediction of genetic merit for direct fertility and health traits as long as they are easier to measure, heritable, and genetically correlated. Considering that changes in (fine) milk composition over the lactation reflects the physiological status of the cow, the mid-infrared (MIR) analysis of milk opens the door to a whole new range of potential indicator traits of fertility and health. Previous studies investigated the phenotypic and genetic relationships between fertility and MIR-predicted phenotypes, most of them being related to negative postpartum energy balance and body fat mobilization (e.g., fat to protein ratio, urea, fatty acids profile). Results showed that a combination of various fatty acids traits (e.g., C18:1 *cis*-9 and C10:0) could be used to improve fertility. Furthermore, occurrence of (sub-)clinical ketosis has been related to milk-based phenotypes such as fatty acids and ketone bodies. Hence, MIR-predicted acetone and β -hydroxybutyrate contents in milk were demonstrated as useful for breeding cows less susceptible to ketosis. Although studies investigating the genetic association among mastitis and MIR-predicted phenotypes are scarce, a wide range of traits, potentially predicted by MIR spectrometry, are worth considering. It includes traits related to the disease response of the cow (e.g., lactoferrin), to the reduced secretory activity (e.g., lactose) and to the alteration of blood-milk barrier (e.g., minerals, citrate). Moreover, direct

MIR-prediction of fertility and health traits should be further considered. To conclude, MIR-predicted phenotypes have a role to play in the improvement of dairy cow fertility and health. However, further studies are warranted to (1) grasp underlying associations among MIR-predicted indicator and fitness traits, (2) estimate the genetic parameters, and (3) include these traits in broader breeding strategies.

Key Words: health, fertility, mid-infrared spectrometry

14 Implementation of mid-infrared calculated tools to select for novel traits in dairy cattle breeding. Eileen Wall*¹, Stephanie Smith¹, Sinead McParland², Vicky Hicks³, and Mike Coffey¹, ¹*Scotland's Rural College, Edinburgh, UK*, ²*Teagasc, Cork, Ireland*, ³*National Milk Records, Chippenham, UK*.

Currently, mid infrared (MIR) spectroscopy of milk samples is used to predict milk fat, protein, and lactose. While the technology has been utilized for milk recording for numerous years, the application of mid-infrared to measure other parameters in milk is a recent development. More recent studies have shown that MIR can predict different milk quality attributes (e.g., Soyeurt et al., 2011, 2012) as well as other performance traits such as energy balance (McParland et al., 2011, 2014), methane emissions (Dehareng et al., 2012) and health and fertility traits. Here we extend the predictions of novel traits from milk MIR to implementation in the industry as part of routine milk recording. We will discuss the system established to routinely capture and used milk spectra in an operational milk recording business. The system established has allowed us to apply prediction equations for a range of traits to national spectra on almost 117,000 animals (over 1 million test-dates) from 355 farms across the UK (from Feb 2013 to Jan 2015). Systems for routinely predicting novel traits have been established and routine extraction of data for the estimation of genetic parameters and breeding values developed. For example, heritability estimates for cow energy balance, body energy content and energy intake were 0.12, 0.23, and 0.15 respectively. Mid-infrared-based traits predictions from routinely collected data at a national level have potential use in genetic improvement of livestock for previously difficult and expensive to record traits.

Key Words: milk mid-infrared, genetic improvement, dairy cows