Interest, Recording and Possible Use of New Phenotypes from Fine Milk Composition

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Introduction

Standard cow milk analysis as used for performance recording or milk pricing has been restricted for decades to fat and protein. Some countries added solids not fat, true protein, urea and lactose and most somatic cell counts (ICAR, 2009). However milk produced by a cow at a given moment under given environmental circumstances (e.g., management, feeding, and climate) is in itself a highly valuable source of information on the status of the animal, the quality of the product (milk), and the interaction environment-animal-product. The aim of this paper is to give a general overview of the current status of research on the interest, the challenges for recording but also the possible use of new phenotypes obtained from milk composition both for genetic improvement and other purposes. The paper will focus on dairy cows; most conclusions can obviously be extended to other milk producing animals.

Milk composition

Until recently milk composition was only quantified for five major traits: milk fat, milk protein, milk urea nitrogen (**MUN**), milk lactose and finally somatic cell count, the later using a different technology. Milk is however a very complex substance with a large number of components. These components reach from components of milk fat or milk protein to vitamins or minerals. For instance, milk fat contains average 96% of triglycerides, which are a glycerol molecule esterified with three fatty acids. For a given content of fat, various fatty acid profiles exist. Similarly, milk protein is an assembly of different protein fractions such as caseins, α-lactalbumins, β-lactoglobulins and other minor proteins (e.g., lactoferrin). The complexity of milk composition is also a rich source of information to define the new phenotypes describing environment-animal-product. At the same time breed differences, at least for major milk constituents have been known for a long time (e.g., Webb, Johnson and Alford (1974)). Similar differences were found and recently confirmed for fatty acid profiles (e.g., Soyeurt, Dardenne, Gillon et al. (2006), lactoferrin (Soyeurt, Colinet, Arnould et al. (2007)) and major minerals (e.g., Cerbulis and Farrell (1976)).

Defining new phenotypes

Animal selection, as herd management, is based on the precise assessment of important traits. Through a better and finer knowledge of milk composition, new phenotypes can be defined. These phenotypes can be used in at least four areas: herd management, environment, animal health, and milk quality. In this paper, the definition of phenotypes related to the fine milk composition is large and includes milk components used as a direct indicator of the considered traits of interest (management, environmental, animal health, and milk quality

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traits) or an indirect indicator trait of these same traits of interest. Knowing these traits will have a positive impact on sustainability of milk production.

Management traits. Since the start of milk recording, the milk fat content, and several years after, the protein content have been used as management traits helping milk producers to fine tune their management and especially feeding systems. MUN and lactose were added more recently, both adding new information, e.g., MUN together with protein allows cross-check protein feeding (e.g., Baker, Ferguson, and Chalupa (1995)). Another example of the use of major milk components is the fat/protein ratio. Brutal changes of this ratio are considered indicators of ketosis or acidosis. Finer knowledge of milk composition would allow the detection of subclincal ketosis thanks to the determination of acetone and β-hydroxybutyrate in milk as suggested by de Roos, van den Bijgaart, Hørlyk et al. (2007). Other fine milk components having large interest are fatty acids. They have a high potential to be used as indicator traits for dairy cow feeding. Long chain fatty acids in milk are strongly related to the ingested long chain fatty acids by cows. Additional management traits are already known to be linked to milk composition. An example is the energy balance which can be related to the modifications in fatty acids in milk (e.g., Lake, Weston, Scholljegerdes et al. (2007)).

Environmental traits. Some management traits can also be directly linked to environmental issues. An example is MUN which is not only a trait indicating nitrogen efficiency of protein feeding, it allows also to assess the amount of extra nitrogen that a cow will excrete (e.g., Jonker, Kohn, and Erdman (1998)). Recently, another research has shown that a second environmental challenge of dairy farming, i.e. the emission of methane, can be linked to fatty acid composition (Chilliard, Martin, Rouel et al. (2009)).

Animal health. After management and environment, the changes in milk composition are also an indirect indicator of the health status of a cow (e.g., Hamann and Krömker (1997)). It is known that the somatic cell count and/or the modifications in the contents of lactose, calcium, and lactoferrin in milk are related to the udder health (e.g., Miller (1984)). As already explained before, the health status of a cow is closely linked to the energy balance which can be monitored by the changes in some milk components.

Milk quality. Quality of milk can be defined in three different ways: the hygienic, the technological, and the nutritional quality. Hygienic quality assumed that the milk is below given threshold for somatic cells and germs per ml of milk, no trace of antibiotics, and a good visual property. The technological quality of milk is related to the specific valorization expected from the produced milk. An example is butter hardness which is directly linked to fatty acid ratios (e.g., Soyeurt, Dardenne, Dehareng et al. (2008)). For cheese, different milk composition traits related to the cheese-making yield were identified. The nutritional quality of milk is based on the contents of milk components having a potential benefit for human health such as the unsaturated fatty acids, calcium, lactoferrin.

Recording new traits

As explained previously, milk labs all around the world quantified mostly only five major milk components. Even if the interest for new phenotypes is nowadays clear, a lack of technology or better of a lack of adequate use of existing technology limited the potential to go further in milk analysis, especially for routine recording of new traits. Recently several studies, mostly done in our group, showed that existing mid infrared (MIR) spectrometry technology can be used to predict other milk components. The MIR technology was already used for a long time to predict milk fat, milk protein, MUN and lactose. However it was shown that also at least some fatty acids (Soyeurt, Dardenne, Dehareng et al. (2006).), lactoferrin (Soyeurt, Colinet, Arnould et al. (2007)), minerals (Soyeurt, Bruwier, Romnee et al. (2009)), acetone and β-hydroxybutyrate (de Roos, van den Bijgaart, Hørlyk et al. (2007)) can also be predicted. This was obviously a very important step because additional phenotypes can be obtained for large numbers of samples with low analysis cost. All analyzed milk samples by a MIR spectrometer generates a MIR spectrum. This spectrum represents the absorption of infrared ray at frequencies related to the vibrations of specific chemical bonds within a molecule (Coates (2000)). To be interpretable, this spectral data must be resumed to express the desired information, i.e. the quantity of milk fat for a given quantity of milk, by using specific calibration equations. By developing new calibration equations it became feasible to predict new traits as major minerals, fatty acids, lactoferrin, acetone, β-hydroxybutyrate, dornic acidity degree, coagulation time. This list is not exhaustive.

As this technology is already used by milk recording, the implementation of these new calibration equations can be easily done if the spectral data can be extracted from the spectrometer and recorded. Storing spectral data allows also using calibration equations at a later stage. Efforts are underway in several countries to adapt to this. Smaller countries with one or fewer labs have here an advantage as it is the case in Luxembourg and in the Walloon Region of Belgium. To our knowledge currently only the Belgian and Luxembourg animal breeding associations are recording all spectra and have accumulated a total of 700,000 and 600,000 test-day spectra from individual cows during the last years. Based on this data, our group was able to initiate a large number of studies on different new phenotypes for their potential interest for herd management, environment, animal health, or milk quality.

Evaluating new traits

Implementing animal breeding for additional traits first requires that animals can be evaluated for them because data is available; the traits show phenotypic variation and are heritable enough. Different steps are required to develop and implement new advanced genetic evaluation systems.

Recording spectral data. As described above few countries have significant spectral data linked to their animal recording and genetic evaluation databases. For larger countries storing this data is still a quiet difficult task as every record contains 1060 data points obtained from MIR.

Predicting new traits from spectral data. Predicting new traits from spectral data needs access to prediction equations. Also in order to guaranty quality and robustness of predictions, which is for example required if values are used for milk pricing, additional steps to certify the results are needed.

Modeling new traits. Multivariate test-day models are required as the new traits have a longitudinal nature during the lactation and they are highly correlated to each other and with some traditional trait as milk, fat and protein. The presence of historical data for correlated traits is required as data currently available for the new traits will be limited to the last few years. Given these fact the type of models that has to be developed is creating new challenges as of the number of traits and the complexity of their relationships. A second challenge in modeling is to make the results useful for management purposes. There is still a large potential of improvement even for classical traits as MUN (e.g., Bastin, Laloux, Gillon et al. (2009)).

Estimation of (co)variance components. Estimating genetic parameters is required. To do this, enough data has to be available. Currently research is underway for a large number of traits. Generally genetic variances were observed and daily heritabilities estimated for new traits range between 0.1 and 0.4 (e.g., Soyeurt, Dardenne, Dehareng et al. (2008)) showing that sufficient heritable genetic differences exist. Because of the lack of historical data correlated traits as milk yield, fat and protein content need to be modeled together with new traits. This requires that (co)variance of those traits and new traits are required. First results show rather strong but very variable links between milk yield, fat content and protein content with fatty acids (e.g., Soyeurt, Dardenne, Dehareng et al. (2008)). Updating of selection indexes will require that (co)variances with other economically important traits will also be needed.

Genetic evaluation. Based on available data genetic evaluations can be done. Test computation with Walloon data for some fatty acids have shown that even with limited data but by making good use of correlated traits, very reasonable levels of reliability can be achieved for a great number of bulls recently used in Belgium. During these runs 1707 bull obtained reliabilities for saturated fatty acid content of 0.50 and more. Research is underway to develop methods to feed back into the genetic evaluation system international breeding values for correlated traits (Gengler and Vanderick, 2008). This would even further enhance the reliability of genetic evaluations for new traits.

Genomic evaluation. By definition traits with limited data look very appealing to use genomic prediction (Meuwissen, Hayes, and Goddard (2001)) to estimate breeding values. However current implementations (e.g., VanRaden (2008)) would require the *a priori* estimation of highly reliable breeding values for a large group of training set sires. This can potentially be replaced by the use of corrected phenotypic records for genotyped cows, however it remains presently unclear if this method would produce prediction equation that are precise enough for sires. Also multi-trait or longitudinal genomic prediction methods based on this approach are only in their infancy, however as explained before the type of data would require multi-trait test-day models. A viable alternative could be the use of an integrated approach combining all available information (phenotypic, genomic and pedigree) exploiting recent methodological advances (Aguilar, Misztal, Johnson et al. (2010)). This method can be integrated in every type of models. It has however some theoretical disadvantages and more research is needed.

New breeding goals

Historically in the majority of countries, selection has favored production traits. During the last years most countries have been shifting towards a more balanced breeding goal for improved milk production without compromising health and fertility. Focused selection for milk production has resulted in impressive improvement in milk production but has also resulted in dairy cows that lose lots of body energy reserves and are in varying degrees of negative energy balance for some parts of the lactation. Consequently, dairy cows are considered less “robust” than they previously have been. More recently, as a result of a general public interest in milk production practices, in milk quality and in the environment, selection pressure in many (if not most) countries tries to shift towards new traits that need to be included in breeding goals. Nowadays with these new phenotypes being available index traits can be diversified to select for these broader breeding goals. Selection can refocus to include additional traits such as milk quality and dairy cow robustness.

Finally, it is important that the inclusion of traits such as environmental sustainability and milk quality does not compromise health, fertility or “robustness” of the cow. The objective will be to improve a balanced and sustainable breeding scheme. Given the complex relationships among production, robustness, milk quality and environmental traits fin balanced selection indexes have to be developed to achieve sustainable improvement of the updated breeding goal. Also, potentially, differentiated selection indexes will be needed as production circumstances could vary (e.g., milk paid for nutritional quality).

Conclusion

Recent advances in milk composition analyses allowed defining new and advanced phenotypes. These new traits are valuable descriptors of the environment, the animal and its product (milk). These advances in milk analysis are based on mid infrared spectrometry exploiting the spectral data generated by the spectrometers during routine milk analysis as done currently worldwide for milk recording. However besides defining these new phenotypes different steps are required to record, to evaluate and to use these new phenotypes for management and breeding. Also updating of selection goals by adding additional traits such as environmental impact, milk quality and dairy cow robustness to increase sustainability of animal breeding is required. Given the complex relationships among production, robustness and milk quality traits fine balanced selection indexes have to be developed to achieve sustainable improvement of the updated breeding goal.

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