Which New Traits are Expected to be Available in the Near Future?

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Abstract

For several decades breeding goals in cattle were strongly linked to increases in milk production. Many functional traits have unfavourable genetic correlations with milk yield, which has led to an accompanying reduction in genetic merit for functional traits. Herd management has been challenged to compensate for these effects, and to balance fertility, udder health, and metabolic diseases in order to maximise profit without compromising long-term welfare. Functional traits, such as direct information on cow health, have also become more important because of consumer interest in animal well-being and demands for healthy and natural products. There are major concerns about the impact of drugs used in veterinary medicine on the spread of antibiotic-resistant strains of bacteria that can negatively impact human health. Sustainability and efficiency are also increasing in importance because of growing competition for high-quality, plant-based sources of energy and protein. Disruptions in global inventories due to climate change also may encourage more emphasis on these traits. For data recording efforts to succeed it is crucial that there is a balance of effort with benefits. The motivation of farmers and other stakeholders involved in documentation and recording is essential to ensure that data quality is high. To keep down the labor costs associated with recording to a reasonable level it is important that to utilize existing data sources. Examples include the use of milk composition data to provide additional information about the metabolic status or energy balance of the animals. Recent advances in the indirect use of mid-infrared spectroscopy to measure the required fine milk composition (e.g., fatty acid composition) have shown considerable promise. There are other valuable data sources in countries with compulsory recording of veterinary treatments and drug use. For countries that rely on recording on a voluntary basis there are also quality assurance systems requesting more documentation. Sources of data outside of the farm include slaughter houses and veterinary laboratories. At the farm level huge amounts of data are increasingly available from automated and semi-automated milking and management systems. Electronic devices measuring physiological or activity parameters can predict physiological status such as estrus, and can also record behavioural traits. In order to develop effective selection programs for new traits, the development of large databases is necessary in order to produce high-reliability predicted transmitting abilities which can be used as inputs for genomic evaluation.

Keywords: phenotypes, novel traits, genomics

Introduction

Due to negative genetic correlations of milk yield with fitness traits a decline in many functional traits has been observed. Herd management is therefore challenged to compensate for these effects and to balance fertility, udder health, and metabolic diseases in order to maximise profit without compromising welfare. Therefore the need for novel traits used for farm management, genetic improvement, and for monitoring parameters of public interest is increasing.

The recording of traits must be primarily beneficial for the stakeholder involved. For individual farmers the use of on-farm data for management decision is of great importance. If other stakeholders, such as veterinarians, are to be motivated to record treatments and diagnoses the data collected has to be beneficial to them, as well. The use of data for farm management is the primary motivation to record information on functional traits. As it is becomes more and more challenging to balance high milk yield, reproduction, and health there is a need for appropriate and timely information for prevention and early measures.

The use of these data for breeding is also valuable, and is important for the long-term improvement of dairy populations. Over the last fifteen years there has been a shift towards increased focus on functional traits in dairy cattle breeding can be observed worldwide. Complex breeding goals with up to 43 functional traits are expressed by Total Merit Indices (TMI) according to a survey carried out by International Committee of Animal Recording (ICAR) in 2012 (Stock *et al.,* 2012). The results, based on 23 countries, show that genetic evaluations are very common for calving, fertility, longevity, feet and legs, and indirect health traits. A further increase in number of traits included in TMI is expected in 22 of 26 countries participating in this survey. A critical precondition for use for genetic improvement is the central availability of data. Public interest in the use of parameters for monitoring (e.g., food safety, surveillance, welfare) is increasing. Regardless of which sources of health information are used, national monitoring programs may be developed to meet the demands of authorities, consumers and producers.

The objective of this paper is to give an overview of expected developments and challenges related to the availability of traits in the near future.

Circumstances

The world population is projected to reach 9 billion people in 2050 according to the latest demographic reports from the United Nations, which means that resources will become more limited and prices for energy and feed (especially grain) will increase. Disruptions in global inventories due to climate change also may encourage more emphasis on novel traits. Cattle producers will be challenged to find ways to reduce greenhouse gas emissions by increasing production efficiency. In this context, there is a need for novel traits that can also be used for both breeding and management. Functional traits, such as direct information on cow health, also may have increased in importance because of interest in animal well-being and consumer demands for healthy and natural products. For example, there are major concerns about the impact of drugs used in veterinary medicine on the spread of antibiotic-resistant strains of bacteria that can negatively impact human health.

These requirements are also part of legal regulations. Pavon (2013) reported that an Animal Health Law has been developed from about 40 European Union (EU) Directives and Regulations, providing a single and robust framework for animal health. In addition to disease prevention (disease awareness, registration, traceability, and biosecurity), disease control and eradication, intra-EU movement, and entry into the EU of animals and animal products will be regulated. A new element will be EU guidelines on antimicrobial-resistant pathogens.

A scientific report on the effects of farming systems on dairy cow welfare and disease (EFSA-Q-2006-113, 2009) concluded that leg disorders, mastitis, and reproductive disorders are considered to be the major components of

poor welfare in dairy cows. Unfavourable genetic correlations of these traits with milk production traits means that the selection pressure applied to dairy cattle over many years is considered to be a major factor leading to poor welfare in dairy cows. In response, the European Commission has called for the development of a set of indicators of animal welfare (Pavon, 2013).

The precondition for recording of reliable data is the motivation of the stakeholders involved. Several countries have conducted surveys of farmers to understand their motivation and needs (Schwarzenbacher, 2013; Steininger *et al.,* 2013). It has been observed that, for farmers, a top priority is genetic progress of functional traits. Increasing milk yield is no longer ranked among the most important traits to select for. Due to increasing herd sizes and limited labor, farmers want robust cows that are easy to handle.

According to Bo (2009) a breeding goal should produce the following outcomes: increased farm income (higher production (milk/beef); reduced production costs (e.g., better fertility, fewer diseases, less losses); easily managed cows (temperament, milking speed), and products that are easy to sell (e.g., animal welfare, ethics, consumer concerns). However, complex breeding goals require a wide range of relevant traits. Trait recording has to have benefits beyond breeding. Additional effort for documentation must produce added value. Easy-to-use electronic systems are a key to long-term-success.

Advances in technology will have an impact on the definition and availability of traits in the future. Recent technological developments have advanced biological understanding of the genetic background of traits (e.g., genomics, proteomics, metabolomics). And novel recessive defects have been identified (Cole *et al.,* 2013). Based on SNP and sequence information recessive haplotypes can be discovered and confirmed within a short time (e.g., Sonstegard *et al.,* 2013). Genomics offer new perspectives for registration by establishing reference populations with "deep" phenotypes and population-wide recording with indicator traits. These advances will lead to

better phenotypes that are closer to the genotype and result in moreefficient selection.

Due to advances in laboratory techniques, the range of traits that are economically feasible to record is increasing. These include metabolites of nutritional interest (lactoferrin) as well as manufacturing properties of milk (e.g., κ-casein). The use of novel traits as indicators for reproductive status, mastitis, and energy balance is under research in several projects.

With increasing herd size, investments in farm technology are growing, and a rapid increase in automation to reduce labor requirements has been observed. The automatic generation of indicator traits for health and fitness is expected to improve the repeatability and lower the cost of those phenotypes.

Expected novel traits in the future

Direct health traits

Several studies show that the use of direct health traits (e.g. mastitis diagnoses) is more effective in breeding for mastitis resistance than somatic cell count alone (Heringstad *et al.,* 2007; Egger-Danner *et al.,* 2012). In addition to the Nordic countries, that have selected for direct health traits for decades, routine genetic evaluation of direct health traits have been implemented in DEA (Germany and Austria) since 2010, France since 2012, and Canada starting in December 2013. Systems for recording of diagnoses are currently being established in other countries as well and will be more available in the future; either through veterinarian diagnoses or producer recorded data. In fact, several studies have found that producer-recorded data from on-farm computer systems is of similar quality to diagnoses recorded by veterinarians for genetic evaluation, and extensive records are potentially available for use in genetic improvement programs (Parker Gaddis *et al.,* 2012). Standardisation of diagnoses is the precondition of use. In 2012 ICAR approved guidelines for Recording, Evaluation and Genetic Improvement of Health Traits (ICAR, 2012). A hierarchical system with a very comprehensive

key of diagnoses (>600), a reduced key of diagnoses (60-100) and simple key with about 10 diagnoses was described. This framework should enable a multidisciplinary use ranging from very detailed information for veterinarians to simple recording of health related observations by farmers. International cooperation for comparability of results across countries is important.

Udder health

Mastitis is the target trait to improve udder health. Until recently, research has focused on indirect measures based on somatic cell count (SCC), such as prolonged elevated somatic cell count (deHaas *et al.,* 2008; Koeck *et al.,* 2010; Urioste *et al.,* 2010). These novel definitions showed higher correlations to mastitis and demonstrated that patterns of SCC provide additional information for genetic evaluations of mastitis resistance than lactation measures of SCC alone. The use of mastitis diagnoses for genetic evaluations has been common for decades in the Nordic countries, followed by Austria, and is becoming common in other countries as well (see "Direct health traits" above). Udder health indices combining SCC and clinical mastitis (and udder conformation traits) are published in some countries.

Electrical conductivity (EC) is available from automated milking systems as an indicator of mastitis. According to Norberg (2005) collecting and applying EC information in a breeding program may be challenging. Recent literature on EC is limited, and is ongoing for indicator traits that may be related to mastitis, such as mid-infrared spectroscopy (MIR). Haeusermann and Hartung (2012) analysed near-infrared spectroscopy, real-time PCR, and IR thermography as indicators of mastitis. They concluded that the development and testing of new mastitis detection methods and sensors is still an important task. On-farm or in-line utilization is not applicable for all techniques, and the definition of a gold standard for mastitis detection remains difficult.

Of interest in the context of udder health is also information about milk yield of individual quarters. Information about bulk milk, which is sampled more frequently than official test days,

might give additional information about the herd status.

Research also has been reported on the use of pathogen-specific information for genetic evaluation (Haugaard *et al.,* 2012; Sorensen *et al.,* 2009*)*. Different bacteria are responsible for different immune responses. De Vliegher *et al.* (2012) showed, based on heifer mastitis, that the effectiveness of prevention programs can be increased when information about pathogens is known.

Reproduction

Reproduction is best described as a complex outcome of related traits, management and environment. Each of the traits describes a different aspect of fertility. To establish a recording scheme for female fertility the following data are desirable: 1) calving dates; 2) all insemination dates, including artificial insemination events and natural mating dates; 3) information on fertility disorders; 4) pregnancy test results; 5) body condition score; 6) hormone assays. Presently, female fertility traits are mainly based on calving and insemination data. The use of fertility-related diagnoses is increasing. Other novel predictors of fertility status, such as pedometers and BCS, are also growing in popularity (Fogh, 2013). Research is also on the way with MIR for pregnancy testing and other tests based on hormonal assays (Gengler, 2013).

Feet and legs

Feet and leg problems are among the three most-frequent culling reasons in dairy cattle, following reproduction and udder health. Feet and legs traits are commonly assessed by breed societies using linear type scoring systems that evaluate the biological extremes of these traits (e.g. straight to sickled legs, steep to shallow claw/hoof depth etc).

Conformation traits that describe feet and legs are have so far been used as indicator traits for claw health. Direct information on claw health status would be better, and conformation traits could be used to increase reliability of estimated breeding values (EBV) (Häggmann

and Juga (2012), Chapinal *et al.,* 2012)). Koenig and Swalve (2006) and Van der Linde *et al.* (2010) showed that the efficiency of breeding programs for the improvement of claw health improves considerably when claw health data are included. Information on lameness is often more easily available that claw health information, and Weber *et al.* (2013) suggest that lameness may be a useful indicator for claw and leg health.

Automated lameness detection based on activity sensors which measure lying time and number of lying bouts may be useful when combined with milking and feeding data in a cow-specific model (De Mol *et al.,* 2013).

In the Nordic countries, Austria, and Southern Germany, veterinary diagnoses of feet and legs traits are recorded routinely. As veterinarians are consulted only in severe cases, incidence rates based on veterinarian diagnoses are much lower than those based on hoof trimming information. Different studies showed that genetic evaluation based on veterinarian diagnosis is valuable (Fuerst-Waltl *et al.,* 2012). For effective improvement of the feet and leg complex it is important to establish systems for centralized storage of data from hoof trimmers. Claw health status at claw trimming is recorded routinely in Norway (Odegard *et al.,* 2013), Denmark, Finland and Sweden (Johansson *et al.,* 2011).

Metabolism

To date, direct traits for metabolic disorders are only rarely used in genetic evaluation. Some countries, such as DEA (Germany and Austria), publish EBV for milk fever. The Nordic countries include metabolic disorders like milk fever and ketoses in the EBV for "other diseases".. In herd management, milk content traits like fat and protein percentage, fat:protein ratio, and milk urea nitrogen are used for early detection of problems associated with metabolism. Recent research is also focusing on the use of this information for genetic improvement purposes (Negussie *et al.,* 2013; Koeck *et al.,* 2013). Due to intervals between test day milk recording, the predictive ability is still limited. However, more frequent information will be in the future available from

AMS. It is assumed that large economic losses are associated with subclinical metabolic disorders such as ketosis. Therefore, the ability to detect subclinical signs of disease at an early stage is important. These methods could be based on serum parameters like non-esterified fatty acids (NEFA) or ß-hydroxybutyric acid (BHBA) concentration (Roberts *et al.,* 2012; Van der Drift *et al.,* 2012), and BHBA is the "Gold Standard" of many cow tests. The availability of such subclinical information will depend on the specificity and sensitivity of the tests, as well as ease-of-use and costs of implementation on-farm. Methods based on MIR have been suggested, but there is not yet a system in place to support the routine collection of large numbers of observations (McParland *et al.,* 2011; Bastin *et al.,* 2012). Other potential indicator traits are rumen activity and body weight change (Fogh, 2013). Body condition scores, and changes in those scores, may be useful for the early detection of metabolic disorders. Melzer *et al.* (2013) showed that there is potential to screen individual cows for a broad array of metabolites, with changes in metabolic profiles correlating with animal health.

Efficiency

An expected increase in prices for grain and energy will increase the focus on efficiency. Efficiency can be defined as units of output per input unit on farm level, as well as of individual animals. A trait of interest is feed efficiency, which commonly is expressed as residual feed intake measured as the difference between actual and predicted dry mater intake (DMI). The greatest challenge to the widespread use of feed intake and feed efficiency measures is the availability of cost-effective information on individual animals (Berry and Crowley, 2013), resulting in a need for indicator traits (Fogh, 2013). Rumen activity might be a future indicator trait for feed efficiency. Other measures based on feed, feces, and urine samples are being developed. Dry matter content in feces, or nitrogen in urine, could be indicator traits for feed efficiency. It is important that the correlations with other traits are well-understood, e.g., RFI and fertility may be unfavourably correlated (Pryce *et al.,* 2013).

Therefore, selection for RFI should be through a multi-trait selection index.

Feed efficiency may also be correlated to methane emissions (Hegarty *et al.,* 2007). Enteric methane is produced as part of the fermentation process has been linked to climate change. Selecting for more efficient cows, methane production could be reduced by up to 26% over a 10 year time-frame (de Haas *et al.,* 2011). There is also variation in the rumen metagenome that appears to predict methane production which could also be exploited (Ross *et al.,* 2013).

Challenges

Predictive biology

Detection of metabolic predictors, or biomarkers, which can be MIR of milk and its components, may become a useful source of information (Gengler *et al.,* 2013). Standard milk analysis undertaken by milk recording by mid infrared spectroscopy generates spectral data that reflects milk characteristics, such as specific ratios of milk fatty acids. Research is currently underway to investigate the use of this data for prediction of indicator traits (RobustMilk, OptiMIR, PhenoFinlait).

A major challenge is the lack of reference data to determine associations among specific diseases and MIR phenotypes. A reliable pool of "healthy" and "sick" animals is needed to develop the prediction. For traits with low heritability and limited reliability and repeatability, this is even more difficult. The reference data set also has to account for different production circumstances, and the comparability of spectra from different instruments is not guaranteed. Individual instruments also require periodic calibration to ensure that results on the same instrument are comparable over time The repeatability of results across different breeds and production circumstances, as well as logistic challenges related to data transfer, require additional consideration. This includes the extraction of data from spectrometers and storage of MIR spectra, standardization of spectra, complex computation of indicators, and implementation

in routine into a milk recording work flow (Soyeurt *et al.,* 2012; Gengler *et al.,* 2013).

Standardization and integration of relevant data sources

Data collection systems that record information at milking and feeding times offer the chance to generate many phenotypes routinely. Different data collection systems provide different data, and data formats and accessibility vary across systems. There is a need for harmonization of trait definitions across systems. Many systems use dedicated computers that do not communicate with external databases. Therefore, data have to be generated from on-farm-equipment and are not centrally available.

Breeding and efficient herd management is facilitated by centrally available data that support benchmarking. Such data provide an opportunity to compare performance between and within farms over time. Often a single parameter does not provide an appropriate benchmark, but indices based on a basket of parameters can provide a better indicator of overall performance (Bradley *et al.,* 2013). Better integration of data has the potential to improve benchmarking.

In most of the countries different data are stored in different databases and little or no communication between systems is available. The Danish System Vetstat (Stege, 2003) and the Austrian Poultry Health Database (Glatzl, 2010) are examples how integration of data could work. Multidisciplinary approaches require linkage of data sources.

Simplicity of use for farmers

The future availability of phenotypic data will depend very much on the motivation of the farmer. It is expected that the number of traits recorded and data available will further increase (Rutten *et al.,* 2012). The challenge will be to ensure that that farmers aren't overwhelmed by this information, and that use of all these traits will still be possible. Easy handling and simple access to data is essential. Labor is a limiting factor on most farms, so tools that condense a

lot of information into a small number of indices are desirable.

Closing the phenomic gap

The limitation in using genomics is phenotypes. This is especially true for novel traits. Traits with a long recording history do have reference populations which enable the prediction of genomic EBV with higher reliability. Due to the potential of genomics, it will be possible to use phenotypes which are expensive to record for breeding in the future. Hocquette *et al.* (2012) suggested that genomic selection is also an opportunity to consider new and complex phenotypes. For novel traits establishing a reference population based on bulls takes very long time as the number of formally progeny-tested bulls is decreasing as well. For closing the phenomic gap between traditional traits and novel traits genotyping of cows is a possibility (Calus *et al.*, 2012). For traits with low heritability, large amounts of data with reliable phenotypes and genotypes (De Roos, 2011) may be needed. Parker Gaddis *et al.* (2013a, b) have shown that genomic EBV can be predicted using fairly small datasets of producer-recorded health data, although most bulls will have modest reliabilities.

Conclusions

Circumstances of production, as well as consumer demand, will have an impact on the availability of traits in the future. Traits connected with animal health, animal welfare, food safety, and efficiency will increase in importance. Advances in technology will enable "better" trait definitions. Phenotypes will have closer biological links to genotypes. Long-term progress requires reliable phenotypes, ideally those that are standardized, have a high repeatability, and are recorded automatically. Farmers want tools for herd management that are easy to use and require little additional work, but achieve the expected output. This is a challenge because there are many different management and production systems, and lots of them are very complex. The collection of reliable phenotypes, especially for health traits

and traits with low heritability, has proven to be a challenge. If different stakeholders are involved in documentation and recording (e.g. veterinarians, nutritionists, and hoof trimmers) it is even more difficult. Nevertheless, examples from the Nordic countries show that it is possible. Technological advances will facilitate the exploitation of those data sources in much more in detail. One example is MIR data, although its routine application has proven to be challenging. New technologies like AMS and a variety of on-farm sensors and monitoring systems, may provide new possibilities forgenerating indicator traits for fertility, mastitis, metabolism, and energy efficiency. In addition to reliability and low price, ease of sampling is important for broad use of a tool. Based on different technological approaches there is a need for harmonization of traits and standardization of data. Additional research will be needed to improve the use of phenotypes from automated systems, and it is essential that on-farms systems communicate with a central database. International organizations like ICAR are needed to define standards for definition of traits so that data collected using different technologies are comparable. The central availability of reliable phenotypes for new traits is necessary for building reference populations for genomic evaluation. To overcome the phenomic gap between traditional traits and novel traits, genotyping of cows should be considered. To make greater progress with novel traits international cooperation is needed in many fields. Multidisciplinary, multi-country approaches are beneficial.

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