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Implementation in breeding programmes

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Genetic improvement is easy when selecting for one heritable and well-recorded trait at a time. Many industrialised national dairy herds have overall breeding indices that incorporate a range of traits balanced by their known or estimated economic value. Future breeding goals will contain more non-production traits and, in the context of this paper, traits associated with human health and cow robustness. The definition of Robustness and the traits used to predict it are currently fluid; however, the use of mid-infrared reflectance spectroscopic analysis of milk will help to create new phenotypes on a large scale that can be used to improve the human health characteristics of milk and the robustness of cows producing it. This paper describes the state-of-the-art in breeding strategies that include animal robustness (mainly energy status) and milk quality (as described by milk fatty acid profile), with particular emphasis on the research results generated by the FP7-funded RobustMilk project

Keywords: MIR, rapid, low cost, dairy, phenotype, genotype robustness

Introduction

Genetic improvement for just one trait at a time (single-trait selection) is relatively easy provided the trait is well defined, easily measured in large numbers, and a proportion of the differences in performance among animals is because of their different genetic makeup (i.e. the trait is heritable). Previous breeding programmes in many dairy cattle populations favoured production over functional traits. Such breeding programmes resulted in rapid rates of improvement for yield but at the expense of performance in other important traits such as fertility (Wall *et al.*, 2007). There may also be unfavourable effects of aggressive selection on yield on other traits not yet known (e.g. environmental footprint).

As breeding goals in most European countries have evolved to include a wider range of traits of economic or societal value (Miglior *et al.*, 2005), constructing such breeding goals has become increasingly complex. This is particularly so when the goal traits vary in heritability or when antagonistic genetic correlations exist among the suite of traits included in the breeding goal, or both. Moreover, the traits now being added to the evolving goal are, generally, becoming less well defined and more difficult to measure, largely because all the easy to measure traits have already been incorporated.

Successful breeding programmes nonetheless require routine access, preferably at a low cost, to large numbers of accurately recorded phenotypes for which genetic or genomic evaluations are to be estimated with the purpose of generating genetic gain. If the chosen traits have economic values, profitability can also rise provided that there are no unwanted negative correlated responses among the traits. There is also much commentary on how best to incorporate public good traits with no direct monetary value to the farmer or breeder (e.g. Wall *et al.*, 2010; Amer 2011; Nielsen *et al.*, 2011). With the implementation of genomic selection, breeders are able to make even faster genetic changes (gain), and therefore it becomes even more important that correlated responses in other traits are monitored and, if necessary, remedial action is taken to correct negative outcomes.

Here we describe the state-of-the-art in breeding strategies that include animal robustness (mainly energy status) and milk quality (as described by milk fatty acid (FA) profile), with particular emphasis on the research results generated by the FP7 funded RobustMilk project (http://www.robustmilk.eu). We extend the discussion to include the potential of mid-infrared (MIR) to predict other traits such as fertility and methane emissions and how these traits might feature in future selection indices.

Phenotyping strategies

'In the age of the genotype, the phenotype is king.' Of course, this is only true now that the routine generation of genotypes has become relatively inexpensive and widely available and is therefore no longer a hindrance to the

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implementation of a breeding programme based on genomically selected animals. Recognising that genomic selection presumes the availability of phenotypes that are relevant to the performance of mature animals, but accessible at early ages, the emphasis is now on collecting appropriate high-quality, low-cost phenotypes to enable the accurate estimation of the effects of the plethora of genomic markers on these traits. Ironically, access to phenotypes of the kind that have been collected for decades in progeny-testing programmes is now the main hindrance to the further exploitation of genomic technology. For all relevant, and especially for new traits, a question arises – will those traits be recorded (or predicted from other traits) in commercial cows in sufficiently large numbers or will they be recorded only in research herds with appropriate facilities? The national strategies for collecting new phenotypes to further exploit genomic technologies need to be developed rapidly.

We are concerned here specifically with phenotypes for robustness and for milk quality. Feed intake is a major component of energy balance and hence robustness. As a result of activity in the RobustMilk project, international collaboration has begun and the pooling of phenotypes already explored (Banos *et al.,* 2012; De Haas *et al*., 2012). This might be an example of an appropriate strategy for the future. However, genotype-by-environment interaction, which describes how animals rank genetically in different environments, must be considered when merging data sets generated in contrasting environments as shown for production traits (Hammami *et al*., 2009).

The methods for acquiring phenotypes in the future ideally should be (1) non-destructive and not affect animal performance, (2) low cost, (3) measured in real-time and (4) measurable temporally. Infrared spectroscopy, for the analysis of milk, fits most of these requirements, and the accuracy of predicting milk quality attributes and robustness from MIR spectroscopy of milk has been described in detail by Berry in this publication. Traits that correlate adequately with milk composition, for example, methane emissions and fertility or that can be predicted directly from spectral data (e.g. minerals (Soyeurt *et al*., 2009) or Lactoferrin (Soyeurt *et al*., 2012)) might therefore be amenable to monitoring using MIR spectrometric analyses of milk.

Alternative phenotyping strategies for milk quality and, in particular animal robustness, exist. The latter include automatic image analysis (including infrared tomography) of animals for the quantification of (changes in) body tissue reserves (Coffey *et al*., 2003) or udder health (Polat *et al*., 2010) as well as sensor technology (Ipema *et al*., 2008). Moreover, associations between milk quality and energy balance have been estimated (Stoop *et al*., 2009). It is expected that research will focus on better (more automated and cheaper) methods of collecting phenotypes in the immediate future to facilitate the maximum realisation of the benefits of genomic technology. However, developments in information technology must also continue to ensure that the ever-increasing quantity of data generated enters a database in real time and that feedback, incorporating all available information stored in the database, is rapidly relayed back to the farmer.

Genomic evaluations

Successful genomic selection breeding programmes rely on accurate estimates of the effects of genomic markers on each trait in the breeding goal. Single-nucleotide polymorphisms (SNPs) are the genetic markers now used in dairy cattle genomic selection programmes. The catalogue of SNP estimates for a given trait is commonly referred to as an SNP key. The accuracy of the SNP key for a given trait is a function of the heritability of the trait and the effective number of animals genotyped for that trait or correlated traits. The SNP key is estimated using a reference population.

Once a SNP key has been developed, an animal with no phenotypes can then have a genomic breeding value predicted using its genotype and the SNP key. The resulting value is synonymous with an estimated breeding value generated using traditional genetic evaluations. Genomic evaluations, however, can only exist for traits where an SNP key has been estimated, and therefore where a reference population of phenotyped and genotyped animals exists for the trait under selection. Calus *et al.* in this publication describe in detail how an SNP key can be derived for a trait like animal robustness. A similar procedure can be undertaken for the estimation of an SNP key for milk quality.

Incorporation of robustness in dairy cow breeding strategies

Robustness may be defined as the ability of cows to remain healthy, fertile and profitable (i.e. maintain homeostasis) under a range of commonly accepted and sustainable farming systems (Ten Napel *et al*., 2009). Dairy cows, like all mammals, are generally in negative energy balance in early lactation (Coffey *et al*., 2002; Berry *et al*., 2006) because feed intake after parturition does not rise in line with the energy demands of increasing milk production. Past breeding programmes that are aggressively selected primarily for milk production increased the extent and duration of negative energy balance in early lactation. The extent and the duration of negative energy balance are known to be deleteriously associated with animal health and fertility (Beam and Butler, 1999). Associations between energy balance and animal health and fertility also exist at the genetic level (Collard *et al*., 2000; Veerkamp *et al*., 2000; Banos and Coffey, 2010).

Robustness can constitute part of a breeding strategy through three main avenues: (1) in the selection index as reflected by the inclusion of health and fertility traits; (2) as a goal trait in the breeding objective capturing the residual impact of energy balance on performance over and above that accounted for by the other goal traits; and (3) through alteration of the estimates of genetic merit depending on the environment in which the animal or its progeny will produce.

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The heritability of health (Berry *et al.*, 2011) and fertility traits (Veerkamp and Beerda, 2007) is low, thereby necessitating a greater quantity of information to generate accurate estimates of genetic merit for these traits within breeding programmes. Because energy balance is known to be moderately heritable and genetically correlated with animal health and fertility (Veerkamp *et al.*, 2001), it could therefore be used as a predictor of the low-heritability fertility and health traits. Body condition score, which is an indirect measure of energy status, is currently used in many national genetic evaluations as a predictor of fertility (Wall *et al.*, 2003) because of lack of sufficient data on energy balance for inclusion in national multi-trait genetic evaluations. Many studies have examined mobilisation of body tissue and partitioning of nutrients in dairy cows (Friggens and Newbold, 2007). It has been suggested that the increased capacity for milk production has resulted in the partial 'shift' of nutrient intake towards production output away from maintaining functional fitness (e.g. Veerkamp *et al.*, 2001). The work in RobustMilk has shown that there is a genetic component to energy balance and we have developed methods to allow us to predict energy balance with field MIR data (McParland *et al.*, 2012).

Wall *et al.* (2008) developed an economic framework to account for body tissue mobilisation. The principal of the economic model was that cows that have higher milk production either have to eat more food to produce this milk (and therefore increase feed costs) or utilise their own body energy or both, potentially at the expense of their metabolic function. This information may be harnessed for selection purposes in terms of developing a breeding goal trait with an economic cost. The effective energy given up by the dairy cow during lactation can be combined with the economic costs of replenishing that body energy on each day of lactation. Simply put, the selection goal trait is the maintenance of energy balance across first lactation with the outcome being a financial breeding value describing the cost of body mobilisation, which may be related to profitability. Methods to derive economic values for three traits were developed. These were the maximum drop in body energy content (min_BEC), the rate of loss of body energy in early lactation (b_early) and the rate of body energy gain (b_late) for different types of calving and grazing systems (Wall *et al.*, 2008). The results show that the economic values for the three traits of body tissue mobilisation change markedly depending on the date of calving. Generally, when the economic value for b_early is positive, the economic value for b_late is negative. For example, the economic values differ markedly for farmers that operate predominantly spring *v.* autumn seasonal calving systems. The economic value, for example, for b_early is positive in an autumn calving system and negative in a spring calving system. It would not be cost-effective for a cow to lose body energy in a spring calving system when the cost of energy from feed is low as any loss in early lactation will need to be repaid towards the end of lactation when feeding indoors and energy is more expensive. The opposite is true for autumn calving when it is economically sensible for a cow to lose body energy when feed is expensive in the winter and regain it when turned out to grass.

Clear differences in the robustness in performance of different strains of Holstein-Friesian cows across environments have been shown from controlled experiments using factorial design arrangements (Pryce *et al.*, 1999; Horan *et al.*, 2004; McCarthy *et al.*, 2007), analyses of national data sets (Calus *et al.*, 2002) or analyses of international data sets (Hammami *et al.*, 2009). Such phenomena of performances of genotypes differing across environments have been termed genotype-by-environment interactions. The extent to which animal traits vary between environments is commonly referred to as their robustness. Animals that perform similarly across different environments can be termed generalists, and animals that perform very differently in different environments are termed specialists.

If energy balance can routinely be predicted with some degree of accuracy (McParland *et al.*, 2012), then it could be included in multi-trait genetic evaluations to augment the accuracy of selection for the low-heritability traits. Generation of energy balance data for inclusion in prediction equations is not trivial and is very expensive. Therefore, prediction of energy balance is currently not possible for many environments. Options for finding proxy traits through which to index energy balance merit exploration. For example, the catabolism of adipose tissue during body condition change results in an increase of C18 FAs concentration in milk and a consequent inhibition of *de novo* synthesis of FAs by the mammary gland (Palmquist *et al.*, 1993; Barber *et al.*, 1997). Milk FA composition is amenable to MIR analysis. As part of the RobustMilk project, McParland *et al.* (2011 and 2012) clearly showed that accurate predictions of energy balance is possible but only where spectral variability represented in the target population is also included in the calibration data set.

Incorporation of milk quality in dairy cow-breeding strategies

Soyeurt *et al.* (2011) documented the potential of MIR analysis of milk, routinely available from all milk samples taken as part of large-scale milk recording to predict the FA content of milk across different breeds and production systems. Infrared spectrometry has been used for decades for the routine determination of major milk components such as fat and protein concentrations. Therefore, milk FA information could be collected routinely at a low cost through the implementation of the relevant FA calibration equations in milk analytical laboratories.

As part of the RobustMilk project, FA contents in milk have been proven to be heritable with sufficient variation to warrant genetic selection (Bastin *et al.*, 2011; Bastin *et al.*, 2012b). Heritability estimates were moderate and indicated that *de novo* synthesised FA (i.e. almost all C4:0 to C14:0 FA and approximately one-half of the C16:0 FA; Grummer, 1991) were under stronger genetic control than FA originating from

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the diet or from body fat mobilisation (i.e. the remaining and almost all the longer chain FA; Grummer, 1991). In addition, heritability estimates were similar over the first three lactations (Bastin *et al.*, 2012b). This indicates that FA profile in milk could be changed by genetic selection (Bobe *et al.*, 2008; Mele *et al.*, 2009; Stoop *et al.*, 2009).

The direct economic value of the milk FA profile remains unclear, as most milk producers do not receive bonuses or penalties with respect to the FA profile in milk. Nevertheless, increasing consumer concern over the relationship between food composition (and particularly in this case, milk composition) and human health warrants inclusion of milk FA in breeding goals. In addition, the desirable range of change of FA contents in milk should be defined. It has been suggested that ideal nutritional milk fat would contain 10% polyunsaturated fatty acids (PUFAs), 8% short-chain fatty acids (SFAs) and 82% monounsaturated fatty acids (MUFAs) (Grummer, 1991). Besides being unrealistic in relation to the typical milk fat profile from a dairy cow (~5% PUFA, 70% SFA and 25% MUFA), such changes in milk fat would alter physical and organoleptic properties of milk (e.g. susceptibility to oxidation; Palmquist *et al.*, 1993). In addition, undesirable effects might be expected on body energy status and environmental impact of dairy cows as both issues have been associated with milk FA profile (Van Haelst *et al.*, 2008; Dijkstra *et al.*, 2011). Extended literature reviews reported the effect of milk FA on human health (e.g. Haug *et al.*, 2007; Ebringer *et al.*, 2008). Overall, a more unsaturated milk fat composition is positively associated with human health. Therefore, as a part of the RobustMilk project, an index (nutritional quality of milk index) was developed (Gengler *et al.*, 2012) on the basis of restricted selection index theory (Kempthorne and Nordskog, 1959). This index puts a negative weight on SFA, a positive weight on MUFA and restricts changes in milk and fat yields to zero. By using this index for a constant fat content, milk fat will be selected to be less saturated with a high contribution from MUFA.

To date, routine genetic evaluations of SFA and MUFA as traits related to human health have recently been achieved in the Walloon Region of Belgium. However, as mentioned above, inclusion of these traits into a total merit index, and therefore breeding goals would require further considerations on all issues related to FA. For instance, higher contents of MUFA would be desirable with regard to the human health aspects, whereas lower contents of MUFA in early lactation would be more desirable from the energy balance status point of view (Bastin *et al.*, 2012a).

Breeding goals in most industrialised dairying nations have been broadening sometimes to include more traits and sometimes to increase selection pressure on existing traits. Inevitably, this reduces the rate of increase in production traits; however, for economic indices, it increases the total economic improvement. Thus, with the addition of milk FAs in the goal, we might expect correlated changes in response for traits already in the goal, that is, a further slowdown in the rate of increase in yield. Such correlated responses need calculating for all traits in the breeding goal and require genetic correlations between all index traits. A suitable relative economic value is needed for the FAs to enable them to take their appropriate place in an overall selection index. Gengler *et al.* (2012) used a restricted index approach that can be used when a sufficient consensus is available on the relative value of a trait.

Conclusions

From the outcomes of the work conducted in the RobustMilk project, and from the interpretation of the literature by Berry in this publication, it seems that MIR analysis of milk has the potential to enhance phenotyping on a broad scale. The accuracy of prediction of individual FAs from MIR ranges from reasonable (0.7) to near unity. The possibility that other relevant traits, such as mastitis, fertility or even methane emissions, might be indexed through MIR spectra is being explored. If reasonable correlations are found, what will be needed to make them useful are more accurately recorded phenotypes to train the MIR data. Once these newly available phenotypes become available on a large scale, genetic (and genomic) evaluations for these traits can be undertaken allowing breeders to make selection decisions on the basis of broader breeding goals that include traits such as FA profile that previously were impossible to include. The RobustMilk project has led to the pooling of rare and expensive data from many research herds to produce results previously unachievable. More importantly, its legacy includes a single database of milk spectral data, feed intake records and genotypes on the same cows. This database may be further exploited to allow the creation of an International SNP Key for feed intake through an initiative called global dry matter intake initiative. This is expected to result in more robust cows producing milk with greater human health properties.

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For more information, please visit the website www.robustmilk.eu, read the other papers in these proceedings or contact the project coordinator: Roel F. Veerkamp (E-mail: Roel.Veerkamp@wur.nl)

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