

# **UPDATE ON ROBUSTMILK – an EU-wide programme to improve the robustness of dairy cows and to make their milk healthier for humans.**

## **What is RobustMilk?**

ROBUSTMILK is a project that has been funded through the EU Framework 7 Programme to join together six world-leading research organisations within EU that are actively working in dairy cattle breeding and have strong links with the dairy industry. It is formally called **Innovative and Practical Breeding Tools for Improved Dairy Products from More Robust Dairy Cattle** but abbreviated to ROBUSTMILK for ease of use (and speed!).

## **Who is involved?**

There are six organisations involved in the project and all have a strong background in dairy cattle breeding. They are all well respected in their own countries and each has a strong reputation for ensuring that research and innovation is disseminated quickly to industry. These organisations are

1. Animal Science Group, Lelystad (Netherlands)
2. The Scottish Agricultural College (SAC Scotland.)
3. Teagasc Moorepark (Ireland)
4. Gembloux Agro-Bio Tech, University of Liège (Belgium)
5. Swedish University of Agricultural Science (Sweden)
6. Wageningen University (Netherlands)

## **What have we done so far?**

### **Database**

The creation of a common database across country partners that includes unique and scarcely recorded measurements for traits underlying individual dairy cow robustness and milk quality. These traits include measures such as feed intake, regular body condition scoring and detailed health and fertility recordings. These databases are held at each of the research partners involved and the first thing to do was to create a framework that enables bringing that data together to make it useable by this and future projects.

We have put together an international database. At present a total of 4,473 animals have phenotypic data stored in the database, linking to 561,940 milk samples. Also we have genotyped these animals with 50,000 markers. The first genome wide association analyses on milk yield, fat to protein ratio and somatic cell count have been undertaken and results published. Regions of the genome associated with milk production were found on chromosomes 9, 10 and 14 and for fat to protein ratio on chromosomes 9, 17

and 27. Furthermore, regions on chromosome 20 were associated with somatic cell count and regions on chromosome 3, 10, 18 and 20 were associated with the variation in somatic cell count.

### **Measuring milk quality**

The groups in Belgium, Edinburgh and Ireland have been very active in developing new methods of accurately and routinely predicting milk quality at little or no extra cost. The same machine in milk laboratories that determines fat and protein percentage in all milk samples (i.e., individual cows and bulk tank samples), also produces much more information which is currently unused. Earlier work in Belgium had already suggested that this unused information can be used to predict individual fatty acid composition in the milk and the lactoferrin content in milk. Fatty acid composition is of interest if we want to improve the quality of the fat in the milk by altering the ratios of the different fatty acids. Lactoferrin is a glycoprotein naturally present in milk which could be interesting as a biologically active food component. It has been also associated with the mastitis resistance in dairy cows. In ROBUSTMILK this methodology was further improved and validated in independent data from research herds from the UK, Ireland and The Netherlands. Accuracy of prediction for particularly the saturated fat content was extremely high and these equations are already being applied in Belgium. The infrastructure is present for applying this technology in other countries. In the UK a recent award has been made for National Milk Records (NMR) to exploit these prediction equations nationally.

The genetic variability of the fatty acids and lactoferrin traits has been studied. Results indicated that these traits are heritable and variable suggesting that they could be changed by genetic selection.

### **Measuring energy balance**

Existing research work on using information gathered from milk samples to predict more difficult to measure traits such as milk fatty acid content have taken an important step further in ROBUSTMILK. ROBUSTMILK set out to answer the research question of whether or not we could identify patterns in the mid-infrared spectrum of milk that were associated with cow robustness or energy balance. The hypothesis was that this approach is already accurately used to predict milk fat and protein percentage and these are known to be associated with energy balance. Equations to predict energy balance from mid-infrared spectra in milk were developed using data from Scottish Agricultural College. The results are very promising. We can predict energy balance with an accuracy close to 75% which far exceeds any previous predictors. This might not be good enough for treatment of individual cows, but for breeding purposes (where many samples are often combined for the whole lactation) this might become an important route for including energy balance in our breeding objectives. The prediction equations are currently being validated using Irish data.

## **Genetic evaluation**

We have developed models that can estimate if the offspring from some sires are more variable than the offspring from other sires, and developed algorithms that are much faster than the currently used ones, thereby reducing the time to undertake routine genetic evaluations for these types of traits. Furthermore, we have developed new traits using SCC and have studied how to better take changes in SCC over the lactation into account as apposed to the current lactation average SCC, and found that heritabilities for these traits were in the range usually found for lactation average SCC (9-13%). We have also shown that we can predict the probability not only of moving from a healthy to a sick state, but also the probability of recovering from a sick state (a trait that has not been studied before) – both based on the dynamics of SCC. This has huge implications for how we genetically evaluate SCC and could result in greater genetic gain for udder health.

## **Feed efficiency**

Although the ROBUSTMILK database might not be massive, it is one of the largest in the world for these specific traits. Most traits recorded on these animals are rare and unique, expensive to record (especially the data on feed intake) and feed efficiency is currently very topical. The first analysis of this dataset suggests that there are about 500 genes causing the variation in feed efficiency between animals, with one gene found that has a relatively strong effect. Interestingly, this gene also affects feed efficiency in poultry. In practice the individual genes found do not have a large enough effect to select on these individual genes, and the best solution to select for feed efficiency will be using genome wide selection. From the first results, we predict that we need feed intake data on at least 5000 to 7500 cows to estimate breeding values with a high enough reliability for publication. This requires the collaboration of even more countries, and this is already underway with collaborations with Australia.

## **Fertility**

Analysis of fertility has been performed using milk progesterone. The shared datasets of four countries demonstrated that the physiological fertility traits had higher heritability than the traditional traits we use such as insemination records. This also indicates that fertility is under greater genetic control than is sometimes anticipated meaning we could make greater improvement for fertility. Performing a genome wide scan, interesting genes were found that might have played a role in the reduction of fertility in the last century. Interesting enough, one of these genes may affect both female and male fertility.

## **Genomic Selection**

Genomic selection is now considered to be the optimal method of genetic evaluation in international dairy cattle populations. Genomic selection is based on utilizing the information on an animal's DNA profile as another source of information alongside other recorded traits such as milk yield, if available. The benefits of genomic selection are greater accuracy of identifying the genetic elite (and worse) animals at a younger age. However, progress in genomic selection is hampered by access to sufficiently large

datasets to estimate the optimal DNA profile for those traits.. ROBUSTMILK has answered the potential of genomically selecting for difficult to measure traits (e.g., feed intake) but has also proven that by combining information from multiple traits the accuracy obtained using genomic selection can be increased thereby increasing genetic gain.

## **What has been produced?**

Primarily, knowledge will be generated and this project has been very prolific in the production of peer reviewed scientific papers (more than 20 so far) but of course when this knowledge is applied, through the strong links between this research group and industry, the ultimate beneficiaries will be EU consumers. For example, once we know the genetic profile of cows that have improved robustness and produce more healthy milk, then we can include this in selection programmes, farmers can choose better bulls to increase the profitability of their herd, and society will benefit from healthier food being produced by better cows. These cows will require less treatment for disease, will live longer and consequently dairy production from them will have less impact on the environment.

A specific product of the project are formulae that allow milk recording organisations to predict individual fatty acids in milk samples rather than simply the whole content of fat. This allows variation between cows in the ratio of saturated to unsaturated fats to be used in selection and management of groups of cows. Already, an additional project called OptiMIR ([www.optimir.eu](http://www.optimir.eu)) has spawned from this project and is rolling the use of these formulae across North West Europe.

## **How will it benefit farmers and society?**

Ultimately, as the research on milk quality is applied in a systematic manner within the food chain such as in the OptiMIR project, healthier milk can be placed on supermarket shelves. At the same time we will know how to do this without compromising the health of the cow and so cows (and farmers) will benefit. Indeed, irrespective of the human health aspects of milk, this project will lead to cows that are more 'robust' which translates into cows that can produce large amounts of milk economically for the farmer, that can remain healthy in so doing and can live a long time without the need for veterinary intervention or drug usage. This benefits both farmers and society but above all, benefits cows and the environment, because herds with cows that live longer have an overall lower impact on the environment.

## **Take home messages**

1. Cows can be improved by selection to be more efficient, more healthy and live longer.
2. Cows can be selected to produce milk that is more healthy for humans using readily available national data.
3. The objective of this project is to attempt to achieve both of the points above simultaneously in an effective and efficient manner .

4. The results to date are very promising: 1) easy ways of predicting fatty acid composition, lactoferrin content in milk and energy balance during routine milk samples, 2) genomic tools that will aid selection for unique traits like feed intake and fertility, and 3) new measures for robustness and mastitis from existing data have all been developed.
5. To exploit genomic selection collaboration is required – the more the merrier and countries or groups unwilling to co-operate will be left behind!

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