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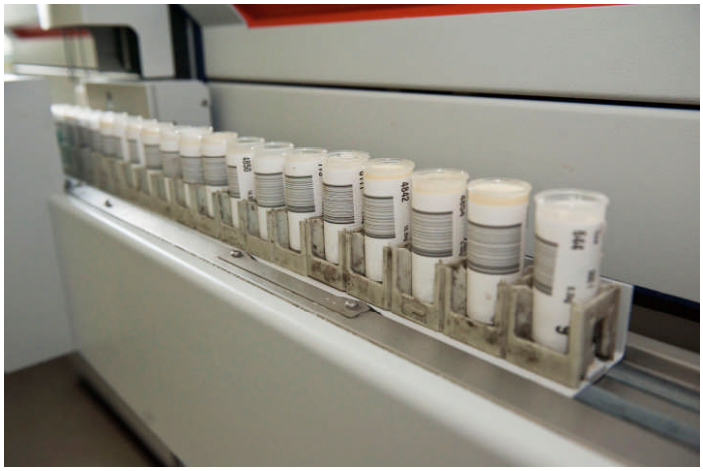
Innovative and practical breeding tools for improved dairy products from more robust dairy cattle



Key external stakeholders:
The Irish Cattle Breeding Federation (ICBF)
International breeding industry
Milk processors and national dairy boards
Dairy farmers
International genetic evaluation bodies
International geneticists, nutritionists and other scientists

Practical implications for stakeholders:
This study

- Developed an international database among 4 countries for the storage of, in particular, difficult to measure traits such as feed intake, to facilitate international genetic and genomic evaluations which would not be possible using individual research institute databases
- Clearly demonstrated that the saturated fatty acid content in milk can be very accurately predicted using infrared spectroscopy, the routine method currently used to analyse the composition of milk samples from Irish (and international) milk recorded cows and bulk milk tank samples
- Demonstrated the ability of infrared spectroscopy of milk to predict body energy status
- Demonstrated that both predicted milk quality and energy status exhibit exploitable genetic variation
- Developed sophisticated statistical models for the analysis of udder health to better reflect the underlying biology
- Identified regions of the bovine genome associated with a range of performance traits included in milk production, the feed intake complex, fertility and milk quality
- Improved genomic selection algorithms to facilitate the joint inclusion of both cow and sire DNA information and field data

Main results:

- Milk fatty acid content can be accurately predicted from milk samples using mid-infrared spectroscopy thereby incurring no additional operation costs over and above the current cost of milk recording and bulk tank testing
- Energy balance can also be predicted from milk mid-infrared spectroscopy and exhibits heritable genetic variation thereby providing the necessary resources for inclusion in a national breeding programme
- Including cow genotypes in genomic selection increases the accuracy of prediction

Opportunity / Benefit:

To improve the accuracy of selection for difficult to measure traits, in particular milk quality and robustness thereby increasing overall herd profitability through a more balanced breeding scheme

Collaborating Institutions:

Wageningen University, Scottish Agricultural College, University of Liege, Swedish University of Agricultural Sciences, Irish Cattle Breeding Federation

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1. Project background:

Dairy cattle have been selected primarily for increased production for over 20 years in many EU countries. This has been mostly as a result of importation of genetic material from North America followed by within-country selection policies specific to each country's local circumstances. In the majority of countries, selection has favoured milk or protein yield whilst in a few countries the focus has been more balanced for improved milk production without compromising health and fertility. Focussed 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 to meet milk production demands, and are in varying degrees of negative energy balance for some parts of the lactation. Consequently, dairy cows are considered less 'robust' than they once were. More recently, as a result of a general public interest in milk production practices and the environment, selection pressure in many (if not most) countries has shifted more towards non-production traits. These non-production traits are mostly those associated with cow health but increasingly, human health is of interest.

2. Questions addressed by the project:

The objective of ROBUSTMILK is to develop new useful and practical technologies to allow dairy farmers and the dairy industry to refocus their selection decisions to include additional traits such as milk quality and dairy cow robustness. It is of utmost importance that farmers can evaluate the consequences of selection for these novel and additional traits within their own milk production systems. Likewise, it is important that the inclusion of traits such as milk quality in selection indices does not compromise health, fertility or “robustness” of the cow. We seek the win-win situation where dairy cow milk is healthy for humans and is also healthy for the cow.

3. The experimental studies:

- The initial task involved the collation of data from research herds in Ireland, the UK, the Netherlands and Sweden as well as milk spectral data from Walloon region in Belgium
- Fatty acid composition and lactoferrin composition of several thousand milk samples from Ireland, the UK, Belgium and the Netherlands were determined using gas chromatography and ELISA laboratory methods, respectively. The true fatty acid and lactoferrin composition were subsequently related to the mid infrared spectrum of those samples using multivariable approaches. Genetic variation was estimated using data from participating countries
- The mid infrared spectrum of milk samples was also related to energy balance information in Irish and UK dairy cows using multivariable regression techniques and the genetic variation in the predicted equations estimated. The prediction equations were also applied to spectral data generated from the Walloon region of Belgium and phenotypic and genetic parameters were estimated
- Alternative statistical approaches accounting for the genetics of residual variation in somatic cell count was estimated using Irish national data
- A total of 1,500 Holstein-Friesian dairy cows from Ireland, the UK, Sweden and the Netherlands were genotyped for over 50,000 genetic markers and their genotypes related to a range of performance variables derived from the international database of research phenotypes

4. Main results:

- Milk fatty acid content can be predicted from milk samples using mid-infrared spectroscopy thereby incurring no additional operational costs over and above the current cost of milk recording and bulk tank testing
- Energy balance can also be predicted from milk mid-infrared spectroscopy and exhibits heritable genetic variation thereby providing the necessary resources for inclusion in an national breeding programme
- Including cow genotypes in genomic selection increases the accuracy of prediction

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- Somatic cell count is not the same genetic trait in seasonal and year-round calving herds, meaning that the same bulls were not the best in both systems. Models were developed that can estimate if the offspring from some sires are more variable than the offspring from other sires, and the developed algorithms were much faster than those previously used
- Regions of the bovine genome putatively associated with several performance traits, particularly on difficult to measure traits, were identified

5. Opportunity/Benefit:

- The mid-infrared spectrum is routinely generated for all individual and bulk milk samples, thus milk fatty acid content can be predicted for all milk samples at no additional cost to milk recording. And since milk fatty acid exhibits genetic variation, the milk fatty acid profile of Irish dairy cows can be altered through animal breeding
- Energy balance status can also be predicted from the routinely available milk mid-infrared spectrum and because it also exhibits genetic variation, energy status can also be improved through animal breeding. However, to date, the predictions can also be used as a management tool. Additional research is required to quantify the benefit of including predicted energy status in multi-trait genetic evaluations for health and fertility
- There is an increase in the quantity of genomic information (with phenotypes) available in Ireland and the tools for combining with sire genotype and phenotype data is now available

6. Dissemination:

(**http://www.robustmilk.eu**)

International conferences: Several invited and contributed presentations at international conferences, including the European Association of Animal Production, INTERBULL, International Committee of Animal Recording, International Society of Animal genetics, Symposium on Applied Biological Science, International Conference on Quantitative Genetics, British Society of Animal Science, British Cattle Breeders Club, NCCC204: The Interface of Molecular and Quantitative Genetics in Plant and Animal Breeding, International Symposium on Animal Functional Genomics, International Cattle Breeders Round Table, American Dairy Science Association Annual meeting, European Society for Domestic Animal Reproduction, and the World Congress on Genetic Applied to Livestock Production.

National Conferences and seminars: Presented at the annual Agricultural Research Forum throughout the duration of the project and at national farmer conferences (e.g., Irish Grassland Association Conference, Teagasc National Dairy Farmers Conference) including G€N€ IR€LAND® user days.

Open Day: Presented at all Moorepark open days.

Industry consultation days

Presented and discussed at several industry meeting days with representatives from the different AI organisations, breed societies, Teagasc extension service, farmer groups and farmers. Also presented to several milk processors and the Irish dairy board.

Farmer discussion groups: Discussed at many farmer discussion groups and seminars.

Press: Results regularly presented in the Irish Farmers Journal, Farming independent, Today's Farm, TResearch, and Moorepark News as well as on radio and television.

Main publications:

Berry, D.P., Bastiaansen, J.W.M., Veerkamp, R.F., Wijga, S., Wall, E., Berglund, B. and Calus, M.P.L. 2012. Genome-wide associations for fertility traits in Holstein-Friesian dairy cows using data from experimental research herds in four European countries. Animal, doi:10.1017/S1751731112000067

Mc Parland, S., Banos, G., Wall, E., Coffey, M.P., Soyeurt, H., Veerkamp, R.F. and Berry, D.P. 2011. The use of mid-infrared spectrometry to predict body energy status of Holstein cows. J. Dairy Sci., 94:3651:3661.

Soyeurt H., Dehareng, F., Gengler, N., McParland, S., Wall, E., Berry, D.P., Coffey, M. and Dardenne, P. 2011. Mid-infrared prediction of bovine milk fatty acids across multiple breeds, production systems and countries. J. Dairy Sci., 93:1657-1667.

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