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Genomic selection in dairy cattle



Key external stakeholders:

The Irish Cattle Breeding Federation (ICBF), breeding industry, dairy farmers, AI technicians, international genetic evaluation bodies, international geneticists.

Practical implications for stakeholders:

This study

- Identified the optimal algorithm for genomic selection in Irish Holstein-Friesian dairy cattle across over 30 traits thereby increasing the accuracy of selection and thus genetic gain.
- Provided industry with an immediately implementable pipeline for genomic selection in Irish Holstein-Friesian cattle and undertook the first national genomic evaluation in Irish Holstein-Friesian cattle.
- Passed the international quality control on national genomic evaluations.
- Generated the pipelines for imputing from lower density genotype platforms to higher density genotype platforms thereby reducing the cost of genomic selection.
- Determined the optimal national breeding scheme for genomic selection in Irish Holstein-Friesian dairy cattle.
- Initiated an international initiative for the exchange of genotypes thereby improving the accuracy of genomic predictions.
- Disseminated the benefits and approaches to optimally exploit genomic selection on farm as well as by breeding companies.

Main results:

- The accuracy of genetic evaluations can be augmented considerably (i.e., from ~32% reliability to ~55% reliability) by exploiting genomic information in national two-step genetic evaluations.
- The cost of genomic selection can be reduced by 66% by using a lower density genotyping platform and imputing to a higher density.
- Genetic gain in Irish Holstein-Friesian cattle can be increased >50% by optimising the national breeding scheme to exploit genomic selection.

Opportunity / Benefit:

Greater accuracy of genetic selection and thus genetic gain for profitability as well as international market share by Irish indigenous breeding companies.

Collaborating Institutions:

ICBF

Teagasc project team:

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External collaborators:

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1. Project background:

Genetic gain is a function of how accurately the genetically elite animals within a population can be identified; the greater the accuracy, all else being equal the greater will be genetic gain. However, being able to accurately identify genetically elite animals at a younger age, without the requirement for a supervised progeny testing scheme can not only increase annual genetic gain further but can also reduce the cost of a breeding program for a given number of animals. Because DNA is 1) responsible for some of the variation in performance among animals, 2) remains the same throughout an individual's lifetime, and 3) is available for birth, being able to optimally exploit DNA information in the national breeding schemes can be very beneficial. Individual differ at millions of sites along their DNA resulting in differences in characteristics and performance; one type of variation in DNA among individuals is called a single nucleotide polymorphism (SNP). Differences in single sites along DNA generally result in only tiny differences among animals but when all the DNA differences between individuals are summed the differences in performance can be substantial. The basis of genomic selection is to quantify the impact of variations in thousands of SNPs in dairy cattle for a range of production traits. Once known, the DNA profile of selection candidate (e.g., young test bulls) can be generated and the sum of all DNA variants for that individual obtained resulting in an estimate of the genetic merit of that individual – this can be available at a very young age.

2. Questions addressed by the project:

- Can low-cost, accurate genomic selection be implemented for a range of performance measures in Irish dairy cattle?
- What is the optimal breeding program to exploit genomic selection in Ireland?

3. The experimental studies:

- This was a desktop study.
- Genotypes (54,001 genetic markers per animal) on several thousand Holstein-Friesian bulls were used to develop the accurate genomic predictions.
- The same genotypes, with a large proportion of genotypes masked to mimic lower density genotypes, were used to test the accuracy of imputation from lower to higher density genotype panels.
- A simulation study, including a cost benefit analysis, was used, based on Irish dairy cattle population parameters, to define the optimal breeding program exploiting genomic selection.

4. Main results:

- The accuracy of national genetic evaluations was augmented through the incorporation of genome-wide genetic marker information; the improvement in accuracy varied by trait which was primarily a function of the effective number of animals used to estimate the genetic marker effects and their relatedness to the candidate animals.
- Genomic predictions were estimated using a genomic relationship matrix commonly referred to as GBLUP.
- Retrospective analysis comparing original genomic proofs of bulls at the time of sale compared to current daughter derived traditional genetic evaluations clearly show an improvement in accuracy of selection of up to 21%.
- The accuracy of imputing (i.e., predicting) the 54,001 genetic markers used in the national genomic evaluations from 3,000 and 6,000 genetic markers was 98 to 99% with a similar effect on genomic predictions.
- Inclusion of female phenotypic and genomic information can lead to a 3-fold increase in the rate of genetic gain compared with a traditional BLUP breeding program and decrease the generation

interval of the males by 3.8 years, while maintaining a reasonable rate of inbreeding.

5. Opportunity/Benefit:

- The accuracy of selection increased with genomic selection and was implemented in the national dairy cattle genetic evaluations for all traits in the national breeding objective, the EBI, in Spring 2009; genomic evaluations for linear type traits followed in 2012.
- In 2009, 34% of semen used was to genomically selected sires which increased to 47% in 2011.
- Simulations clearly show that a 50% increase in genetic gain is achievable with genomic selection; this is worth €8 million annually which is cumulative and permanent; greater genetic gain has been observed since the implementation of genomic evaluations.

6. Dissemination:

International conferences: Presented at many international conferences, invited and contributed, such as the European Association of Animal Production, British Society of Animal Science, British Cattle Breeders Conference, INTERBULL, ICAR, American Dairy Science Association Annual meeting, New Zealand Society of Animal Production, International Society of Animal Genetics, Recent Advances in Animal Nutrition Annual Conference (Nottingham), and the World Congress on Genetic Applied to Livestock Production.

International workshops and seminars: Presented at several international workshops and seminars including the University of Pretoria, South Africa, and Massey University, New Zealand, Lincoln University, Nebraska

National Conferences and seminars: Presented at the Agricultural Research Forums through the duration of the project and at national farmer conferences (e.g., Irish Grassland Conference) including GENE IRLAND® days.

Open Day: Presented at all Moorepark open days.

Breeding 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.

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. and Kearney, J.F. (2011) 'Imputation of genotypes from low-to high-density genotyping platforms and implications for genomic selection.' *Animal*, 5 (8): 1162-1169.

McHugh, N., Meuwissen, T.H.E., Cromie, A.R and A. K. Sonesson (2011) 'Use of female information in dairy cattle genomic breeding programs.' *Journal of Dairy Science*, 94: 4109-4018.

Wickham, B.W., Amer, P.R., Berry, D.P., Burke, M., Coughlan, S., Cromie, A., Kearney, J.F., McHugh, N., McParland, S. and O'Connell, K. (2012) 'Industrial perspective: capturing the benefits of genomics to Irish cattle breeding.' *Animal Production Science*, 52: 172-179.

Popular publications:

Berry, D.P., Cromie, A., McHugh, N. and Kearney, F. (2010) 'Genomic selection in Ireland - from zero to hero in one year.' In: *British Cattle Conference*, BCBC, p46-50.

Berry, D.P., Howard, D., Waters, S. and Kearney, F. (2008) 'Genomic selection to increase EBI.' In: *National Dairy Conference*, Rochestown Park Hotel, Cork, 4 pages.

Berry, D.P., Kearney, F. and Harris, B. (2009) 'Genomic selection in Ireland.' In: *Proceedings of the Interbull International Workshop: Genomic Information in Genetic Evaluations*, Uppsala, Sweden, Bulletin No. 39, 29-34.

7. Compiled by: Dr Donagh Berry