Project number: 6408
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Multi breed genomic selection in dairy and beef cattle

Key external stakeholders:
The Irish Cattle Breeding Federation (ICBF)
Scientists
Stakeholders in the breeding industry

Practical implications for stakeholders:
This study

- Developed a low-cost and reproducible bespoke genotyping platform concurrent with the associated downstream pipelines to generate the necessary DNA information for use in genomic evaluations of dairy and beef cattle
- Developed two-step genomic evaluations used nationally in the largest cattle multi-breed genomic evaluation globally

Main results:

- The accuracy of prediction of genetic merit can be augmented through the integration of DNA information in the evaluations
- The cost of genomic evaluations can be reduced considerably by using a lower density genotype platform of carefully selected and informative DNA variants

Opportunity / Benefit:

- Accelerated genetic gain through the exploitation of DNA information in the four selection pathways governing genetic gain

Collaborating Institutions:
Irish Cattle Breeding Federation

Teagasc project team:	Donagh Berry (PI), Deirdre Purfield
External collaborators:	Francis Kearney (ICBF), Ross Evans (ICBF), Andrew Cromie (ICBF)

1. Project background:

Simulations, undertaken within-breed, suggest that genomic selection can increase genetic gain by >50%. However, interest in alternative dairy cattle breeds and crossbreeding is increasing, necessitating an across-breed genomic evaluation. Beef cattle breeding and sheep breeding are based on many different breeds and crossbreds, which when coupled with their smaller population size, signify a requirement for across-breed genomic evaluations. Genomic selection uses information on the DNA of an animal to supplement the traditional genetic evaluations; this results in increased accuracy of selection. The increase in accuracy of selection is a function of, amongst others, the size of the population used to estimate the SNP (i.e., pieces of DNA) effects. The cost of genotyping however remains a stumbling block to both the generation of a large reference population but also the update of the technology – reducing the number of SNPs genotypes could translate to a reduced cost per genotype. Based on preliminary research in Ireland, the size and structure of the beef population in Ireland does not lend itself to accurate within-breed genomic selection as currently implemented in dairy cattle in Ireland; therefore across-breed genomic selection must be pursued but this is not trivial.

2. Questions addressed by the project:

- To develop an low-cost informative bespoke genotype platform pertinent to Irish dairy and beef cattle for the generation of genotype information on millions of animals
- Develop the pipelines for a two-step genomic evaluation scalable to millions of genotyped animals
- Scan the genome, using imputed whole genome sequence data, for signal suggesting putative mutations associated with performance traits in dairy and beef cattle

The experimental studies:

- This study was desktop based
- Algorithms were develop to optimize the selection of SNPs informative for the Irish population which could be subsequently accurately imputed to whole genome sequence
    - Alternative imputation algorithms and software suites were also compared on efficiency and efficacy of genotype imputation
- Pipelines were develop for data editing, genomic evaluations and post-hoc blending of direct genomic evaluations with traditional evaluations

3. Main results:

- **Development of multi-breed beef genomic evaluations:** Two-step national beef genomic evaluations were officially launched in 2016. These evaluations are currently the largest official national genomic evaluation globally in cattle. The accuracy of prediction of genetic merit increased following the information of DNA information into the genetic evaluations
- **Custom genotyping panel- Irish Dairy and Beef:** A bespoke genotyping panel was developed which included the SNPs included in the national dairy genomic evaluations as well as strategically selected SNPs to enable accurate imputation to higher density genotype panels. SNPs to impute microsatellites marker for parentage assessment were also included on the SNP manifest.
- **Development of imputation pipelines:** Imputation pipelines for the efficient and accurate imputation of SNP panels to medium (50k), high density (770k) and whole genome sequence (40 million) have been created. The pipelines for imputation to medium density are implemented within the national genomic evaluations.
- **Breeding programs:** the mathematical methodology to set limits to animal movement in genetic merit between consecutive genetic evaluation runs has been incorporated into the ICBF quality assurance system; the impact of relationships among bulls and unequal bull usage within a bull team for a herd's breeding program have been incorporated in the national sire advise system run by the ICBF.
- **Genomic regions of interest:** Several regions of the genome were identified as associated with a range of performance traits

4. Opportunity/Benefit:

- To reduce the cost of genotyping by using more carefully selected SNPs pertinent to the Irish dairy and beef cattle populations
- More accurate prediction of genetic merit through the appropriate incorporation of genomic information into national genetic evaluations
- Genomic regions putatively associated with performance traits identified for further investigation

5. Dissemination:

International conferences

Presented at many international conferences, invited and contributed, such as the European Association of Animal Production, INTERBULL, International Society of Animal Science, American Dairy Science Association Annual meeting, and the World Congress on Genetic Applied to Livestock Production

National Conferences and seminars

Presented at the Teagasc Dairy and Beef Open Days

Main publications:

Berry, D.P., Wolfe, A., Byrne, N., Sayers, R., Dodds, K.G., McEwan, J.C., Oconnor, R.E., McClure, M. and Purfield, D. (2017). Characterization of an X-chromosomal non-mosaic monosomy (59,XO) dairy heifer detected using routinely available single nucleotide polymorphism genotype data. Journal of Animal Science 1042-1049

Bouwman A.C., H.D. Daetwyler, A.J. Chamberlain, C.H. Ponce, M. Sargolzaei, F.S. Schenkel, G. Sahana, R. Govignon-Gion,S. Boitard, M. Dolezal, H. Pausch, R.F. Brøndum, P.J. Bowman, B. Thomsen, B. Guldbrandtsen, M.S. Lund, B. Servin, D.J. Garrick , J. Reecy, J. Vilkki, A. Bagnato, M. Wang, J.L. Hoff, R.D. Schnabel, J.F. Taylor , A.A. E. Vinkhuyzen, F. Panitz, C. Bendixen, L.-E.Holm, B. Gredler, C. Hozé, M. Boussaha, M.-P. Sanchez, D. Rocha, A. Capitan, T. Tribout, A. Barbat, P. Croiseau, C. Drögemüller, V. Jagannathan, C. Vander Jagt, J.J. Crowley, A. Bieber, D.C. Purfield, D.P. Berry, R. Emmerling, K.-U Götz, M. Frischknecht, I. Russ, J. Sölkner, C.P. Van Tassell, R. Fries, P. Stothard, R. F. Veerkamp, D.Boichard, ME. Goddard and B.J. Hayes. 2018. Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics. 50: 362-367.

Purfield, D., McClure, M. and Berry, D.P. (2016). Justification for setting the individual animal genotype call rate threshold at eighty-five percent. Journal of Animal Science 94:4558-4569

6. Compiled by: Dr. Donagh Berry