Project number: 6740
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Multi-Breed sheep genetic and genomic evaluations

Key external stakeholders:
Sheep Ireland (ICBF)
Scientists
Stakeholders in the breeding industry
Genotyping laboratories

Practical implications for stakeholders:
This study:

- Proved that genetic variability exists for health traits and dagginess in Irish sheep which has resulted in national genetic evaluations for these traits now being used by the industry.
- Demonstrated that a strong genotype concordance exists between genotyping platforms and service providers enabling strong bargaining power on the cost of genotyping.
- Illustrated how the cost of genotyping on a medium density chip platform (needed for genomic evaluations) can be reduced by combining a carefully selected lower density genotype platform with imputation strategies.
- Proved that parentage can be accurately assigned with just 250 carefully selected genomic variants spread across the genome; these genomic variants are now used in Ireland for parentage discovered by Sheep Ireland.
- Developed the logistics for scrapie genotyping using custom genotyping platforms.

Main results:

- Exploitable genetic variability exists in lameness, mastitis and dagginess in Irish sheep; each of which have an economic value derived in this study.
- Genotypes can be used for parentage discovery as well as breed determination.
- Genotypes of parents can be predicted from their offspring; when the genotype of the dam was also available. Acceptable prediction of genotypes of the sire could be achieved with just seven genotyped progeny with an equivalent accuracy achievable without the genotype of the dam needing the genotypes of 15 progeny.

Opportunity / Benefit:

- National genetic evaluations for lameness and dagginess are now available and included within the national sheep breeding indexes.
- Parentage discovery algorithms are embedded within the Sheep Ireland database and run with each new genotype entry.
- Breed composition of animals can be accurately predicted from routinely available genomic information.

Collaborating Institutions:

Sheep Ireland

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1. Project background:

Genetic gain is a function of the accuracy of the genetic/genomic evaluations. Genetic gain achieved in Ireland to date has been small (4c/lamb/year). Genetic gain in New Zealand, with similar breeding goals to Ireland, is currently NZ$0.60/lamb/year. Therefore huge potential exists to increase the rate of genetic gain in Ireland. More stable genetic evaluations through greater accuracy will instil greater farmer confidence in the genetic evaluations thereby increasing uptake. The national breeding objective in sheep was established in 2008. The genetic parameter estimates currently used in the genetic evaluations, however, were based on small datasets available in 2008 or in some cases international estimates were used. Moreover, data on many potential fixed effects were not available at that time. Sufficient Irish sheep data now exists to apply skillsets, such as model building and variance component estimation procedures, initially developed in cattle to be now applied sheep. This will enable the development of more pertinent statistical models and re-estimation of the genetic parameters; the published results will be peer-reviewed. Genetic evaluations in health traits are non-existent in Irish sheep and the potential of exploiting genome-wide genomic information in Irish sheep has never been explored

2. Questions addressed by the project:

- What is the extent of genetic variability in health traits and dagginess in Irish sheep?
- Can the cost of genotyping be reduced by changing between genotyping vendors and service providers with no loss in accuracy or through the reduction in the number of genomic variants genotyped coupled with imputation to higher density?
- What is the level of parentage errors in Irish sheep and how does it impact genetic gain? Can genotyping help resolve these errors?

- **The experimental studies:**
- Most of the study revolved around the analyses of the national sheep database.
- A total of 31,315 animals from 242 flocks had data recorded as part of this project. These data were uploaded into the Sheep Ireland database and as well as being used in the national genetic evaluations, were also used for research purposes.
- Animal linear mixed models were used to estimate the contribution of genetics to difference in susceptibility to disease.
- Genotypes on 22,000 animals were also generated from a whole range of different breeds
- Scrapie genotypes from known animals differing in scrapie were also available

3. Main results:

- Genetic parameters for lameness, dagginess and mastitis have been quantified
- With greater than 22,000 animals now genotyped, the current parentage error rates are 8.3% and 5.6% for sires and dams, respectively. The prevalence of animals having both the dam and sire incorrect is 2.7%. Recent developments now mean that of the sires that are incorrect, the correct sire for 40% of these animals can be accurately predicted from genotyped sires on the database. The correct dam can be successfully predicted for 36% of animals previously identified as having a dam mismatch.
- Scrapie can be genotyped using custom genotyping panels with 100% concordance to the gold standard.
- Routinely used genotype panels can be used to detect some karyotype abnormalities; the first dizygotic twins in any species were detected.
- Genotyping costs can be reduced by using 6,000 carefully selected genomic variants and imputing up to high density.
- Genotypes of parents can be generated in-silico, based on progeny genotypes and the accuracy of generating these parental genotypes is improved if the genotype of the mate (i.e., the other parent of

the progeny) is also available.

- When the genotype of the dam was also available, acceptable prediction of genotypes of the sire could be achieved with just seven genotyped progeny with an equivalent accuracy achievable without the genotype of the dam needing the genotypes of 15 progeny.

4. Opportunity/Benefit:

- National genetic evaluations for lameness and dagginess are now available and, with the economic values derived in this project, are now used by Irish sheep breeders in their breeding programmes to reduce their respective incidence through sustainable breeding.
- Over 22,000 Irish sheep have now been genotyped with many breeders (part) paying for genotyping; parentage validation and, where necessary, discovery are now routinely being undertaken.
- Additional benefits from genomics other than genomic evaluations have been demonstrated such as parentage discovery, breed prediction, karyotype detection and reporting of major genes such as scrapie

5. Dissemination:

International conferences

Presented at many international conferences, invited and contributed, such as the European Association of Animal Production, International Society of Animal Science, Sheep Breeders Round Table, the World Buiatrics Congress, and the World Congress on Genetic Applied to Livestock Production

National Conferences and seminars

Presented at the Teagasc Sheep Open Days as well as many national sheep events

Main publications:

O'Brien, A.C., McHugh, N., Wall,E., Pabiou,T., McDermott,K., Randles, S., Fair, S. and Berry, D.P. (2017). Genetic parameters for lameness, mastitis and dagginess in a multi-breed sheep population. Animal 11:911-919

Berry D.P., O'Brien A., Wall E., McDermott K., Randles S., Flynn P., Park S., Grose J., Weld R., McHugh N., 2016. Inter- and intra-reproducibility of genomics from sheep technical replicates on Illumina and Affymetrix platforms. Genetic Selection Evolution 48:86. Doi:10.1186/s12711-016-0267-0

Berry, D. P., A. O'Brien, J. O'Donovan, N. McHugh, E. Wall, S. Randles, K. McDermott, R. E. O'Connor, M. A. Patil, J. Ho, A. Kennedy, N. Byrne, and D. C. Purfield. 2018. Aneuploidy in dizygotic twin sheep detected using genome-wide single nucleotide polymorphism data from two commonly used commercial vendors. Animal. 12:2462-2469.

6. Compiled by: Dr. Donagh Berry

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