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Long term sustainable breeding strategies for consistently superior health in cattle



Key external stakeholders:

The Irish Cattle Breeding Federation (ICBF)
Scientists
Stakeholders in the breeding industry
Veterinarians
Animal Health Ireland

Practical implications for stakeholders:

This study

- Proved that genetic variability exists in a wide range of cattle health traits implying that breeding for these traits can be fruitful.
- Quantified the impact of current dairy and beef breeding objectives on genetic change in animal health.
- Contributed to the knowledge required to generate national genetic and genomic evaluations were launched for tuberculosis and liver fluke for dairy and beef cattle with accompanying dissemination on how to use this new information source.
- Quantified the economic cost of different diseases in Irish cattle.
- Refined the economic values within the dairy national breeding index, the EBI, were updated based on lameness incidence recorded in the study cattle.

Main results:

- Inter-animal genetic differences contribute up to 14% of the variability in susceptibility to a wide range of diseases in Irish cattle including infectious bovine respiratory disease, bovine viral diarrhoea, serological response to Mycobacterium avium ssp. paratuberculosis, bovine tuberculosis, liver fluke, ostertagia, neospora, different lameness and claw traits, scour, pneumonia, and both calf and cow mortality.
- Validation of the genetic evaluations for many of these traits proved that genetically divergent animals had different incidences of the diseases (once exposed)
- Although genomic regions associated with these health traits were detected using the largest studies undertaken globally, the proportion of variation in susceptibility explained by each individual variant was negligible.

Opportunity / Benefit:

- National genetic and genomic evaluations for tuberculosis (first ever in Ireland) and liver fluke (first ever globally) were launched and are now publicly available. The aim is to include new traits into the national breeding indexes two years after they are first launched. Irish farmers can now use these genetic evaluations to select for animals less susceptible to these diseases

Collaborating Institutions:

Irish Cattle Breeding Federation, Animal Health Ireland, Wageningen University.

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1. Project background:

There continues to be very significant advances in efforts to control disease in cattle, with the potential for significant improvements to both performance and welfare. These advances have included improved understanding of disease pathophysiology and epidemiology, as well as the development of products such as antibiotics and anthelmintics for improved disease control. Concurrently, there have been considerable advances in animal breeding and genetics, relevant to animal disease control. These advances are of considerable veterinary interest, noting that observed animal performance is the outcome of the interaction between the animal's genetic makeup and the specific environment it was exposed to. Logically, therefore, improved genetic merit has the potential to complement current approaches to animal disease control. Improvement in animal health through genetic selection is advantageous because genetic gain is cumulative and permanent, since the genes introduced into a population can persist for many generations. Unravelling the genetic architecture of health and disease resistance not only facilitates knowledge development on potential for breeding for improved health status but also generates knowledge for biomedical research in animals and humans including applications such as vaccine development.

2. Questions addressed by the project:

- What is the extent of genetic variability in a wide range of health traits in Irish dairy and beef cattle?
- What are the genetic correlations between these health traits and other performance traits thus helping quantify the impact of prevailing breeding goals on predicted genetic response in animal health?
- Are there any genetic markers that explain a proportion of the genetic variance in animal health?
- What are the economic costs of the different health traits in Irish cattle

The experimental studies:

- Most of the study revolved around the analyses of the national cattle database.
- Detailed phenotypes on up to 10,979 cows from 69 dairy herds were collected. Phenotypes collected included pre-breeding reproductive tract ultrasound measurements, body condition score and locomotion score in the spring and autumn, detailed hoof ailments, as well as 9 diseases namely BVD, IBR, salmonella, Neospora, liver fluke, Johne's disease, pneumonia, Leptospirosis and Ostertagia as well as a post-breeding pregnancy diagnosis. All cows were also genotyped.
- Animal linear mixed models were used to estimate the contribution of genetics to differences in susceptibility to disease. Whole genome sequence data were imputed for all animals and related to the disease traits after accounting for nuisance factors in the statistical model.

3. Main results:

- Examples of the heritabilities for a selection of the different health traits in both dairy and beef cattle (young and old) were: Neospora (0.02 to 0.09), pneumonia (0.0449), pregnancy (0.02), ostertagia (0.07), scour (0.0228), IBR (0.10), BVD (0.01), lameness (0.08 to 0.26), liver fluke (0.01 to 0.09), and mortality (mostly <0.05). More importantly, considerable exploitable genetic variability existed for all traits.
- The pipelines were developed to generate national genetic and genomic evaluations (which have now been deployed) for TB and liver-fluke in Irish cattle. The TB evaluations are only the second such evaluations published globally and the liver-fluke evaluations are the first ever national

evaluations published.

- The three national breeding objectives, EBI (Dairy), the Replacement Index (Beef) and the Terminal Index (Beef), are having a favourable impact on the genetic trend for liver fluke-liver damage. It was estimated that liver damage caused by liver fluke will reduce by 0.71, 0.68 and 0.07 percentage units per generation from selection on the EBI, Replacement Index and Terminal Index, respectively. Additionally, selection on the current dairy breeding objective, the EBI, will generate animals with a reduced antibody response to liver fluke and *Ostertagia* as well as an increasing the antibody response to *Neospora*. By including liver damage caused by liver fluke into the national breeding objectives, after accounting for economic cost of treatment and saleable liver loss, further reductions in prevalence of live fluke can be achieved. At an economic cost of €6.92 in the EBI, liver fluke prevalence would reduce by 0.85 percentage units per generation. For the beef indexes, an economic cost of €21.58 for the Replacement Index would reduce liver fluke prevalence by 0.73 percentage units per generation and for the Terminal Index a cost of €15.44 for liver fluke would result in 0.11 percentage units per generation reduction in liver fluke. Also the economic weighing for liver fluke only had a marginal impact on the genetic gain in the other traits in the breeding objectives.
- Based on selection on EBI, the expected annual response in young animal mortality is -0.22 percentage units, in cow mortality is -0.08 percentage units, in mobility score (measured on a 4-point scale) is -0.002 units, in the individual hoof health traits (measured on a 4-point scale) of overgrown sole, white line disease, and sole hemorrhage is -0.001 units, -0.002 units, and +0.004 units, respectively, as well as in the immune response traits to BoHV-1 and tuberculosis is -0.12 percentage units and -0.14 percentage units, respectively. Based on selection using the beef Replacement Index, the observed predicted annual response in young animal mortality is -0.03 percentage units, in cow mortality is -0.12 percentage units, and in tuberculosis is -0.03 percentage units. Based on selection using the beef Terminal Index, the observed predicted annual response in young animal mortality is -0.01 percentage units, in cow mortality is -0.06 percentage units, and in tuberculosis is -0.08 percentage units.
- There was little or no genetic variability in sensitivity to liver fluke prevalence levels among cattle for milk production and carcass traits. Some genetic variability in sensitivity among dairy cows did exist for fertility traits measured across herds differing in liver fluke-prevalence.
- Genome wide association studies on parasites, Johne's disease and TB identified a large number of genomic regions associated with these health traits. Parasites and TB were both linked to the olfactory system of cattle suggesting that animals use an avoidance strategy to minimise infection to disease by odour cues. The proportion of variance in the health traits explained by these genomic regions was very small and, therefore, unlikely to add much in genomic evaluations and not worth pursuing.

4. Opportunity/Benefit:

- National genetic and genomic evaluations for TB and liver fluke were released; economic values were also derived so both traits can be included in the national breeding indexes in a few years.
- Regions of the genome detected to be associated with some of the traits which other scientists can explore further but the results from the present study suggest limited usefulness in cattle breeding.

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, 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:

Twomey, AJ, DP Berry, RD Evans, ML Doherty, DA Graham, DC Purfield. 2019. Genome-wide association study of endo-parasite phenotypes using imputed whole-genome sequence data in dairy and beef cattle Genetics Selection Evolution 51 (1), 15

McGovern, SP, DC Purfield, SC Ring, TR Carthy, DA Graham, DP Berry. 2019. Candidate genes associated with the heritable humoral response to *Mycobacterium avium* ssp. *paratuberculosis* in dairy cows have factors in common with gastrointestinal diseases in humans. Journal of dairy science 102 (5), 4249-4263

Ring, SC, DC Purfield, M Good, P Breslin, E Ryan, A Blom, RD Evans, ML Doherty, DG Bradley, DP Berry.

2019. Variance components for bovine tuberculosis infection and multi-breed genome-wide association analysis using imputed whole genome sequence data. PloS one 14 (2), e0212067

6. **Compiled by:** Dr. Donagh Berry
