



Unravelling the genetics of animal health

Ever wonder why all the cattle in a herd don't get infected during a contagious disease outbreak? Is genetics a major component of the animal health puzzle?

Importance of animal health

Advancing the health and welfare of Irish dairy and beef cattle provides an opportunity to capitalise on increased productivity, while also taking cognisance of the responsibility of cattle production to be environmentally sustainable and socially acceptable. Strategies available for the control of cattle diseases in Ireland consist of herd management and biosecurity protocols, including vaccination and national eradication programmes. Antibiotic and anthelmintic treatments are used as mainstay treatments for bacterial and parasitic infections, respectively. Despite this, the persistently high prevalence of many diseases on farm reduces animal performance and farm viability. Furthermore, the incorrect usage of antibiotics and anthelmintic treatments is contributing to antimicrobial and anthelmintic resistance. Therefore, sustainable and cost-effective strategies to improve animal health status warrant investigation. Animal breeding is one such potential strategy.

Breeding as a strategy to improve health

Breeding programmes have historically exploited the vast quantity of performance data available to achieve rapid on-farm improvements. Approximately half of the observed on-farm gains in reproductive and performance metrics in Irish cattle are attributable to genetic improvement. The same genetic advancements in animal health have not materialised. Lack of

genetic differences among cattle (i.e., genetic variability) is unlikely to be the underlying reason, but the lack of data to decipher genetically divergent animals for health has hampered progress. Nonetheless, international pressure to improve overall cattle health and well-being has led to the generation of many health datasets at research centre and national level. These datasets provide a rich opportunity to explore the extent of inter-animal genetic variability for health status. Analysis of these datasets can quantify the genetic variation for health traits and also the potential gains achievable from including health characteristics in national breeding goals.

Obtaining health data

In 2015, the HealthyGenes project (funded by the Research Stimulus Fund) was launched to address the paucity of available health records in cattle. That project aspired to generate a large database of animal records for a range of diseases including hoof health, body condition score, locomotion, infectious bovine rhinotracheitis (IBR), Johne's disease, liver fluke, *Neospora caninum* and stomach worms on over 10,000 dairy cows. Additionally, tuberculosis (TB) test results from the national TB eradication programme, liver fluke data from the Beef HealthCheck programme on slaughtered animals, and farmer-recorded details of incidences of mastitis and lameness, were available.

Table 1: Prevalence of TB and liver fluke infection in cows identified as being high or low risk for infection based on estimated genetic merit for susceptibility to TB and liver fluke.

Genetic merit prediction	Cow prevalence	Herd prevalence
TB		
High risk	9%	10%
Low risk	7%	10%
Liver fluke		
High risk	47%	48%
Low risk	41%	45%

Genetic variability exists for animal health

Recent research has revealed that 10% of the inter-animal variability in susceptibility to bovine TB is due to genetic differences among animals. A validation study was subsequently carried out to determine whether or not predicting animal genetic merit for TB susceptibility at birth, using only TB data from its relatives, could accurately predict the likelihood of an animal succumbing to TB. Considering only exposed herds, cattle in the worst 20% for predicted genetic merit for TB, deemed to be 'high risk', were compared to cattle in the best 20% for predicted genetic merit for TB, deemed to be 'low risk'. Following these animals throughout their life, 9% of the high-risk animals succumbed to TB versus 7% of the low-risk animals (Table 1). Therefore, predicting the genetic merit of cattle for susceptibility to TB infection would empower farmers to select cattle genetically more resistant to TB as candidate parents of the next generation. Such a strategy can complement the national TB eradication scheme. Similar conclusions are evident for Johne's disease, where up to 15% of the inter-animal variability in serological response is due to transmittable genetic effects.

Large variability in the prevalence of IBR existed among progeny of different sires. The progeny of some sires only had a 5% prevalence of IBR, while the progeny of other sires had a 90% prevalence, despite animals residing in common herds and being of similar age (Figure 1). Additionally, breeding for IBR resistance has been shown to have a favourable impact on genetic merit for both fertility and mortality in cattle. If more routine access to IBR (and other health data) becomes available through national programmes, the incidence of such diseases could be reduced through breeding, concurrent with traditional schemes.

Using data on livers examined by veterinarians at slaughter, significant genetic variation between cattle for liver fluke infection was detected. Although liver fluke infection was only 1% heritable, large exploitable genetic variation existed among the 95,522 animals analysed. Estimates of genetic merit for

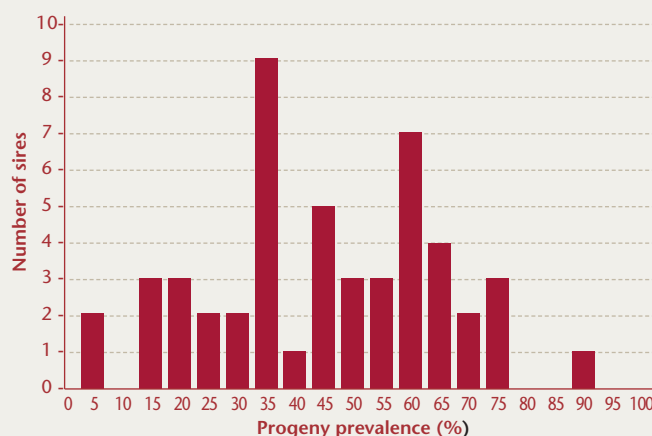


FIGURE 1: Prevalence of positive blood tests for IBR in female progeny of sires with ≥25 daughters in ≥5 herds.

susceptibility to liver fluke infection were derived for animals at birth and were followed throughout their life. A six-percentage unit difference in the prevalence of liver fluke damage existed between cows predicted to be genetically high risk versus those predicted to be genetically low risk (Table 1). Therefore, genetic evaluations are a useful tool to breed cattle that are less susceptible to liver fluke, which will complement current control strategies.

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