

Breeding for reduced liver fluke infection



It is now possible to identify cattle that are less likely to be diagnosed with liver fluke infection at slaughter. This is because there are genetic differences among cattle in their ability to resist liver fluke infection. Breeding values for resistance to liver fluke will be available from January 2019 on www.icbf.com

Importance of liver fluke

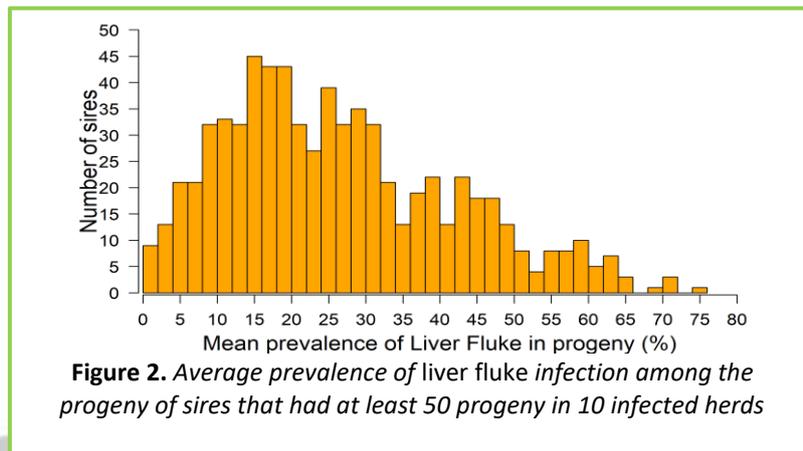
Liver fluke is a widespread problem. One in every 5 cattle slaughtered in Ireland are diagnosed with liver fluke infection (Figure 1). Almost all dairy and beef herds are at risk of liver fluke infection. If properly used, anthelmintic treatments can control liver fluke, but they do have limitations in dairy herds because of the associated milk withdrawal. In addition, anthelmintic treatments are often incorrectly used thus, their usage can contribute to anthelmintic resistance.



Figure 1. Liver diagnosed with liver fluke at slaughter (Source: AHI)

Breeding is complementary to traditional control strategies

It is often believed that environment and management determine whether cattle become infected with liver fluke. However, like many other traits the genetic makeup of cattle also determines their ability to fight off liver fluke infection. Ground breaking Irish research has revealed large variability in the prevalence of liver fluke infection (ranging from 0 to 75%) among the progeny of sires in liver fluke infected herds (Figure 2). Furthermore, 1% of the inter-animal variability in liver fluke infection is controlled by the genetic ability of cattle to resist (i.e., fight off) liver fluke infection. Although the transmissible genetic variability for liver fluke infection is relatively small, it is similar to fertility which has improved through breeding. Up to half of the performance gains that have been achieved in fertility traits over the past 20 years have been due to genetic improvement, despite the low heritability of fertility traits. The benefit of breeding is that it is permanent and cumulative. Therefore, animal breeding is a sustainable way to reduce the prevalence of liver fluke in herds which will compliment traditional control strategies.



Disentangling genetics from environment

One of the main challenges and components of genetic evaluations for any trait, especially disease traits, is disentangling genetics from environmental effects. For the genetic evaluation of liver fluke, strict criteria are used to maximise the likelihood that only animals exposed to the parasite are considered in the genetic evaluation. In brief, only liver fluke results from cattle that resided with herd-mates that were diagnosed with liver fluke infection are included in the genetic evaluation for liver fluke. Like all other traits, the genetic ability of cattle to resist liver fluke infection is compared to their herd-mates, ensuring comparisons are made between cattle with a similar likelihood of exposure to the parasite as well as management protocols (e.g., grazing group, age).

Did you know?
Livers diagnosed with liver fluke cannot be used for human consumption, resulting in an economic loss to the industry

Understanding breeding values for resistance to liver fluke

Each animal's breeding value for resistance to liver fluke is expressed as the predicted prevalence of liver fluke in that animal's progeny. Therefore, lower breeding values, which mean fewer progeny are expected to be diagnosed with liver fluke, are more desirable. For example, a bull with a breeding value of 10% for resistance to liver fluke is predicted to produce progeny where, on average, 1 in every 10 of his progeny will be diagnosed with liver fluke infection.

Does breeding for resistance to liver fluke really work?

Yes. Cattle with lower breeding values for resistance to liver fluke have are likely to be diagnosed with liver fluke infection at slaughter compared to their herd-mates which have higher breeding values for resistance to liver fluke. Using only liver fluke information from their ancestors, breeding values for cattle were predicted prior to slaughter (i.e., the liver fluke result of these cattle was not used in the genetic evaluation). When these cattle were slaughtered, 36% of cows predicted to be in the highest risk group for infection were diagnosed with liver fluke. In comparison, 30% of cows predicted to be in the lowest risk group for infection were diagnosed with liver fluke.

What animals have breeding values for resistance to liver fluke and where can I find it?

For 2019, only AI bulls will have a breeding value for resistance to liver fluke which will initially be published on www.icbf.com in the format of a Microsoft Excel file. Breeding value for resistance to liver fluke will eventually be incorporated into the EBI, Euro-star Indexes, animal profiles, reports etc.

For scientific peer-reviewed publications on the genetics of liver fluke see:

- Twomey, A. J., R. G. Sayers, R. I. Carroll, N. Byrne, E. O. Brien, M. L. Doherty, J. C. McClure, D. A. Graham, and D. P. Berry. 2016. Genetic parameters for both a liver damage phenotype caused by *Fasciola hepatica* and antibody response to *Fasciola hepatica* phenotype in dairy and beef cattle. *Journal of Animal Science*. 94(10): 4109-4119. <https://doi.org/10.2527/jas.2016-0621>
- Twomey, A. J., R.I. Carroll, M. L. Doherty, N. Byrne, D. A. Graham, R. G. Sayers, A. Blom, and D. P. Berry. 2018. Genetic correlations between endo-parasite phenotypes and economically important traits in dairy and beef cattle. *Journal of Animal Science*. 96(2):407-421. <https://doi.org/10.1093/jas/sky008>
- Twomey, A. J., D. A. Graham, M. L. Doherty, A. Blom, and D. P. Berry. 2018. Little genetic variability in resilience among cattle exists for a range of performance traits across herds in Ireland differing in *Fasciola hepatica* prevalence. *Journal of Animal Science*. 96(6): 2099-2112. <https://doi.org/10.1093/jas/sky108>