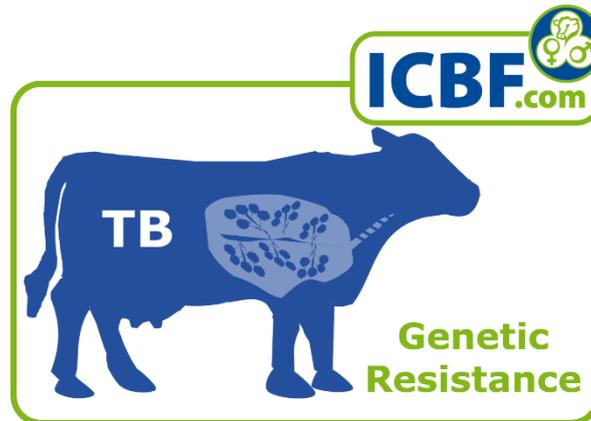


## Identify cattle at high risk of being diagnosed with TB before they enter your herd



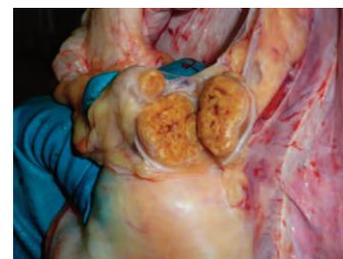
**New research has revealed that some cattle are more likely to be diagnosed with TB than others due to their genetic makeup. Protect your herd by using breeding values for resistance to TB which will be available from January 2019 on [www.icbf.com](http://www.icbf.com)**

### **What is bovine Tuberculosis and why does it need to be eradicated?**

Bovine TB is an infectious disease of cattle that can elicit disease in other animals and humans. Clinical signs of TB in cattle are rarely observed in Ireland due to the rigorous surveillance and culling protocols associated with the TB eradication program. Nevertheless, the annual operational costs (€84 million in 2017) as well as other costs to the farmer (e.g., labour) associated with the TB eradication program in Ireland are extensive. Nonetheless, Ireland needs to eradicate bovine TB to attain a high health status in humans and cattle as well as to maintain access to export markets.

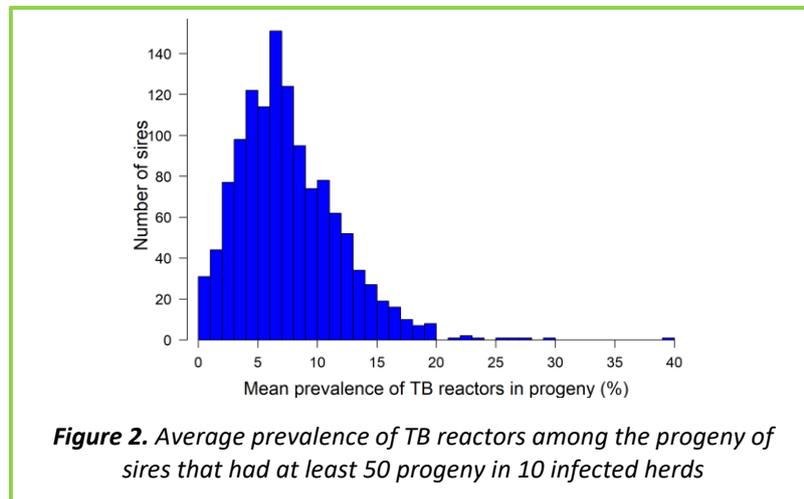
### **Alternative strategies are required to hasten the eradication of bovine TB**

Even though the bovine TB eradication program has been operational in Ireland for nearly 70 years TB remains prominent in Ireland; 4.89% of cattle herds were infected with TB in 2017 and 17,266 reactor cattle were removed (Figure 1). Therefore, it is timely that an alternative strategy be explored to complement the existing TB eradication program and hasten the eradication of bovine TB. Genetic selection is one such complementary strategy. Recent research by Teagasc and ICBF, in conjunction with the DAFM and UCD, have identified that certain family lines of cattle tend to have a higher prevalence of TB reactors than other cattle. For example, among beef and dairy AI bulls that sired many progeny across multiple TB infected herds



**Figure 1.** Suspect bovine TB lesion  
(Source: DAFM)

(i.e.,  $\geq 50$  progeny in  $\geq 10$  TB infected herds) there was much variation in the prevalence of TB reactors in their progeny. Bulls were used in areas considered to be TB blackspots as well as areas with a lower TB prevalence. For some bulls that had many progeny in TB infected herds, none of their progeny became TB reactors while other bulls produced progeny (that were also in the same TB infected herds) where 4 out of every 10 progeny were diagnosed as TB reactors (Figure 2).



### Quantifying the contribution of genetics to bovine TB prevalence

It is well acknowledged that both environmental (including wildlife interactions) and herd management factors influence whether cattle become TB reactors and subsequently, whether a herd has a TB-breakdown. Until now it has not been considered that genetic differences among cattle may influence their ability to fight off TB infection.

**Did you know?**  
12% of the differences observed in the prevalence of TB infection among cattle are controlled by transmissible genetic effects

Nonetheless, innovative Irish research has revealed that 12% of the variability in TB infection is controlled by the animal's genetic ability to fight off TB infection (i.e., resistance). The benefit of using animal breeding to complement the existing eradication program for TB is that breeding is permanent and cumulative.

### Strict criteria ensure only cattle exposed to bovine TB inform genetic evaluations

For the genetic evaluation of resistance to TB, strict criteria are used to maximise the likelihood that only cattle exposed to the bovine TB causing bacterium are used to inform the genetic evaluation. Only bovine TB results (i.e., whole-herd results and post-mortem results) from cattle that resided with herd-mates diagnosed with TB infection are included in the genetic evaluation. Like all other traits, the genetic ability of cattle to resist TB infection is compared to their herd-mates, thus ensuring comparisons are made between cattle with a similar likelihood of exposure to the bovine TB causing bacterium as well as management protocols (e.g., grazing group, age).

For example, among a herd of 100 dairy cows where 2 cows become TB reactors, the genetic evaluation compares the 2 TB reactors with the other 98 non-infected cows; the genetic evaluation also accounts for differences in the age of cows. Test results from other management groups in the herd (e.g., calves, weanlings) are not used to inform the genetic evaluation if no animal in that management group was infected with bovine TB. That said, breeding values are predicted for all cattle in that herd (e.g., the calves and weanlings that were deemed not exposed to the bovine TB causing bacterium) and cattle in other herds as an indicator of their level of resistance to bovine TB should those cattle ever become exposed to the bovine TB causing bacterium in the future. It is because of the genetic relationships among cattle in TB infected management groups with other cattle that breeding values can be generated for all cattle, irrespective of whether they have been exposed to the bovine TB causing bacterium.

### **Understanding breeding values for resistance to TB**

Each animal's breeding value for resistance to TB is expressed as the predicted prevalence of TB in that animal's progeny. Therefore, lower breeding values, which mean that fewer progeny are expected to be diagnosed with TB, are more desirable. For example, a bull with a breeding value of 10% for resistance to TB is predicted to produce progeny where, on average, 1 in every 10 of his progeny will be diagnosed as a TB reactor, either during a whole-herd test or at slaughter.

### **Breeding for resistance to TB can prevent your herd from a TB-breakdown**

Cattle with lower breeding values for resistance to TB are less likely to be diagnosed with TB during their lifetime compared to their herd-mates which have higher breeding values for resistance to TB. Using only TB information from their ancestors, breeding values for cattle in herds undergoing a TB-breakdown were predicted at birth (i.e., TB results of these cattle was not used in the genetic evaluation). When the TB test results of these cattle were confirmed, the number of TB reactors was 26% higher in cattle with the worst breeding values for TB resistance compared to cattle in the same herds with the best breeding values for TB resistance. The implications of preventing just one TB infection could avert a subsequent 1.5 to 4.9 secondary TB infections which arise from cattle-to-cattle transmission of TB. Therefore, breeding strategies can play a fundamental role in the acceleration of the eradication of TB without having any major negative ramifications on other traits.

### **Achieving the most profitable and healthy herd**

To achieve the most profitable herd that is also more resistant to TB select cows and bulls for breeding that have the highest overall index (i.e., EBI, Replacement Index, or Terminal Index) with the lowest breeding value (i.e., lowest predicted prevalence) for resistance to TB.

**What animals have breeding values for resistance to TB and where can I find it?**

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

**For recent scientific peer-reviewed publications on the genetics of bovine TB see:**

- Richardson, I. W., D. G. Bradley, I. M. Higgins, S. J. More, J. McClure, and D. P. Berry. 2014. Variance components for susceptibility to *Mycobacterium bovis* infection in dairy and beef cattle. *Genetics Selection Evolution*. 46:77.  
<https://doi.org/10.1186/s12711-014-0077-1>
- Ring, S. C., D. C. Purfield, M. Good, P. Breslin, E. Ryan, A. Blom, R. D. Evans, M. L. Doherty, D. G. Bradley, and D. P. Berry. 2019 Variance components for Bovine Tuberculosis Infection and Multi-Breed Genome Wide Association Analysis Using Imputed Whole Genome Sequence Data. *PLoS ONE*. Under Review.