

Advancements in genomic evaluations

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Summary

- Genomic selection uses DNA information to help predict the future performance of an animal and its progeny.
- To minimise the risk associated with using genomic bulls, a bull team appropriate for the herd size should be used.

Introduction

Genomics is the study of an individual's DNA. All genes are composed of DNA, and it is the variation within the DNA that makes cows different. Therefore, knowing the DNA of a new-born calf, and how this DNA affects performance, enables prediction of how well that animal and its future progeny will perform. This is the basis of genomic selection, which incorporates DNA information into national genetic evaluations to more accurately identify the genetically superior candidate parents of the next generation.

How does it work?

The first step in genomic selection is to establish a reference population. The reference population is a large genotyped population of animals with accurate performance information such as milk yield or fertility. The associations between the DNA and performance measures are then derived from this population. Several thousand animals are required to form a good reference population; presently there are over 8,000 informative animals within the Irish Holstein-Friesian reference population. Increasing the size of the reference population is essential to ensure genomic prediction estimates are accurate. The average reliability of genomic proofs of young animals is now 63%. A recent validation exercise revealed the accuracy of genomic evaluations is 16%-35% more accurate than evaluations based solely on parental average. New research clearly shows that there is a further benefit if genotyped cows are also included in the reference population; the accuracy improves a further 5–10% over just using information on sires (Table 1).

Table 1. Accuracy of predictions for now proven bulls based on parent average, genomic evaluations based on just a sire reference population or also including cows

Trait	Parent average	Genomic evaluations — sire reference population	Genomic evaluations — sire+cow reference population
Milk	0.55	0.64	0.71
Fat	0.44	0.59	0.65
Protein	0.48	0.65	0.68

Value of genotyping females in the herd

The current cost of genotyping all female calves in a herd is €22/head (incl. VAT). This is considerably cheaper than overseas, where genotyping costs range from €31 in Australia to €90 in Canada. The cost of genotyping female dairy calves can be recouped through better selection of herd replacements. This is illustrated in the Figure 1, where the breakeven genotyping cost at a 21% replacement rate assuming 80% of females genotyped

are retained is €49, more than double the actual cost. For example, a herd that keeps 80% of heifer calves as replacements and has a replacement rate of 21% has an expected net benefit of genotyping of €33 per heifer retained. Genomic information can also be used to confirm parentage, identify lethal/major genes, estimate inbreeding and predict the breed composition of an animal.

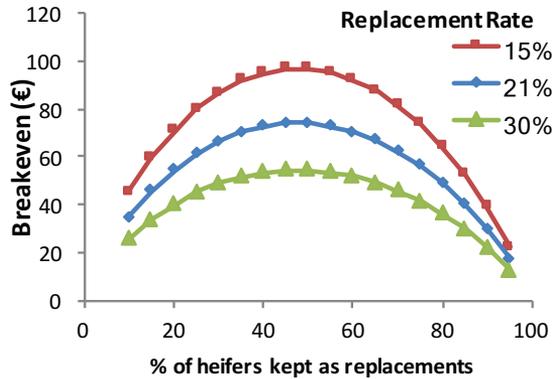


Figure 1. The breakeven cost of genotyping females for different replacement rates

Minimising risk

Despite the recent increases in reliability with genomic selection, it is important to acknowledge that the EBI of an individual animal can still change over time as more information accumulates. To minimise the potential risk of using genomically selected bulls, a bull team should be used with the minimum team size being dependent on the herd size (Table 2); this achieves a bull team reliability of 95%. For example in a 100 cow herd, equal usage of eight unrelated genomic sires is recommended to mitigate proof fluctuation. While using daughter proven bulls instead of genomic bulls can reduce risk on an individual bull level, it reduces genetic gain. This was seen when comparing seven high EBI genomic bulls and seven high EBI daughter proven bulls from the 2011 active bull lists with their 2017 EBI. Results showed that, on average, the team of seven genomic bulls were €52 ahead of the daughter proven bull team in 2011 to 2017.

Herd Size (Incl. heifers)	Recommended minimum number of unrelated bulls
51–100	7
101–150	8
151–200	10
201–250	11
251–300	12
301–400	14

Conclusions

Genomic selection is accelerating the rate of genetic gain in EBI through the more accurate identification of genetically elite males and females. It is, however, important to minimise risk associated with genomic selection by using large bull teams.