# An evaluation of applying genomic information to the females in a dairy herd



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# Introduction

Progeny testing has been the foundation for the genetic improvement of dairy cattle for over half a century and in combination with the widespread use of Artificial Insemination (AI) has led to rapid genetic gains. However, progeny testing results in a long generation interval and is ineffective at selecting for difficult and expensive traits to measure, such as feed efficiency (Weigel *et al.*, 2015).

Genomic evaluation compares the genetic-make up of a population of dairy cows with each animals future performance. This identifies areas of the DNA which are linked with improved traits, so any dairy cow's DNA can then be compared to this information to provide an estimate of its future performance and traits (Thomasen *et al.*, 2012).

The rate of genetic gain is determined by the breeders equation:

 $\frac{Genetic \ Progress}{Year} = \frac{Accuracy * Selection \ Intensity * Genetic \ Variation}{Generation \ Interval}$ (Willis, 1998)

Assuming that genetic variation is constant, genomic selection increases the accuracy of selection compared to parent average, increases the selection intensity through screening a wider range of animals and reduces the generation interval by removing the need for progeny testing, leading to greater genetic gain.

As the cost of genomic testing reduces, with a low density evaluation costing £32 in the UK (NMR, 2014), applying genomic technology to improve the selection of females in the dairy herd becomes more cost effective. The aim of this poster is to demonstrate the potential of genomic technology for the females in a dairy herd.

# Do genomic traits correlate with future performance?

It is important to demonstrate that genomic predictions are an accurate representation of future performance, if farmers are to invest in genotyping animals.

Figure 1 demonstrates the relationship between two different selection methods for PTA Milk on subsequent performance.



For example, if the top 75% of heifers are retained, there is a 107.5 kg difference in first lactation yield between heifers selected by sire's PTA milk and genomic PTA milk. If this gain in yield is replicated throughout the cows lifetime, the September 2015 average margin over purchased feed cost of 17.15ppl (AHDB Dairy, 2015) is applied and the cost of a genomic evaluation is £32 (NMR, 2014), the increased profitability from each animal is £27.

In practice the economic gain would be higher as the increased genetic gain would improve future generations. The trait or index by which the animals are selected will increase profitability depending on their individual effects. For example, a herd with poor fertility would see greater benefit from selecting for high genomic PTA Daughter Pregnancy Rate (DPR), than a herd with excellent fertility. Genomic evaluations improve the reliability of selection for traits with low heritability, such as fertility and lameness traits. Figure 2 compares days open in the first lactation compared with heifers sorted by sire's PTA DPR and genomic PTA DPR.



<sup>(</sup>Source: Weigel et al., 2012)

Figure 2: Average days open in first lactation for 240 Holstein cows in the Allenstein Dairy Herd at UW-Madison, according to quartile for genomic PTA for daughter pregnancy rate at 12 months of age and quartile for sire's current PTA for daughter pregnancy rate

Heritability is the proportion of the phenotype which is attributed to the genetics of the animal (Willis, 1998). The low heritability of daughter pregnancy rate (h<sup>2</sup>=0.04; VanRaden *et al.*, 2009) results in no strong correlation between sire's PTA DPR and first lactation days open. However, there is a clear relationship with genomic PTA DPR. This suggests that genomic evaluations provide more accurate predictions of future performance for low heritability traits than traditional methods such are PA and sire PTA.

# How do I collect samples for genomic evaluation?

There is a wide variety of DNA sampling methods suitable for genomic evaluation, including blood, hair, semen and ear punch. Blood sampling may not be suitable for twins (Wiggans, 2011). The pros and cons for each method are described in Table 1.

(Source: Weigel et al., 2015)

Figure 1: Average first lactation ME 305-day milk yield for 411 Holstein cows in the Allenstein Dairy Herd at UW-Madison, according to quartile for genomic PTA milk at 12 months of age and quartile for sire's current PTA for milk yield.

Figure 1 identifies that sire PTA does effectively sort heifers for PTA milk, however genomic predictions are much more accurate. This is demonstrated by a difference of 4,801 pounds and 2,366 pounds between the top and bottom quartiles for genomic PTA milk and sire's PTA milk respectively.

Correct sampling techniques for hair, blood and ear punch have been described by ZoetisGenetics (2014), and can be viewed by scanning the QR code below. Using the correct procedures will maximise the chance of collecting a viable sample for genomic evaluation.

Table 1 identifies the positive and negative aspects of each method of DNA sampling. It can be concluded that hair sampling is the optimal method. NMR (2014), only accept hair samples for their genomic evaluation service.



#### Table 1: Positives and negatives of each DNA sampling method

Method of Sampling	Positives	Negatives
Blood	May be taking blood samples for other diagnostic tests	Requires veterinary assistance Not suitable for twins
Hair	No additional equipment required Easy and quick to sample	Requires 20-25 hairs to ensure laboratory can collect reliable sample
Semen	Historical data available, frozen semen from deceased bulls ensure samples can still be taken	Non-applicable for females
Ear punch	Easy and quick sampling method Can be conducted when ear tagging calves	Requires purchase of Tissue Sampling Unit, or Tissue Sampling Ear Tags

(Source: Wiggans, 2011; ZoetisGenetics, 2014; Allflex, 2015)

# How can genomic evaluations be applied to a herd?

#### Selecting Replacements

The widespread use of sexed semen and reduced culling rates has led to an excess of females on many farms. Genomic testing has the potential to sort replacement heifers to a higher level of accuracy than traditional methods such as Parent Average and sire's PTA. Inferior animals can then be removed as parents of the next generation (Weigel *et al.*, 2012) and ensure the most profitable animals are kept.

The greater the selection intensity, the greater the pro-rata genotyping costs if all animals are genotyped. The greater the amount of pedigree information, the lower the economic return as the improvement in reliability is smaller. Genotyping all animals is more efficient when many selection decisions are being made (Weigel *et al.*, 2012).

A herd may employ a strategy of identifying the top 10% of heifers for embryo transfer, the 10<sup>th</sup> to 50<sup>th</sup> percentile for sexed semen insemination, the 50<sup>th</sup> to 75<sup>th</sup> percentile for conventional semen and to remove the genetics of the 75<sup>th</sup> to 100<sup>th</sup> percentile. The method of separating heifers depends on the farm, but would likely be an index, such as £PLI or NM\$. In this strategy, four selections are made, therefore the benefits from improved accuracy are multiplied.

#### Marketing pedigree heifers

Genomic selection requires no previous pedigree information, so presents the opportunity to identify valuable females in herds which previously had no experience in pedigree breeding.

A heifer that has been genomically tested has breeding values with similar reliability to a cow with three to four lactations and superior information regarding low heritability traits such as fertility and lameness (Pritchard *et al.*, 2013). This will lead to a premium for genomically tested heifers. Elite heifers should be preselected, as poor genomic evaluations may lead to a lower sale price.

#### Parentage verification



Identifying animals through genomic evaluation will ensure that carrier females are not bred with a carrier bull. However, selection against carrier sires will only marginally improve future fertility. A carrier bull will reduce average conception rate by carrier frequency divided by 4 (VanRaden *et al.*, 2011). For example, if average conception rate is 40% and the carrier frequency is 4%, the average loss in conception rate is 0.4 percentage points. This is insignificant compared to the variation in conception rate between sires and herds.

# Conclusions

Genomic PTA's have been shown to be an accurate representation of future performance and more reliable than sire PTA or Parent Average. The greatest benefit to be found from genotyping females is to improve the reliability of selection decisions. This will prevent heifers of low genetic value from entering the herd. Genomic evaluations can also be used for the marketing of pedigree heifers, parentage verification, improving the accuracy of mating plans and avoiding mating carriers of deleterious recessive alleles.

It is likely many herds would benefit from genotyping some, or all of the herd. The economic gains increase with the number of decisions the information is used for. Herds should only genotype if they expect to recover the cost of testing, if all heifers enter the herd regardless of genetic value, it is not worthwhile genomic testing.

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The rate of parentage misidentification is estimated at between 11 and 15% (Banos et al., 2001; Weigel et al., 2012; Gelderman et al., 1986). Genomic evaluations automatically verify the paternity of calves, if the dam is genotyped, the maternity of the calf can also be verified (Pryce and Hayes, 2012). This will improve the accuracy of pedigrees and mating plans

#### Mating plans

Inbreeding impacts profitability by affecting fitness and production traits (Smith *et al.*, 1998). Mating plans reduce inbreeding by selecting appropriate matings.

#### Avoiding deleterious recessive alleles

Genomic evaluations test for deleterious recessive alleles as part of the evaluation. DUMPS, BLAD and fertility haplotypes are included in UK evaluations (Holstein UK, 2013). performance of dairy cattle. Journal of Dairy Science, 81, pp.2729-2737.

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