

Genotyping dairy females can improve the reliability of genomic selection for young bulls and heifers and provide farmers with new management tools

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Abstract

To date, genomic selection has been successfully applied to male pathways of selection in dairy breeding schemes. Farmers can already achieve higher annual rates of genetic gain through using genomically tested bulls in their herds. As genotyping costs continue to fall, it will likely become increasingly popular to capture extra value from genotyping females. Genotyping females can 1) improve the reliability of genomic selection (of both bulls and heifers) by increasing the number of animals in the reference population, provided some of the females eventually get records through herd recording; 2) assist in the identification of elite females; 3) identify the best heifers to become herd replacements; 4) provide better prediction of the true value of an animal's genetics, that may correlate to sale price; 5) achieve certainty of parentage of individual cows; 6) avoid inbreeding through the use of genomic assisted mating plans, where relationships between animals are quantified at the genomic level and 7) avoid genetic defects that could arise from mating cows to bulls that are known carriers of genetic diseases that are the result of a single lethal mutation.

Introduction

Genomic selection refers to selection decisions based on genomic breeding values (GEBV). The GEBV are calculated as the sum of the effects of dense genetic markers that are approximately equally spaced across the entire genome, thereby potentially capturing most of the quantitative trait loci (QTL) that contribute to genetic variation in a trait. GEBVs are now being used to identify and market the best bulls in many

countries around the World (Pryce and Daetwyler, 2012). The main advantage in using genomic breeding values is a reduction in generation interval, which can lead to double the rate of genetic gain than conventional progeny-testing systems (Schaeffer, 2006). The benefit of genotyping females has been assessed in terms of their impact on rate of genetic gain through increasing the reliability of selection in female selection pathways (e.g. McHugh et al., 2011). However, there are several other reasons why females should be genotyped. One is to improve and maintain the reliability of genomic prediction and the other is for farm management purposes. As the cost of genotyping continues to fall, we may start to see entire herds becoming genotyped rather than just elite females or partial herds.

The contribution of females to the reference population

One risk of replacing progeny-testing with breeding schemes that screen large numbers of young bulls and only select a small number of these for widespread use, is that fewer bulls will be added to the reference population on an annual basis than in the past. This would decrease the reliability of genomic prediction as the distance between the current dairy population and the majority of animals in the reference population increases (Lillehammer et al. 2010). Countries with small populations may be more affected by this issue than larger populations (McHugh et al. 2011). Considerable effort has gone into increasing the size of current reference populations and this effort must continue to ensure reference populations remain relevant to selection candidates. One of the strategies used to increase reference populations is to share genotypes.

Genotyping of cows is another way in which a larger reference population can be achieved. In August 2010, the only country including females in their reference population was the USA (Wiggans et al., 2011). However, genotyped females need to be incorporated cautiously, as there could be a risk that some of them are preferentially treated and therefore their phenotypes could be biased. Instead, directly targeting a group of randomly selected cows may be more beneficial. In Australia, the size of the male reference population is around 3000 Holstein males, so adding genotyped females to the reference population could improve the reliability of breeding values.

Recently, the Australian Dairy Futures Cooperative Research Centre's 10,000 Holstein Cow Genomes project and Jer-nomics project embarked on collecting DNA samples and genotyping 10,000 Holstein and 4000 Jersey cows (from commercial herds). This information has recently (April, 2012) become part of the Australian reference population. This has led to a 4-8% improvement in the reliability of breeding values depending on trait. Table 1 shows the increase in reliability of genomic breeding values for 437 young Holstein bulls achieved by adding close to 10,000 cows to the reference population.

Table 1. The reliability of genomic breeding values of 437 young bulls when bulls only were included in the reference population and when cows were also included

Trait	Bulls only	Bulls + cows	Change
Protein	54	61	8
Fat	54	61	8
Milk	54	61	8
Survival	30	36	7
Fertility	33	37	4
Somatic cell count	43	51	7
Milking speed	49	53	4
Temperament	49	53	4
Likability	49	53	4
Mammary system	39	44	5
Overall type	38	44	6
Udder depth	38	43	5
Udder texture	33	38	5

Having the entire sequences of bulls may help to increase the accuracy further. The idea behind sequencing key ancestors of cattle breeds, is that we will have the causative mutations in the data set, i.e. we will be able to capture more of the genetic variation in a trait. The 1000 bull genomes project has started with an aim to provide researchers with a large database for genomic prediction and genome wide association studies in all cattle breeds (<http://1000bullgenomes.com/>).

In addition to their contribution to the reference population, there are a number of reasons why farmers might consider genotyping females to improve their profitability. These will be discussed in the remainder of this paper.

Improving profitability through genotyping females

Low density SNP arrays have been developed (e.g. Boichard et al., 2012) and are now available commercially at a cheaper price than the 50K SNP panel. The LD array costs €9 in Ireland (Donagh Berry, personal communication) and is the SNP array most farmers will use to genotype their cows.

Reliabilities of greater than 60% are now being achieved for many traits, this is equivalent to a cow with 3-4 lactation records and much higher than a heifer's reliability without genomic selection (which is approximately 30% depending on trait). An approximation of reliability can be calculated as a function of the number of records and heritability of a trait (Cameron, 1997) as: $n/(n+\lambda)$, where n is the number of records and λ is $(1-h^2)/h^2$, where h^2 is the heritability of the trait. Having genomic breeding values on heifers obviously aids in identifying elite females to become dams of the next generation and securing higher prices for exceptional sale heifers. Genotyping young heifers will help to alleviate concerns over preferential treatment, as the genomic part of the breeding value should be less biased than the part derived from pedigree relationships. This could either see positive implications for pedigree sale prices of genotyped heifers/embryos, or simply that genotyping of sale heifers becomes the norm.

A logical way of profiting from genotyping females is to select female replacements on the basis of the genotype results. Obviously a major limitation in dairy cattle breeding is the number of replacements that are available – deteriorating levels in herd fertility means that in most cases, there are only sufficient replacements to sustain the herd. However, advances in reproductive technologies, such as sexed semen and embryo transfer, means that there are opportunities to select in the cow to breed cow pathway.

For selecting replacement heifers using EBI, assuming a standard deviation of EBI of €62 (Donagh Berry personal communication) and genotyping costs are €29/cow, the net profit of genotyping 40 heifers to select the top 20 as replacements (per 100 cows) would be worth €46/cow per cow discounted over four lactation. This is after spreading the cost of genotyping over the replacements kept. However, using parent average estimated breeding value information is free and can already be used to select replacement heifers. If genotyping is used solely as a tool to select replacements, the cost would need to be €15/cow before it becomes economically worthwhile. This calculation excludes rearing and sale costs, as it is assumed that there is no deliberate rearing of extra heifers specifically to sell i.e the benefits are just considered to be the average merit of the heifers retained versus those sold. Currently, there is a lively export market of heifers from Australia to China. The net profit (i.e. sale minus rearing costs) for in-calf heifers is approximately AU\$500 (€390), making it attractive to rear and sell extra heifers for the export market. If extra heifers are reared specifically for selling, genotyping may make it easier to decide which animals to sell or keep.

Extra value from genotyping can also be captured by using other strategies that are described in the rest of this paper.

Avoiding inbreeding

Pryce et al. (2011) showed that controlling inbreeding using a genomic relationship matrix could reduce the rate of inbreeding by 1 to 2% with very little loss in genetic gain in profit, from controlling inbreeding. However, pedigree did a reasonably good job as well, reducing inbreeding by around half the amount of genomically controlled inbreeding when both pedigree and genomically controlled inbreeding were assessed

on the genomic scale. As pedigree is “free”, the value of controlling inbreeding using genomic relationships rather than pedigree relationships is small and by itself does not justify genotyping females. A 1% reduction of inbreeding, valued at AU\$5 per annum or AU\$14.20 discounted over four lactations, or (€1.09), can be achieved.

For farmers using large groups of genomically tested sires, it may be difficult to manually work out which cow to mate to which bull i.e. avoiding matings between relatives. This could mean that computerised mating plans become more common. However, it seems likely that, in the short-term, only part of the herd is likely to be genotyped. One strategy is to replace part of the pedigree relationship matrix with genomic relationships (e.g. Legarra et al. 2009). So pedigree only is used for some of the relationships and genomic relationships are used between bulls and cows where available.

Parentage verification

Genomic tools to verify the paternity of calves are now available with 100% certainty when more than 300 SNPs are genotyped on an animal and its sire (Hayes, 2011). A calf can also be assigned to its dam provided the dam has also been genotyped. Using genotyping to resolve parentage may be particularly useful for herds with large numbers of calves being born over relatively short periods, where it is often logistically not possible to work out the sire and dam of a calf. The value of this is likely to be in reducing stress and reliance on staff around calving when a lot of calves are born over a short-period. Currently, Holstein Australia uses a service provided by the University of Queensland to verify parentage. The procedure uses 22 microsatellites and costs \$36.30 (Matthew Shaffer, personal communication, Holstein Australia, 2011). As with SNP data, both parents need to have microsatellites for full parentage verification.

A total net profit of €85 per replacement retained (i.e. after including genotyping costs) is possible through 1) selecting replacements 2) pedigree ascertainment and 3) controlling inbreeding. Using genomic information is better than relying on pedigree information for these decisions, although, the advantage is small (€2.90 per replacement). If the cost of genotyping halves to €15, then the benefits become even

more attractive, as we calculate that there is a €30.90/replacement advantage of genotyping over using pedigree information.

Conclusions

The industry is likely to benefit from genotyping unselected females, as the Australian experience has demonstrated a lift of 8% in bull reliabilities from adding a population of 10,000 genotyped cows. As genotyping costs reduce for low density SNP chips, the prospect of using this technology on commercial dairy farms becomes very attractive. This is especially true if genotyping is used for several strategies, such as mating plans to control inbreeding, select the best replacements and parentage verification. The situation is different for farmers raising extra heifers for sale purposes who may realise better sale prices from genotyped high genetic merit heifers.

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