

Effective Use of Genomics in Commercial Dairy Farms

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Introduction

Genomic selection refers to selection decisions based on genomic-estimated breeding values. These genomic breeding values are calculated using genetic markers across the entire genome. This technology has revolutionized dairy cattle breeding. Indeed, genomic selection has the potential to increase genetic gain considerably by reducing generation intervals and increasing selection intensity and selection accuracy. This has transformed dairy cattle breeding programs worldwide because the rate of genetic progress for economically important traits can be approximately doubled using genomics^{1,2}. Not surprising, thousands of animals are genotyped every year, and this genomic information is fully integrated into national genetic evaluations. Genomic testing is intensively used by pedigree breeders to identify the most elite males and females in the populations; this group of elite animals represents the sires and dams of the next generation of young bulls. However, it is important to emphasize that genomic selection also offers great benefits for commercial producers^{3,4}. As such, the main objective of this article was to assess the potential value of genomics to commercial dairy farmers.

Effective Use of Genomics: Sire Selection

Progeny testing has been the basis of genetic selection programs in dairy cattle breeding. It has led to remarkable genetic gains in production traits; e.g., predicted transmitting ability (PTA) values of US Holsteins bulls have increased by 81 lbs. of milk per year over the last three decades. However, it is important to note that progeny testing is a very time-consuming process. For instance, at least 4.5 years are required for collecting semen of a potential elite bull, rearing his offspring, and finally predict his genetic merit based on his offspring's performance. If we decide that the bull is good enough to use in the entire population, then his first sons and daughters will be born when he is about 5.5 years of age. This long generation interval limits the rate of genetic progress. In this context, the use of genomic testing, namely the use of genetic markers across the genome to predict breeding values, allows us to identify and select animals at an early age. This drastic reduction in the generation interval has a very positive impact on the rate of genetic gain.

Dairy sire selection has dramatically changed with the arrival of genomics. Nowadays, dairy farmers have basically two main options when they make sire selection decisions: use proven (progeny-tested) bulls or use young genomic-tested bulls (i.e., young bulls with no progeny that have been evaluated using only their own genomic data). The National Association of Animal Breeders (NAAB) distinguishes these two groups of bulls as the *active* (A) bulls, progeny-tested bulls with performance information in at least 10 daughters, and the young *genomic-tested* (G) bulls, young bulls that have not yet milk-recorded offspring. It is important to remark that the number of young genomic-tested bulls currently in the market far exceeds that of progeny-tested bulls. For instance, of the 2,741 Holstein bulls available in the market in August 2016, 2,172 (79%) were young genomic-tested bulls. Similarly, in Jersey, 403 of the 534 available bulls had G status.

The key concept regarding young genomic-tested dairy bulls is that, on average, these young bulls have greater predicted genetic merit values than the proven bulls. **Figure 1** shows the average PTA value for lifetime net merit (NM\$) for the group of active (A) and genomic (G) Holstein and Jersey bulls marketed to US dairy farmers in August 2016. The difference in the average PTA NM\$ between these groups is remarkable: the net merit of young genomic-tested bulls is \$270 and \$124 greater than for progeny-tested bulls in Holstein and Jersey breeds, respectively. Notably, if we rank the (A + G) bulls based on PTA NM\$ values, and then we consider only the top 100, we find that 98% and 87% of these elite Holstein and Jersey bulls, respectively, are young genomic bulls. It is worth noting that if we consider that the changes achieved through genetic selection are cumulative and permanent, then it is expected that the new generations (e.g., G bulls) have (on average) greater genetic merit than the older generations (e.g., A bulls). Now, in the case of the young genomic-tested dairy bulls, higher genetic values are accompanied by lower reliability values. Indeed, the reliability of PTA NM\$ values of young bulls is 26% and 19% lower than for proven bulls in Holstein and Jersey breeds, respectively (**Figure 1**). This is not surprising considering that the young genomic-tested bulls do not have progeny yet.

The question is how we proceed in this scenario, i.e., we should use young genomic-tested bulls because they have greater PTA values, or instead, we should use proven bulls because they have more reliable PTA estimates. At this point, it is important to remark that sire selection decisions should be always based on PTA values. As such, we should not select or exclude sires based only

on reliability; however, we should use the value of reliability as a guide to decide how intense we want to use a bull. Therefore, when we consider the dilemma young genomic vs. proven dairy bulls, the best strategy is to use a group or team of young genomic-tested bulls. **Table 1** shows how the reliability of the genetic merit of the team (calculated simply as the average genetic merit) increases as we include more young bulls in the team. For instance, if the REL values of individual young genomic-tested bulls is 70%, then REL of the average genetic merit for a team of three young bulls is about 90%, and if we increase the group size to six or even twelve young bulls, we achieve REL values for the group average between 95% and 98%.

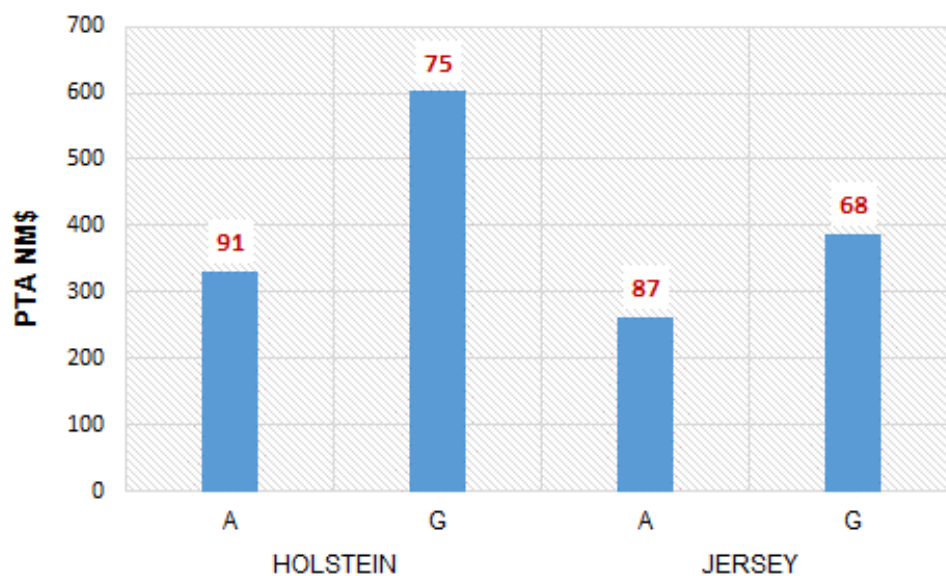


Figure 1. Average *predicted transmitting ability* (PTA) values (in the y-axis) and the corresponding *reliability* (REL) values (above the bars) for *Lifetime Net Merit* (NMS) for active (A) and genomic (G) Holstein and Jersey bulls marketed to US dairy farmers. Based on August 2016 Council on Dairy Cattle Breeding (CDCB) genetic evaluations.

Table 1. Change in the reliability of the group genetic merit (calculated as the average genetic merit of the group) as function of the number of young genomic-tested bulls in the group.

No. of genomic-tested bulls in the group	Reliability of the group genetic merit
1	70
3	90
6	95
12	98

Effective Use of Genomics: Replacement Heifer Selection

The selection of replacement heifers in commercial dairy farms has been traditionally characterized by very low intensity of selection, because in general farmers retain nearly every heifer calf as a future herd replacement. However, recent improvements in herd management have reduced involuntary culling rates and improved reproductive efficiency, which has led to the ability to produce excess heifers. Additionally, the use of sexed semen can also generate a considerable surplus of heifer calves. In this context, the selection of replacement heifers is feasible. The key question here is: how do we select the necessary replacements? In other words, how can we identify superior or inferior heifer calves accurately? The use of genomic testing, namely the use of genetic markers across the genome to predict breeding values, allows us to identify and select heifers at an early age.

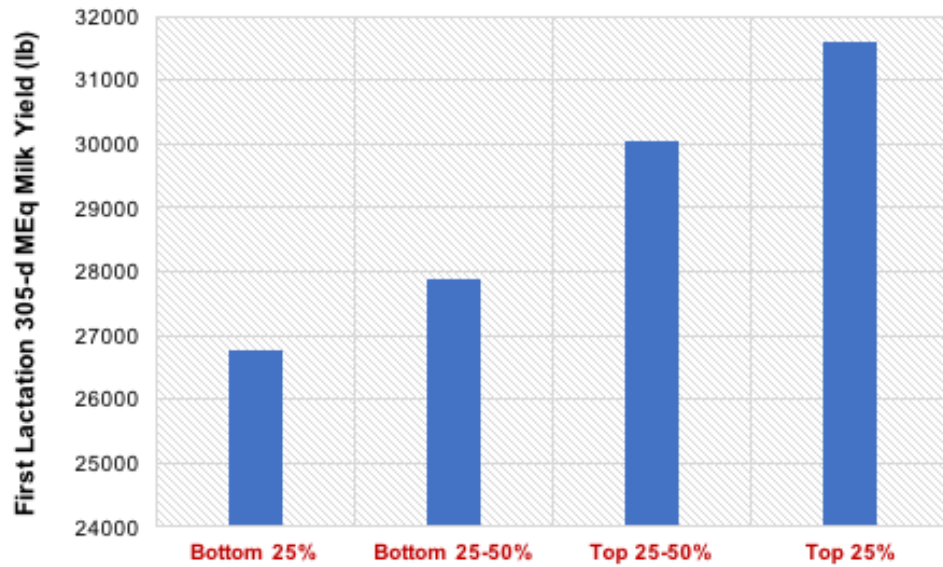
What are the advantages of using genomics for selecting heifer calves? The key point is try to estimate as precisely as possible the genetic merit of a heifer at a young age. In the absence of genomic information, the selection or culling of a given heifer calf is based on the average genetic merit of her parents. The reliability of this information typically ranges from 0 when we do not know the parents to 0.40 if we have access to complete pedigree information. Now, if we use genomic testing, then the reliability of the genomic-predicted genetic merit of the heifer calf ranges from 0.55 to 0.75 depending on the trait of interest and the amount of pedigree data available. Interestingly, this genomic prediction early in life is generally more reliable than the traditional predicted transmitting ability (PTA) estimated using several lactation records on both the cow and her daughters. Therefore, genomic testing allows us to make accurate selection (culling) decisions at an early age; and these decisions are more reliable than those than can be achieved using pedigree information alone.

Probably one of the key points regarding the use of genomics for selecting herd replacements is to demonstrate that the results of the genomic testing are highly correlated with future phenotypic performance. Recently, colleagues at the University of Wisconsin-Madison ⁵ compared early genomic predictions with subsequent production and reproduction performance in the first lactation of Holstein cows (**Figure 2**). Cows were ranked based on their own genomic PTA values (predicted at 12 months of age), and then these alternative quartile rankings (from top 25% to

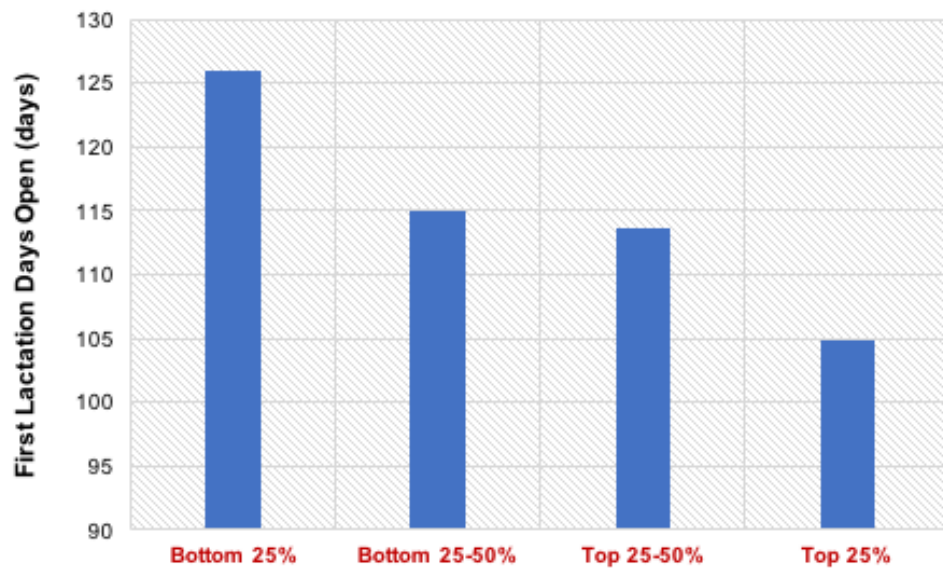
bottom 25%) were compared with the actual phenotypic performance in first lactation. If there is an association between genomic testing and future performance, then we expect that the best heifers in terms of genomic values show greater phenotypic records. Indeed, for milk production, the observed difference between the top and the bottom quartiles was equal to 4,800 lbs. (Top **Figure 2**). For female fertility, the actual difference in days open between those heifers classified as top 25% and those classified as bottom 25% was equal to 21 days (Bottom **Figure 2**). Therefore, these findings show that early genomic predictions (performed on calves or yearling heifers) can be effectively used as predictors of future performance. In other words, genomic testing can be used to make accurate selection decision at a young age.

Genomic information on individual animals can be used to reduce feed costs and improve the genetic level of herd replacements. Indeed, the identification of genetically inferior heifer calves allows early culling of these animals, significantly reducing the cost of rearing replacements. Alternatively, these genetically inferior heifers can be inseminated with beef semen to produce high-value crossbred beef calves. Note that these cows inseminated with beef semen are in fact removed as parents of the next generation. On the other hand, the identification of superior heifers through genomics can be combined with the use of advanced reproductive technologies to rapidly propagate these animals and generate superior replacements. For instance, high-genetic-merit heifers can be used as donors in either an in-vitro fertilization program or an embryo transfer program. Instead, these superior heifers can be inseminated using sexed semen from top sires.

It is worth noting that genotyping replacement heifers has extra benefits other than making proper selection and mating decisions, including parentage verification, controlling inbreeding, and avoiding the spread of genetic disorders through genomic-enhanced matings. Arguably, these benefits add value to genomic testing.



Ranking of Genomic-Predicted Genetic Values (GPTA) for Milk



Ranking of Genomic-Predicted Genetic Values (GPTA) for DPR

Figure 2. Production [305-d mature-equivalent (MEq) milk yield] and reproductive performance (days open) in first lactation according to the ranking of genomic values. The rankings were calculated based on genomic predicted transmitting ability (PTA) values estimated at 12 months of age. [Adapted from Weigel et al., 2015, Western Dairy Management Conference ⁵].

Conclusions

Genomics has revolutionized dairy cattle breeding. Nowadays, young genomic-tested bulls represent the vast majority of semen available in the market. Notably, these genomic bulls have on average greater genetic merit than proven bulls. Therefore, commercial dairy farmers have now a unique opportunity to capture the benefits of genomics selecting superior young genomic-tested bulls. Now, these young bulls have reliability values about 70%, and hence, farmers should manage the risk associated with imprecision in PTA estimates by using a group of young bulls, rather than focusing too heavily on individual animals. Moreover, dairy farmers can use genomic testing to support more accurate selection or culling replacement decisions. It is worth noting that those producers that combine genomic testing with other management decisions, such as early culling to reduce feed cost or the use of advanced reproductive technologies to rapidly propagate the best females in the herd, will obtain the greatest benefits of this technology.

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