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Potential gains in lifetime net merit from genomic testing of cows, heifers, and calves on commercial dairy farms

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ABSTRACT

The objective of this study was to quantify the gains in genetic potential of replacement females that could be achieved by using genomic testing to facilitate selection and culling decisions on commercial dairy farms. Data were simulated for 100 commercial dairy herds, each with 1,850 cows, heifers, and calves. Parameters of the simulation were based on the US Holstein population, and assumed reliabilities of traditional and genomic predictions matched reliabilities of animals that have been genotyped to date. Selection of the top 10, 20, 30, . . ., 90% of animals within each age group was based on parent averages and predicted transmitting abilities with or without genomic testing of all animals or subsets of animals that had been presorted by traditional predictions. Average gains in lifetime net merit breeding value of selected females due to genomic testing, minus prorated costs of genotyping the animals and their unselected contemporaries, ranged from $28 (top 90% selected) to $259 (top 20% selected) for heifer calves with no pedigrees, $14 (top 90% selected) to $121 (top 10% selected) for heifer calves with known sires, and $7 (top 90% selected) to $87 (top 20% selected) for heifer calves with full pedigrees. In most cases, gains in genetic merit of selected heifer calves far exceeded prorated genotyping costs, and gains were greater for animals with missing or incomplete pedigree information. Gains in genetic merit due to genomic testing were smaller for lactating cows that had phenotypic records, and in many cases, these gains barely exceeded or failed to exceed genotyping costs. Strategies based on selective genotyping of the top, middle, or bottom 50% of animals after presorting by traditional parent averages or predicted transmitting abilities were cost effective, particularly when pedigrees or phenotypes were available and a relatively small proportion of animals were to be selected or culled. Based on these results, it appears that routine genotyping of heifer calves or yearling heifers can be a cost-effective strategy for enhancing the genetic level of replacement females on commercial dairy farms. Increasing the accuracy of predicted breeding values for young females with genomic testing might lead to synergies with other management tools and strategies, such as propagating genetically superior females using advanced reproductive technologies or selling excess females that were generated by the use of sex-enhanced semen.

Key words: genomic testing, replacement heifer, genetic selection

INTRODUCTION

Since the introduction of the BovineSNP50 (**50K**) BeadChip by Illumina (San Diego, CA) in late 2007, vast numbers of dairy cattle have been genotyped worldwide, and the resulting genomic information has been fully integrated into national genetic evaluation systems (Hayes et al., 2009; VanRaden et al., 2009). The majority of animals that were genotyped initially were young males and potentially elite females, because the cost of the 50K array often precluded its use for routine genomic testing of cows, heifers, and calves on commercial dairy farms. Recent research has shown that genotypes from a low-density array with approximately 3,000 (**3K**) SNP can be used effectively for imputation of 50K genotypes from an ancestral reference population, and genomic-predicted transmitting abilities (**GPTA**) derived from these imputed genotypes are almost as accurate as 50K predictions for a fraction of the cost (Weigel et al., 2010a,b; Zhang and Druet, 2010; Dassonneville et al., 2011). Illumina introduced a 3K bovine SNP array in 2010, and several for-profit companies and non-profit organizations offer genotyping services to dairy farmers based on this platform.

The availability of less expensive genotyping options, such as the Illumina 3K array, coupled with the development of a bioinformatics infrastructure that allows efficient and almost transparent integration of the resulting genotypes into the national genetic evalu-

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ation system (Wiggans et al., 2011), is a major step in extending the technology of genomics beyond AI companies and pedigree breeders and into the hands of commercial dairy farmers. However, genotyping a large number of cows, heifers, or calves on a commercial farm represents a significant financial investment. Therefore, cost-benefit studies should assess the financial viability of routine genomic testing and identify genotyping strategies that will maximize gains in the accuracy of selection, culling, mating, and management decisions.

The objective of the present study was to evaluate, via simulation, the expected gains in lifetime net merit (**LNM$**) that could be achieved on commercial dairy farms through routine genomic testing of females using a low-density (e.g., 3K) SNP panel, while considering alternative strategies that involve full genotyping or selective genotyping of animals within a given age group.

MATERIALS AND METHODS

Data were simulated to mimic a commercial dairy operation with 1,000 lactating cows, and 100 replicates were carried out. Each herd contained 1,850 total females that were distributed among 8 age groups: 450 heifer calves (<12 mo), 400 yearling heifers (12–24 mo), 350 first-parity cows (24–36 mo), 250 second-parity cows (36–48 mo), 170 third-parity cows (48–60 mo), 120 fourth-parity cows (60–72 mo), 70 fifth-parity cows (72–84 mo), and 40 sixth-parity cows (84–96 mo). Parameters of the population were chosen based on the current population of US Holstein cows, as evaluated by the USDA-ARS Animal Improvement Programs Laboratory (Beltsville, MD), with mean PTA for LNM$ of $45, standard deviation (**SD**) of LNM$ equal to $198, and genetic trend in LNM$ of $28 per year. True transmitting abilities (**TA**) were generated by sampling from a normal distribution with the aforementioned mean and SD. Values for parent average (**PA**), PTA, and GPTA included prediction errors that were drawn from a normal distribution with mean zero and SD equal to the product of the square root of assumed reliability (**REL**) and the genetic SD; assumed REL values are described in the next section. Selection decisions were carried out based on PA, PTA, and GPTA within each age group, so that the potential gains associated with genotyping animals of various ages could be assessed. Whereas TA are typically used to select parents of the next generation, profitability of the current generation is a function of breeding values (**BV**), which reflect animals' genetic contributions to their own phenotypes. Therefore, TA were converted to BV (i.e., multiplied by 2) before computation of the difference between LNM$ of animals that were selected based on GPTA and LNM$ of animals from the same age group that were selected based on traditional PA or PTA. The simulation strategy used in this study, which involved simulation of true and estimated breeding values in a single generation, was simplistic compared with alternative approaches, such as simulation of a base population followed by hundreds of generations of random mating or directional selection (e.g., Casellas and Varona, 2011). However, the objective of the present study was not to predict long-term rates of genetic gain or investigate the effects of selection on allele frequencies and other genetic parameters, but rather to generate breeding values for hypothetical dairy herds in which the utility of genomic information could be evaluated within a single generation.

To facilitate an economic assessment of the costs and benefits of genomic testing, the average gain in BV for LNM$ was compared with the prorated cost of genotyping per selected individual. The prorated cost of genotyping was computed as the current cost of DNA extraction and 3K SNP genotyping ($40) times the proportion of animals tested, divided by the product of the percentage of animals retained after testing and the discounted number of times each animal's genetic superiority would be expressed. We assumed that each female would generate her own replacement, and that her daughter and granddaughter would do the same. We further assumed a generation interval of 4 yr and a discount rate of 5% per year. Therefore, the number of discounted expressions per animal was as follows: $1.00 + 0.5 \times (1.05)^{-4} + 0.25 \times (1.05)^{-8} + 0.125 \times (1.05)^{-12} = 1.65$. As an example, if all animals within a given age group were genotyped and the top 20% were selected, the prorated genotyping cost would be $(\$40 \times 1.0) \times (0.20 \times 1.65)^{-1} = \$121.20$. Alternatively, if the bottom 50% of animals within a given age group were genotyped and the top 90% were selected, the prorated genotyping cost would be $(\$40 \times 0.5) \times (0.90 \times 1.65)^{-1} = \$13.47$. Incorporating contributions to future generations into prorated genotyping costs facilitated simple comparisons of genotyping costs with expected gains in LNM$ in the current generation; such comparisons would have been difficult using an alternative approach such as computing cumulative discounted net returns in LNM$ over a 20-yr planning horizon.

Three classes of animals were considered based on the availability, or lack thereof, of pedigree information: no pedigree, known sire, or full pedigree. Assumed REL values, which are shown in Table 1, were a function of 3 factors: extent of available pedigree information, number of phenotypic records (for lactating cows), and presence or absence of a 3K genotype. Without genomic testing, assumed REL ranged from 0.00 (heifer calves) to 0.27 (sixth-parity cows) for animals with no pedigree information, 0.22 (heifer calves) to 0.48 (sixth-parity cows)