Effective Use of Genomics in Sire Selection and Replacement Heifer Management

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Introduction

For more than half a century, progeny testing has been the foundation of genetic selection programs in dairy cattle, and it has led to rapid genetic gains in traits such as milk production, for which breeding values of bulls and cows have increased by roughly 200 pounds per year. However, progeny testing is expensive and time-consuming due to a long generation interval in cattle, and it is not an effective method for improving traits that are difficult or expensive to measure routinely on commercial dairy farms, such as feed efficiency. Whole genome selection, more commonly known as genomic selection, refers to using information about single nucleotide polymorphisms (SNP) markers in the cattle genome to predict the genetic merit of young animals that have no offspring or performance data at the time selection decisions are made. The information obtained by genomic testing a young heifer or bull is compared with genomic data from a reference population of older animals of the same breed. The Council on Dairy Cattle Breeding (CDCB) provides routine genomic predicted transmitting abilities (PTA) for US dairy cattle, and more than 800,000 dairy bulls, cows, heifers, and calves have been tested to date.

Genome-Tested Young Sires

Virtually every bull offered to US dairy farmers has been chosen based on the results of genomic testing. The National Association of Animal Breeders (NAAB) denotes young genome-tested bulls with no milk-recorded offspring as “G” status (genomic), whereas older bulls that have 10 or more milking daughters in the US are denoted as “A” status (active).

Table 1. Average PTA values and corresponding reliability (REL) values for milk yield, daughter pregnancy rate (DPR), and Lifetime Net Merit (NM$) for active and genomic bulls marketed to US dairy farmers, based on December 2014 CDCB genetic evaluations.

Breed	**Status**	**No.**	**Milk (lb)**		**DPR (%)**		**Net Merit ($)**	
			PTA	**REL**	**PTA**	**REL**	**PTA**	**REL**
Brown Swiss	Active	33	251	89	0.1	69	149	84
	Genomic	43	576	62	0.3	50	315	59
Holstein	Active	618	515	94	0.3	82	240	90
	Genomic	1,499	860	76	1.1	68	479	73
Jersey	Active	104	411	93	-0.2	75	238	87
	Genomic	317	650	69	-0.3	52	366	65

As shown in Table 1, the number of young "G" status bulls currently in the marketplace far exceeds that of "A" status bulls that have completed progeny testing. The difference in average genetic merit between these groups is striking – Net Merit of young bulls is $166, $239, and $128 greater than for progeny tested bulls in Brown Swiss, Holsteins, and Jerseys, respectively. The price we pay for higher predicted genetic merit is lower reliability, a difference of 25% for Brown Swiss, 17% for Holsteins, and 22% for Jerseys (these losses in reliability are proportional to the size of the corresponding genomic reference populations for these breeds). The best strategy for managing the risk associated with lower reliability of young genome-tested bulls is to increase the number of different bulls that are used, as shown below in Table 2. The REL values of individual genomic bulls range from 70 to 76%, whereas the REL of average genetic merit for a team of three bulls ranges from 90 to 92%. Increasing team size to six provides 95 to 96% REL for the team average, and increasing team size to twelve leads to 98% REL.

Table 2: Example PTA and REL for Net Merit of active and genomic Holstein bulls versus REL of a team of the same bulls, where Team REL = [1 – (1 – average REL of individual bulls in the team)/(number of bulls in the team)], with REL expressed as a proportion (93% REL = 0.93).

Bull Type	**Individual NM PTA ($)**	**Individual NM REL (%)**	**Team of 3**		**Team of 6**		**Team of 12**	
			PTA	**REL**	**PTA**	**REL**	**PTA**	**REL**
Active	256	93	266	97	344	99	235	99
	461	86						
	81	98						
	295	89	422	98				
	328	96						
	643	93						
	85	88	83	96	127	98		
	270	85						
	-106	87						
	-138	92	170	97				
	340	93						
	309	91						
Genomic	314	72	222	91	374	96	454	98
	416	76						
	-63	74						
	499	73	525	91				
	496	71						
	581	73						
	585	70	621	90	535	95		
	712	71						
	566	70						
	182	74	449	92				
	611	75						
	553	75						

Genomic Results from the UW-Madison Herd

Demonstrating the relationship between genomic predictions and future performance is the key to gaining farmers' confidence in this technology. Over the past three years, every heifer calf in the Allenstein Dairy Herd at UW-Madison has been tested with a Zoetis low-density chip (CLARIFIDE®). Our research and teaching herd consists of 764 cows, with a rolling herd average of 28,362 pounds of milk, 1,076 pounds of fat, and 894 pounds of protein on 2X milking. The protocol calls for testing upon arrival at our heifer rearing site, the Marshfield Agricultural Research Station, and more than 1,000 calves have been tested to date. Of these, roughly 400 have entered the milking herd, and we can compare their early genomic predictions with their subsequent lactation performance. The analysis was based on sorting heifers into quartiles based on their sires' current PTA values or their own genomic PTA values predicted at 12 months of age. Note that sire misidentification errors discovered through genomic testing (about 5% in our herd, compared with 15% nationally) were corrected prior to carrying out the analyses described below. A total of 411

Holstein cows were beyond 60 days in milk, and their predicted performance was compared with actual 305-day mature equivalent (ME) milk yield in first lactation, as shown below in Figure 1.

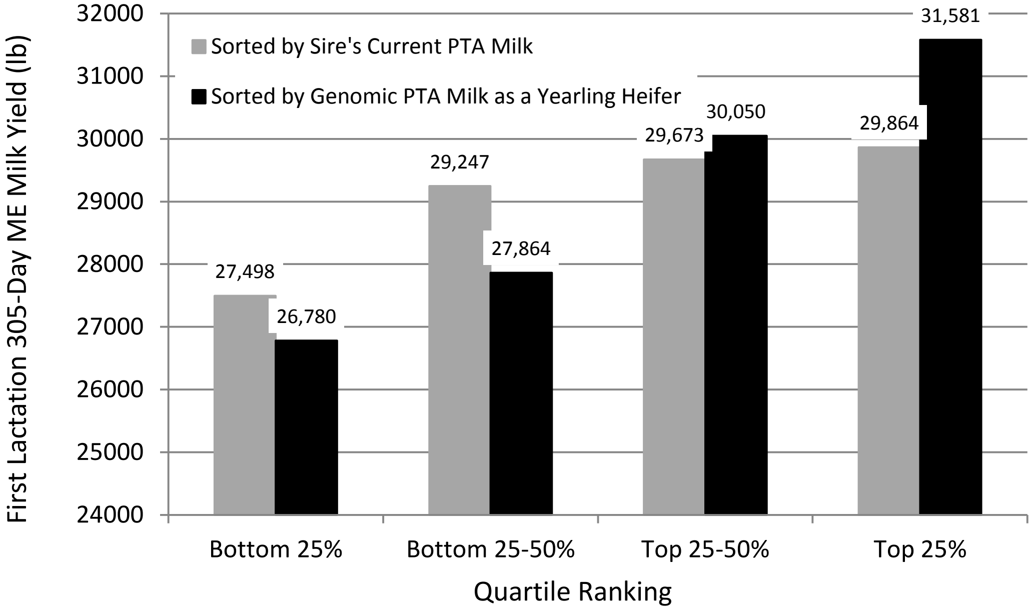


Figure 1. Average first lactation ME 305-day milk yield for 411 Holstein cows in the Allenstein Dairy Herd at UW-Madison, according to quartile for genomic PTA milk at 12 months of age and quartile for sire's current PTA for milk yield.

As shown in Figure 1, the difference between the top and bottom quartiles in actual 305-day milk yield when cows were sorted by current sire PTA was 2,366 pounds per lactation, whereas this difference was 4,801 pounds when cows were sorted by genomic PTA at 12 months of age. This indicates that genomic data of young calves and heifers can be used to predict future lactation performance effectively, and that genomic predictions provide much greater accuracy than simply using information from their sires.

What would have been the cost of selection errors made by culling the bottom 25% of our heifers based on sire PTA values rather than their own genomic PTA information? The difference in actual milk yield between the top 75% of cows based on sire PTA (29,595 pounds) and the top 75% of cows based on early genomic PTA (29,832 pounds) is 237 pounds per lactation. If we multiply this by 2.75 lactations per cow, we get a difference in lifetime production of 652 pounds. After subtracting the cost of extra feed to produce this milk (43% of the value of extra milk) and multiplying by a 3-year average mailbox price of $20.39 per hundredweight, we get a gain in lifetime net revenue of $76 per animal. The total gain for all 309 heifers retained as herd replacements would be $23,484. The cost of genomic testing is roughly $45 per animal, so the total cost of testing 411 heifers is $18,495, which leads to a net profit of $4,989 after accounting for testing costs. In practice the gain would be greater, because a portion of the genetic improvement is passed along to daughters, granddaughters, and so on. And, of course, the primary reason a farmer would consider culling young animals with poor genetic merit is to reduce feed costs during the rearing period. Assuming a rearing cost of $2.30 per day during the post-weaning period, we could have saved approximately $147,798 in feed costs by culling the 102 heifers with lowest genomic

PTA values at 3 months of age. The ability of a farmer to cull a significant proportion of genetically inferior heifer calves depends on several management factors, such as survival rate in pre-weaning calves, pregnancy rate in yearling heifers and lactating cows, and involuntary culling rate in the milking herd.

We also analyzed the data of 240 Holstein cows that were beyond 250 days in milk at the time of the analysis, and their female fertility, as measured by daughter pregnancy rate (DPR) was compared with their actual days open in first lactation, as shown in Figure 2.

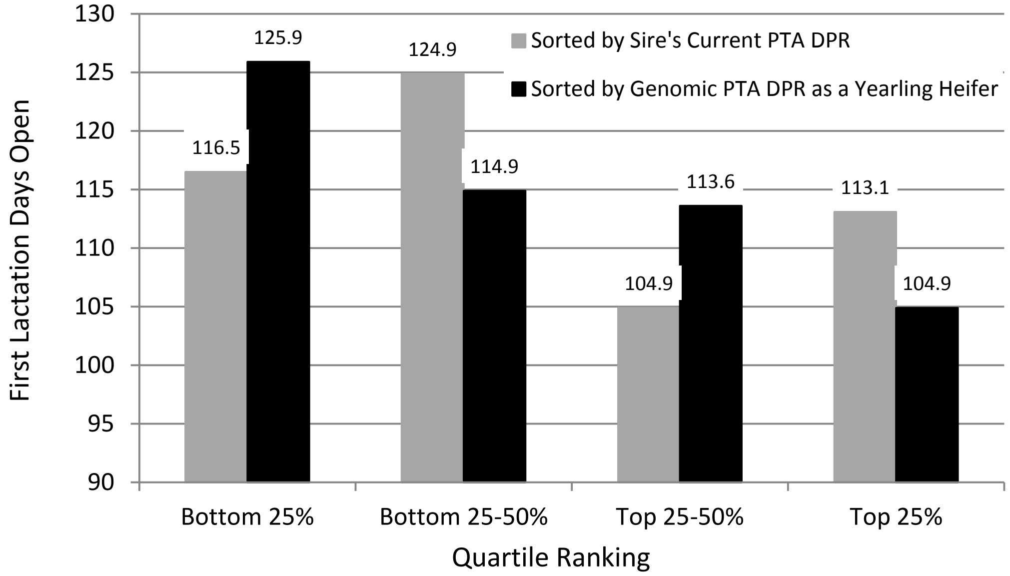


Figure 2. Average days open in first lactation for 240 Holstein cows in the Allenstein Dairy Herd at UW-Madison, according to quartile for genomic PTA for daughter pregnancy rate at 12 months of age and quartile for sire's current PTA for daughter pregnancy rate.

As shown in Figure 2, the difference in actual days open in first lactation was quite large when heifers were sorted by genomic PTA, with the top and bottom quartiles differing by 21.0 days. When we sorted animals by sire PTA, this difference was only 3.4 days, so genomic predictions were significantly more accurate as predictors of future reproductive performance. At a typical value of $2.00 to $3.00 per additional day open, it is clear that savings in labor, technician, and semen costs can help offset the cost of genomic testing.

What about udder health? We compared the genomic predictions for somatic cell score (SCS) with actual average monthly log somatic cell count (SCC) in first lactation for 216 Holstein cows. As shown in Figure 3, there was a clear increase in first lactation log SCC when cows were sorted based on genomic PTA for SCS as a yearling heifer, and the difference between highest and lowest quartiles for genomic PTA (2.38 vs. 1.56) was much greater than for sire PTA (2.20 vs. 1.56). Thus, genomics can also be used to identify heifers that are more likely to suffer from clinical or subclinical mastitis than their contemporaries once they enter the milking herd.

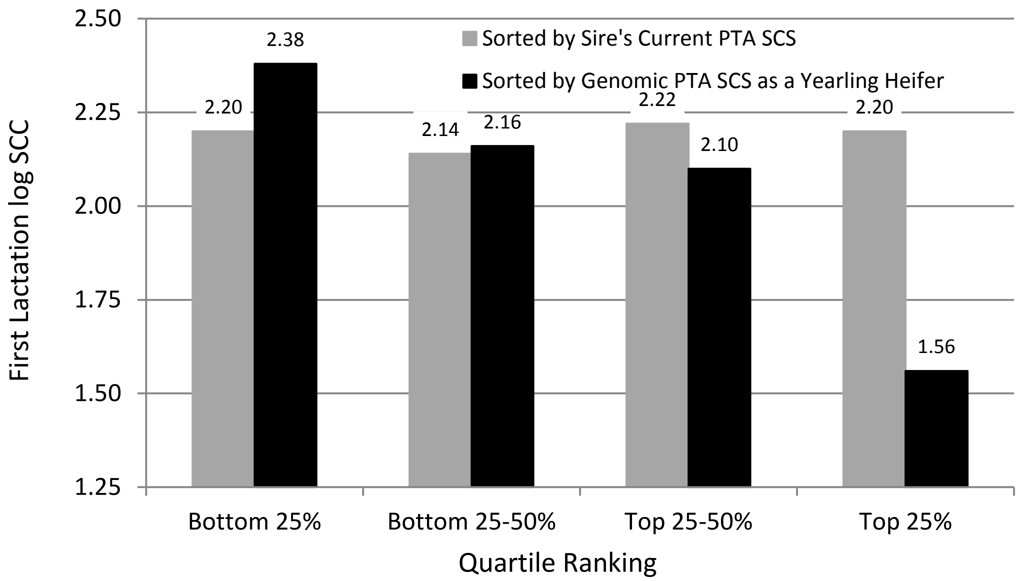


Figure 3. Average log somatic cell count in first lactation for 216 Holstein cows in the Allenstein Dairy Herd at UW-Madison, according to quartile for genomic PTA for somatic cell score at 12 months of age and quartile for sire's current PTA for somatic cell score.

Genomic Results from a Leading Commercial Herd

To confirm the results from the UW-Madison herd, a second analysis was carried out using data from one of the top commercial dairies in Wisconsin, where genomic testing is part of the management routine for all heifer calves. This herd has 920 Holstein cows, with a rolling herd average of approximately 31,000 pounds on 3X milking. All animals with genomic predictions in August 2013 were used in the analysis, and the genomic predictions were compared with their subsequent first lactation performance. Cows with first calving prior to August 2013 were excluded, so none of these animals had performance data of their own at the time of genomic predictions. All cows had the chance to complete at least 60 days in milk for the milk, fat, protein, and SCS analyses (407 cows) or 250 days in milk for the days open analysis (192 cows).

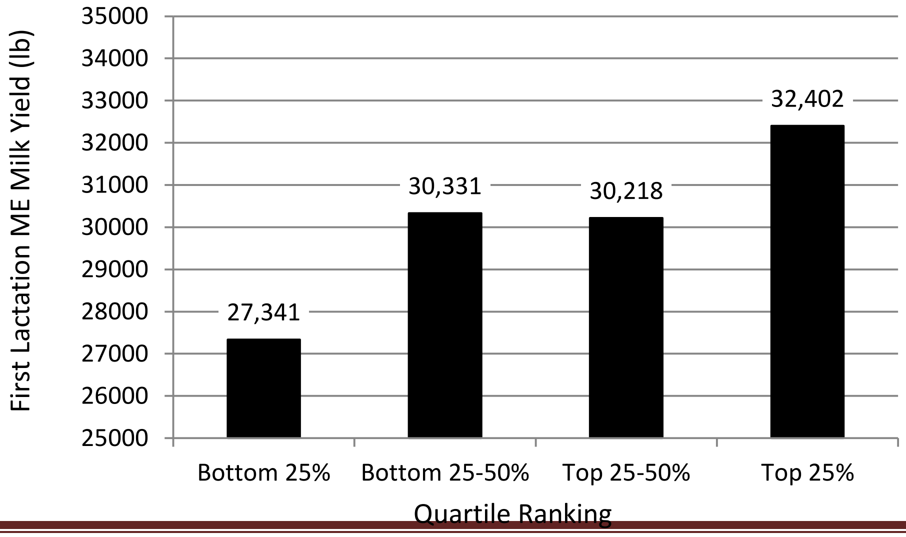


Figure 4. Average standardized 305-day ME milk yield in first lactation for 407 Holstein cows in a leading commercial herd, according to quartile for genomic PTA for milk yield as a yearling heifer.

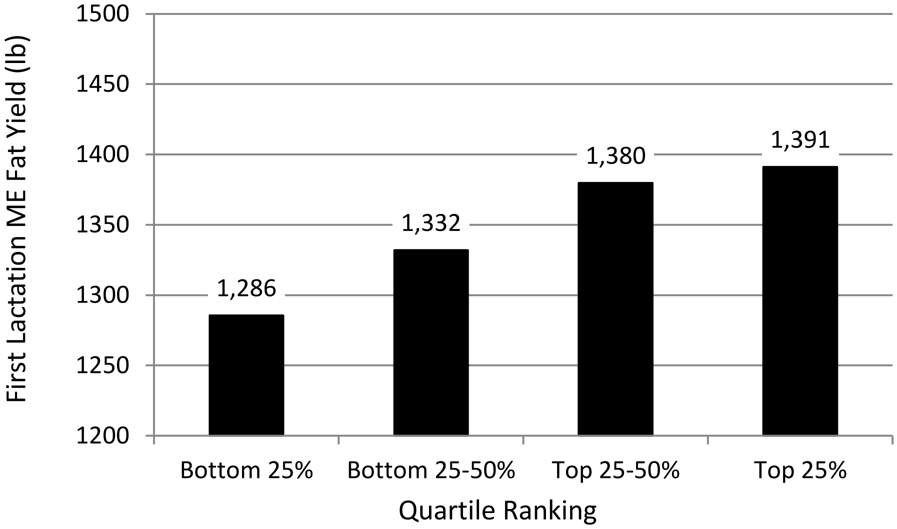


Figure 5. Average standardized 305-day ME fat yield in first lactation for 407 Holstein cows in a leading commercial herd, according to quartile for genomic PTA for fat yield as a yearling heifer.

As shown in Figures 4 and 5 above, as well as Figure 6 below, genomic predictions as a yearling heifer were exceptionally effective as predictors of future lactation performance. Differences in average first lactation yield between the highest and lowest quartiles were 5,061 pounds of milk, 105 pounds of fat, and 93 pounds of protein. More importantly, with respect to early identification and culling of genetically inferior heifer calves to reduce feed costs, differences between the third quartile (bottom 25-50%) and fourth quartile (bottom 25%) were 2,990 pounds of milk, 46 pounds of fat, and 50 pounds of protein.

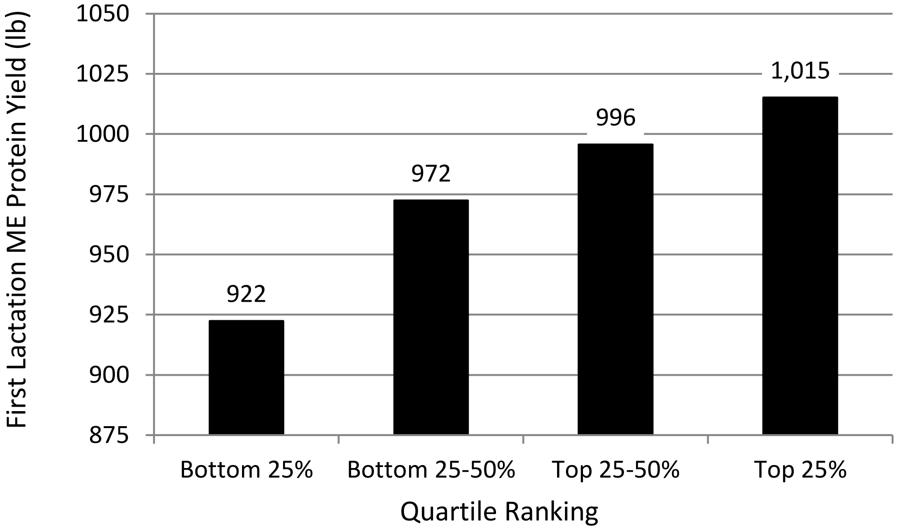


Figure 6. Average standardized 305-day ME protein yield in first lactation for 407 Holstein cows in a leading commercial herd, according to quartile for genomic PTA for protein yield as a yearling heifer.

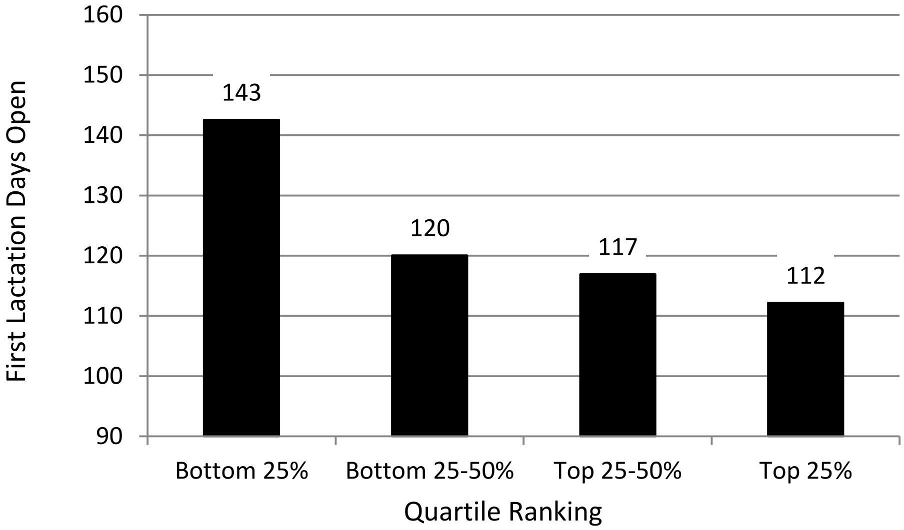


Figure 7. Average days open in first lactation for 192 Holstein cows in a leading commercial herd, according to quartile for genomic PTA for daughter pregnancy rate as a yearling heifer.

As shown in Figure 7, early genomic predictions were quite effective for identifying heifers that will have inferior reproductive performance in the future. Cows that were in the bottom quartile of genomic PTA for daughter pregnancy rate averaged 143 days open, as compared with 120, 117, and 112 for the three other quartiles. Likewise, as shown in Figure 8, early predictions for somatic cell score identified animals that were more likely to suffer from clinical or subclinical mastitis in the future, with average first lactation SCS of 2.48 for the cows with poorest genomic predictions and 2.03, 1.97, and 1.92 for the other three quartile groups.

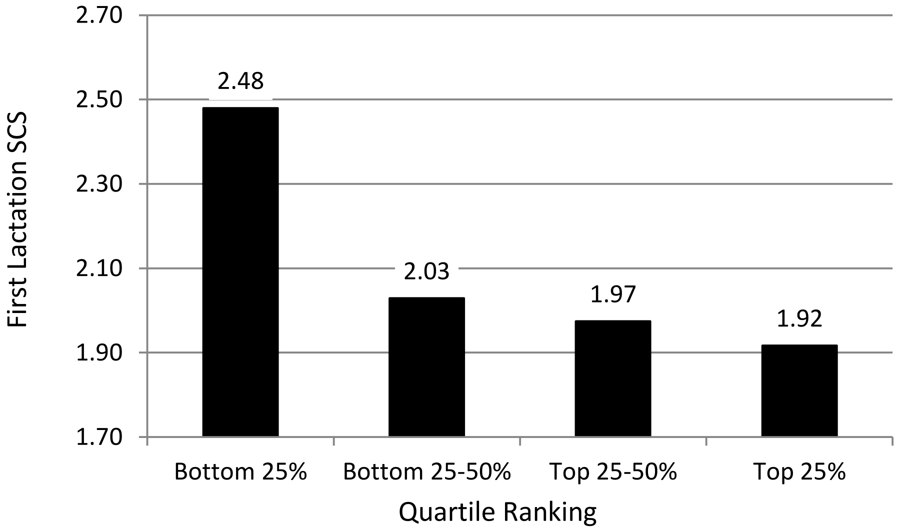
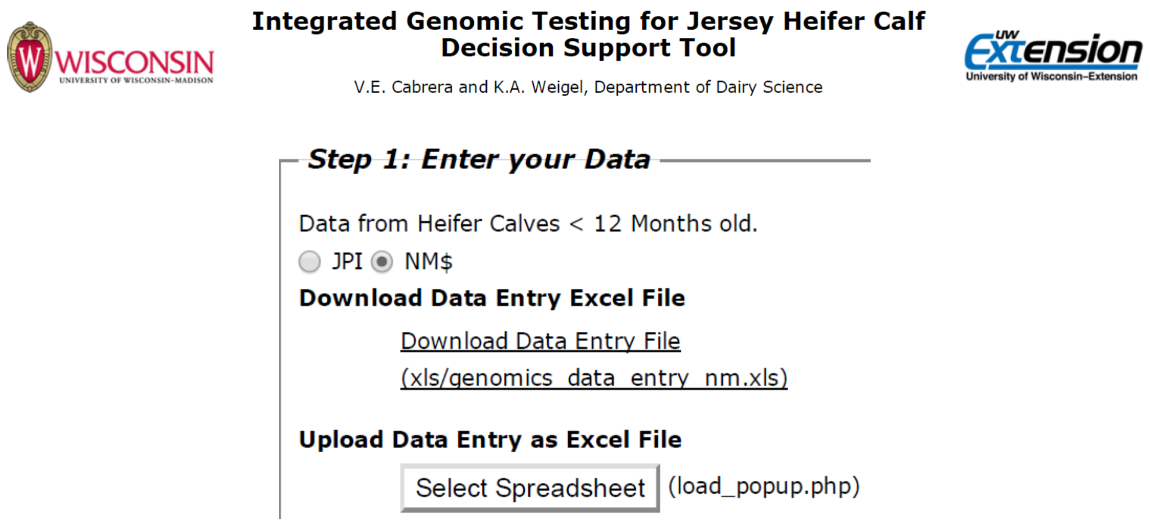


Figure 8. Average somatic cell score in first lactation for 192 Holstein cows in a leading commercial herd, according to quartile for genomic PTA for somatic cell score as a yearling heifer.

Which Animals are Good Candidates for Genomic Testing?

Should a farmer invest in genomic testing of every heifer calf on the farm? This decision depends on the intended use of the genomic results. If the objective is to identify elite heifers for the purpose of marketing embryos, for example, then testing the calves with poorest pedigrees might not be sensible. Likewise, if the only objective is to cull genetically inferior animals, then testing heifers with the top pedigrees might not be useful. Several decision tools are now available to assist farmers with such decisions, as described below:



Integrated Genomic Testing for Jersey Heifer Calf Decision Support Tool

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Step 1: Enter your Data

Data from Heifer Calves < 12 Months old.

○ JPI ● NM$

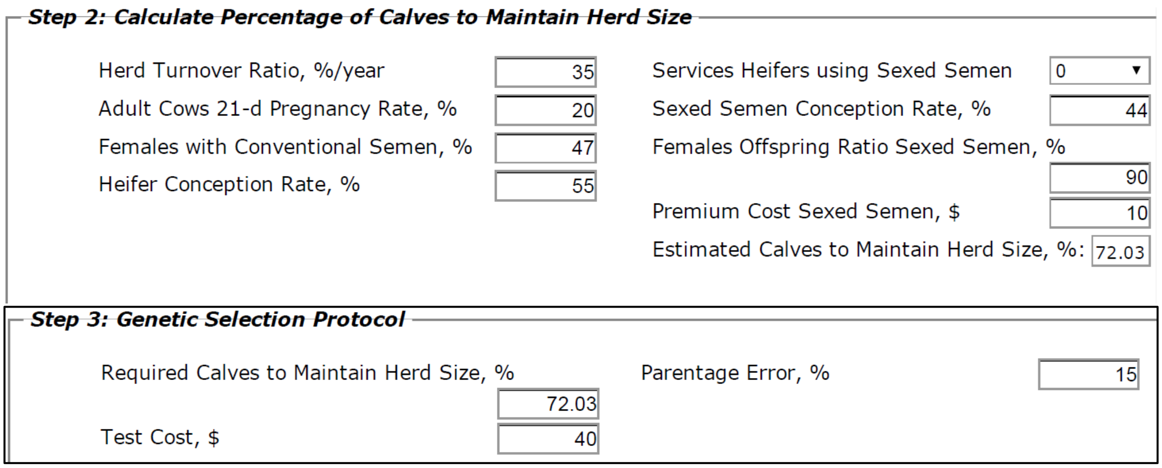
Download Data Entry Excel File

Download Data Entry File (xls/genomics_data_entry_nm.xls)

Upload Data Entry as Excel File

(load_popup.php)

Figure 9. Screen shot of a decision support tool for helping farmers determine which heifer calves are good candidates for genomic testing (http://dairymanagement.wisc.edu/tools/genomics).



Step 2: Calculate Percentage of Calves to Maintain Herd Size

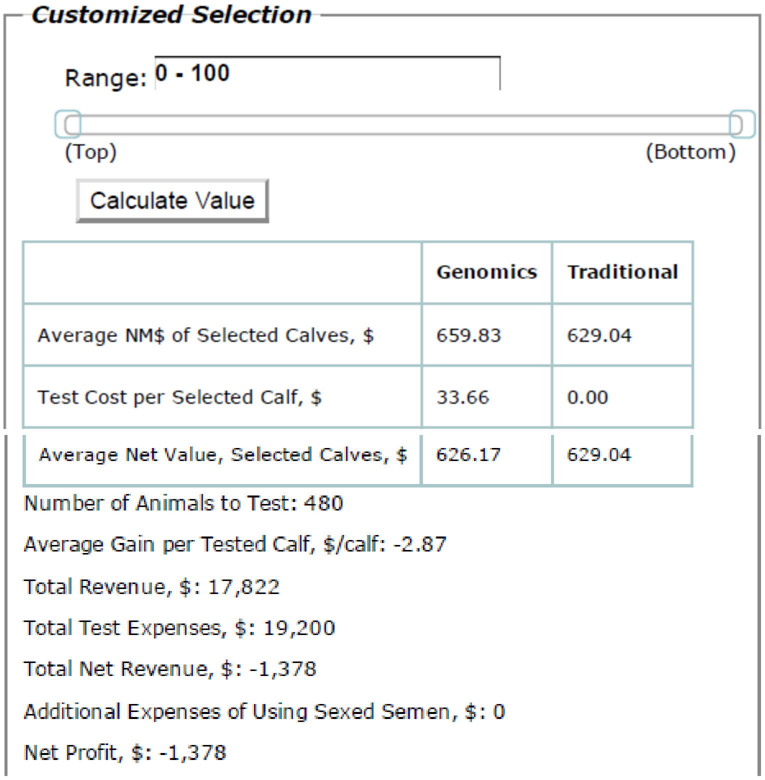
Herd Turnover Ratio, %/year: 35
Adult Cows 21-d Pregnancy Rate, %: 20
Females with Conventional Semen, %: 47
Heifer Conception Rate, %: 55
Services Heifers using Sexed Semen: 0
Sexed Semen Conception Rate, %: 44
Females Offspring Ratio Sexed Semen, %: 90
Premium Cost Sexed Semen, $: 10
Estimated Calves to Maintain Herd Size, %: 72.03

Step 3: Genetic Selection Protocol

Required Calves to Maintain Herd Size, %: 72.03
Test Cost, $: 40
Parentage Error, %: 15

Figure 10. Screen shot of the user interface for the aforementioned genomic decision support tool, using an example data set and default parameters (http://dairymanagement.wisc.edu/tools/genomics).

As shown in the example in Figure 10, a typical herd with 35% turnover rate and 20% pregnancy rate will need to keep a minimum of 72% of heifer calves as herd replacements, leaving the opportunity to reduce rearing costs by culling 28% of calves identified as genetically inferior. The results in Figure 11 suggest that testing every heifer calf (range 0-100) may not be optimal.



Customized Selection

Range: 0 - 100

	Genomics	Traditional
Average NM$ of Selected Calves, $	659.83	629.04
Test Cost per Selected Calf, $	33.66	0.00
Average Net Value, Selected Calves, $	626.17	629.04

Number of Animals to Test: 480

Average Gain per Tested Calf, $/calf: -2.87

Total Revenue, $: 17,822

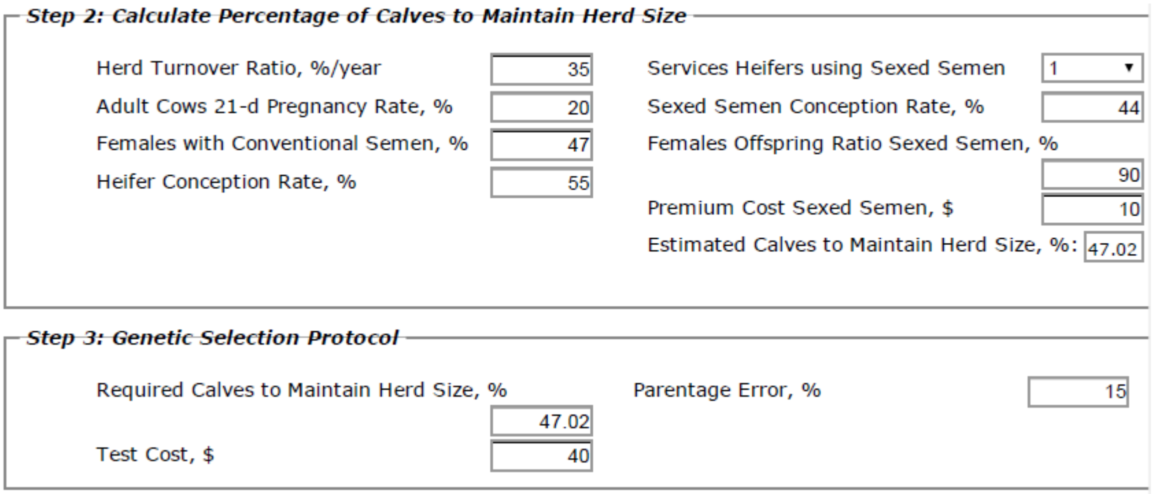
Total Test Expenses, $: 19,200

Total Net Revenue, $: -1,378

Additional Expenses of Using Sexed Semen, $: 0

Net Profit, $: -1,378

Figure 11. Screen shot of results from the aforementioned genomic decision support tool, using example data and default parameters (http://dairymanagement.wisc.edu/tools/genomics).



Step 2: Calculate Percentage of Calves to Maintain Herd Size

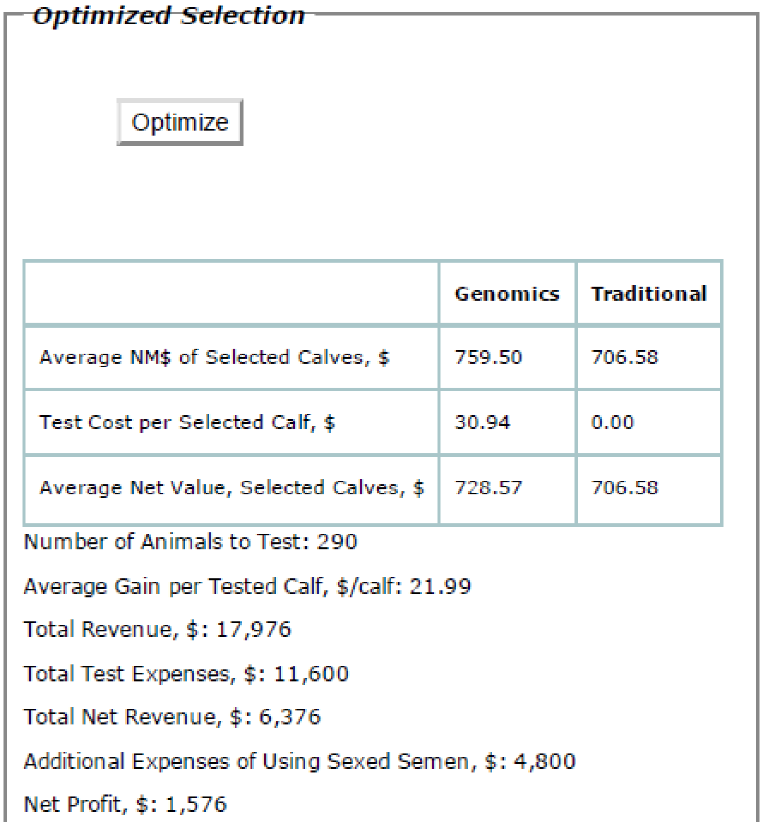
Herd Turnover Ratio, %/year: 35
Adult Cows 21-d Pregnancy Rate, %: 20
Females with Conventional Semen, %: 47
Heifer Conception Rate, %: 55
Services Heifers using Sexed Semen: 1
Sexed Semen Conception Rate, %: 44
Females Offspring Ratio Sexed Semen, %: 90
Premium Cost Sexed Semen, $: 10
Estimated Calves to Maintain Herd Size, %: 47.02

Step 3: Genetic Selection Protocol

Required Calves to Maintain Herd Size, %: 47.02
Test Cost, $: 40
Parentage Error, %: 15

Figure 12. Screen shot of the user interface for the aforementioned genomic decision support tool, using example data and default parameters (http://dairymanagement.wisc.edu/tools/genomics).

Sexed semen can be used to create more selection opportunities, as shown in Figure 12, and allowing the program to optimize the proportion of calves that are tested (in this case, 290 out of 480 total calves) can lead to a more profitable genomic testing strategy (Figure 13).



	Genomics	Traditional
Average NM$ of Selected Calves, $	759.50	706.58
Test Cost per Selected Calf, $	30.94	0.00
Average Net Value, Selected Calves, $	728.57	706.58

Number of Animals to Test: 290

Average Gain per Tested Calf, $/calf: 21.99

Total Revenue, $: 17,976

Total Test Expenses, $: 11,600

Total Net Revenue, $: 6,376

Additional Expenses of Using Sexed Semen, $: 4,800

Net Profit, $: 1,576

Figure 13. Screen shot of results from the aforementioned genomic decision support tool, using example data with sexed semen and optimization (http://dairymanagement.wisc.edu/tools/genomics).

Other Tools and Opportunities

The key to successful implementation of genomic testing in the long term is development of additional tools that will allow farmers to take an appropriate action for every heifer, depending on the outcome of the genomic test. Such actions might include culling, insemination with sexed semen, use as an embryo donor or recipient, or insemination with beef semen. The Holstein Association USA, in cooperation with Zoetis, has developed a genomic selection “dashboard” for managing the information from your cows, heifers, and calves. In addition to the typical young stock reports, herd reports, and individual cow pages, which show genomic PTA and REL values for production, health, and type traits, there are a number of tools for monitoring and benchmarking the genetic level of your herd, as shown below.

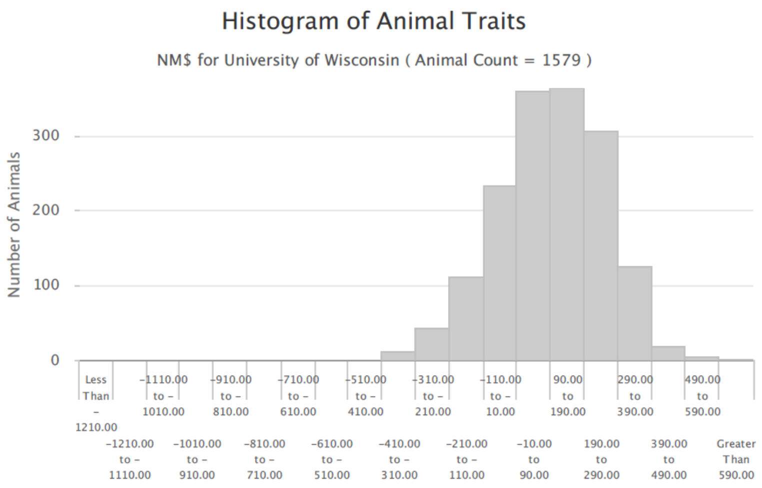


Figure 14. Screen shot of a histogram of Net Merit predictions for genotyped animals in the UW-Madison Allenstein dairy herd, using the Enlight genomic management tool (www.enlightdairy.com).

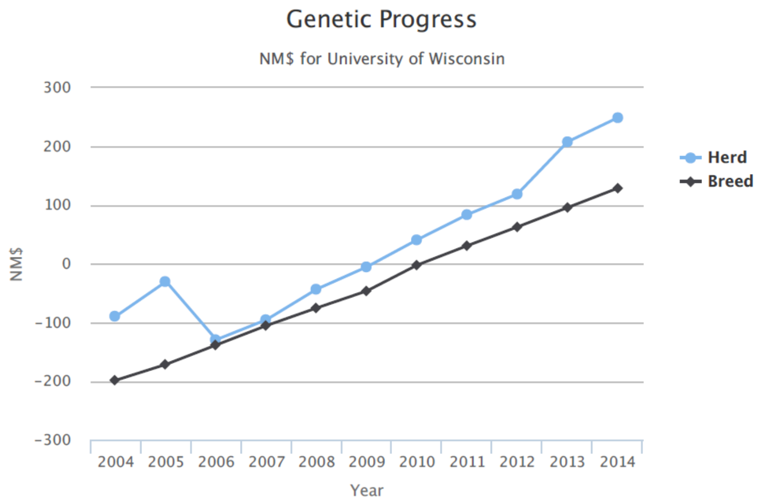


Figure 15. Screen shot of the trend in genetic progress for Net Merit of genotyped animals in the UW-Madison Allenstein dairy herd, using the Enlight genomic management tool (www.enlightdairy.com).

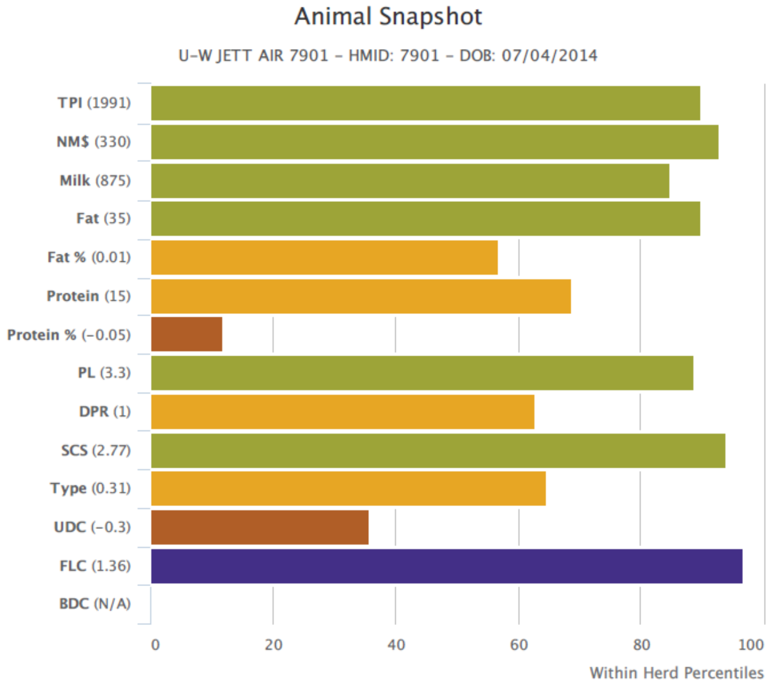


Figure 16. Screen shot of the genomic profile of an example heifer calf in the UW-Madison Allenstein dairy herd, using the Enlight genomic management tool (www.enlightdairy.com).

Additional information is also available, such as data regarding known genetic defects and conditions (e.g., BLAD, Mulefoot, red coat color) and yet-to-be-mapped genetic disorders (e.g., HH1, HH2), and this can be extremely useful for avoiding carrier by carrier matings.

Take Home Messages

- Genomic testing has become fully integrated into dairy cattle selection programs in North America, and nearly every potentially elite bull, cow, heifer, and calf is genotyped.
- Young genome-tested bulls represent the majority of semen in the marketplace, and farmers should manage the risk of their lower reliability values by selecting teams of bulls, rather than focusing too heavily on individual bulls.
- The ability of early genomic predictions to identify heifer calves that will be inferior or superior for production, health, and fertility traits later in life has been firmly established using data from both experimental and commercial herds.
- Decision support tools have been developed that will allow farmers to more effectively identify candidates for genomic testing, evaluate the expected costs and benefits of genomic testing, and monitor their inventories at the herd level and individual animal level.
- Herds that develop standardized protocols for genetic management of replacement animals, including genomic testing, culling, breeding, mating, and related decisions, will reap the greatest benefits of this technology.

Notes: