Using Genomics on the Farm

Dr. Kent A. Weigel
Department of Dairy Science, University of Wisconsin
1675 Observatory Drive, Madison, WI 53706
kweigel@wisc.edu

Introduction

In the past three years, tens of thousands of North American dairy cattle have been genotyped using the Illumina BovineSNP50 BeadChip, and alternative high-density and low-density genotyping chips have recently become available. These technologies became possible due to sequencing of the bovine genome and were developed via collaboration between Illumina Inc., the USDA Agricultural Research Service, the National Association of Animal Breeders, and other commercial and academic partners. A key breakthrough is the ability to carry out thousands of DNA marker tests simultaneously, for a cost of less than ½ ¢ per marker. Single nucleotide polymorphism (SNP) markers represent base changes (A, T, C, or G) within the DNA sequence of a cow or bull – a sequence that consists of approximately 3 billion base pairs distributed over 30 pairs of chromosomes. These SNP markers can be genotyped in an efficient and automated manner, in contrast to the labor-intensive genotyping methods that were used previously. Another key breakthrough is the finding that, once a large number of genetic markers become available for an individual animal, it is possible to estimate that animal's breeding value based on associations between marker genotypes and milk yield, somatic cell score, productive life, daughter pregnancy rate, and other key traits that were observed in other animals of the same breed. The most important animals in this process are the dairy bulls represented in the Cooperative Dairy DNA Repository, which was formed more than 15 years ago, when ABS Global, Accelerated Genetics, Alta Genetics, Genex Cooperative, Select Sires, Semex, and Taurus Service began storing semen samples from young bulls entering their progeny testing programs for the purpose of genetic research.

Validation of Genomic Predictions by USDA

In a widely cited study by scientists at the USDA-ARS Beltsville Agricultural Research Center, a total of 5,369 Holstein bulls and cows that were born from 1952 to 1999 were genotyped with the Bovine SNP50 BeadChip (VanRaden et al., 2009; Cole et al, 2009). Genotypes and phenotypes of these animals were used to estimate the effects of 38,416 SNP markers on production, type, longevity, udder health, and calving ability. Next, the estimated SNP effects were used to compute the genomic predicted transmitting abilities (PTAs) of 2,035 young Holstein bulls born from 2000 to 2003 that had no progeny of their own. Finally, the 2009 PTAs of bulls in the latter group, which were based on information from their progeny, were compared with their traditional parent averages and the genomic PTAs computed from 2004 data. The same process was repeated in Jerseys (using 1,361 older bulls and cows for prediction and 388 young bulls for validation) and Brown Swiss (using 512 older bulls and cows for prediction and 150 young bulls for validation). Results in Table 1 show the increase in reliability due to genomic information, as compared with the reliability from pedigree information only.

Table 1. Reliability changes due to the inclusion of genomic data in national genetic evaluations in the validation study of VanRaden et al. (2009).

Trait	Increase in Reliability due to Genomics		
	Holstein	Jersey	Brown Swiss
Lifetime Net Merit	+24%	+8%	+9%
Milk Yield	+26%	+6%	+17%
Fat Yield	+32%	+11%	+10%
Protein Yield	+24%	+2%	+14%
Fat Percentage	+50%	+36%	+8%
Protein Percentage	+38%	+29%	+10%
Productive Life	+32%	+7%	+12%
Somatic Cell Score	+23%	+3%	+17%
Daughter Pregnancy Rate	+28%	+7%	+18%
Final Classification Score	+20%	+2%	+5%
Udder Depth	+37%	+20%	+8%
Foot Angle	+25%	+11%	-1%

As shown in Table 1, gains in reliability from genomic information were significant for almost all traits and breeds, ranging from -1% for foot angle in Brown Swiss to +50% for fat percentage in Holsteins. Gains were largest for traits for which single genes with large effects had already been discovered, such as fat percentage (DGAT1 gene on chromosome 14; Grisart et al., 2004) and protein percentage (ABCG2 gene on chromosome 6; Cohen-Zinder et al., 2005). For each trait, we can combine a young animal's pedigree with information regarding its SNP genotypes to obtain a genomic PTA of much greater accuracy. For a heifer calf, reliability of the genomic PTA is greater than the information we could obtain by measuring several lactation records on the animal and its daughters. For a young cow, genomic information can be combined with her lactation records to obtain a genomic PTA that is significantly more informative than her traditional PTA. For a bull calf, reliability of the genomic PTA is equivalent to what we could obtain by measuring performance on 25 or 30 of his progeny test daughters. Improvements in accuracy can even be obtained for bulls that have completed progeny testing, although the gain in information for a bull that already has performance data from 80 to 100 daughters is much smaller. Gains in reliability for Jerseys and Brown Swiss have not been as great as for Holsteins. However, this difference is largely due to the fact that fewer progeny tested bulls have been genotyped, and results for these breeds will be improved by combining information from North American sires with that of key populations internationally.

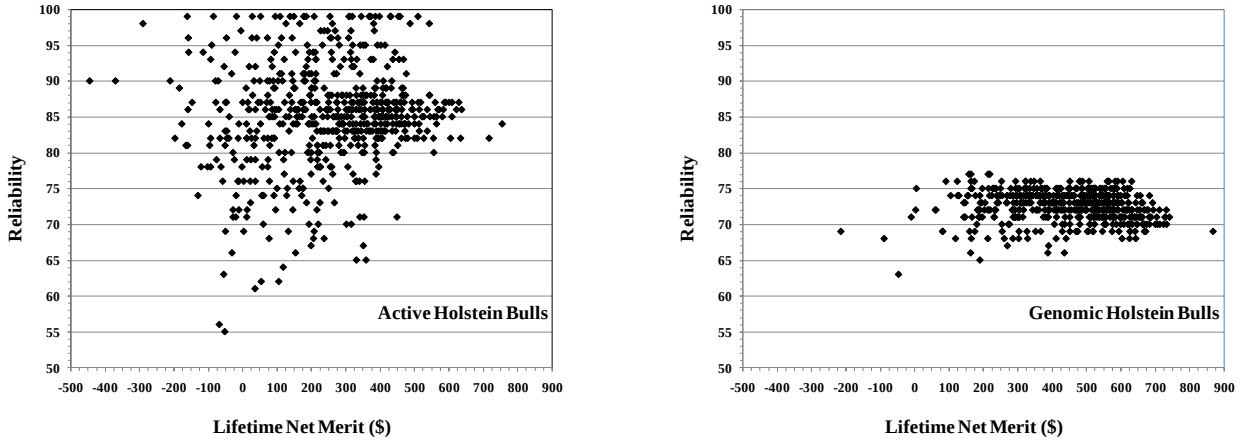
Impact on Sire Selection Decisions

The artificial insemination (AI) studs are in the midst of tremendous change because of this technology. Virtually every young bull entering an AI company today is DNA tested on the farm and selected from a group of 5 to 10 young bulls with similar pedigrees. Therefore, we know that each of these bulls has received a favorable sample of genes from its parents. The

genomic PTA for a young bull typically has reliability in the range of 60 to 75%, as opposed to only 30 to 40% for its traditional parent average. North American AI companies are now marketing semen from hundreds of young bulls that have genomic PTAs but no daughters of their own. These young bulls have replaced older, proven bulls that were at the low end of the sire line-up, and many of these bulls are being used for contract matings. Because buyers now have the ability to distinguish between sets of full siblings that have the same parent average, the premium for securing first choice from a flush is much greater, and buyers at consignment sales and dispersals now pay a premium for young animals with favorable genotypes.

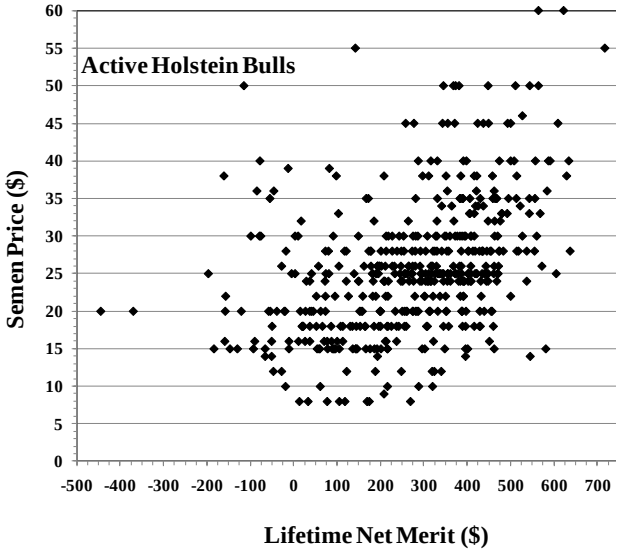
What about commercial producers? While these producers may not yet be genotyping young females on their farms, they are seeing semen on the market from hundreds of young bulls with genomic breeding values and no progeny. These bulls have attractive pedigrees, because they're younger than the current proven bulls, but their reliabilities are lower, as shown in Figure 1.

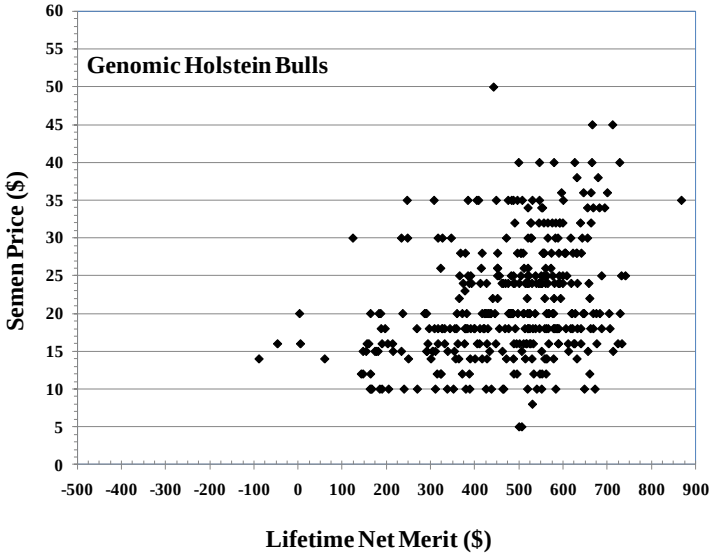
Figure 1. January 2011 PTA for Lifetime Net Merit versus reliability for Holstein bulls with active status based on progeny testing (left) and genomic status based on DNA testing (right).



Because reliabilities of young, genome-tested bulls are lower, producers should avoid heavy use of one or two top bulls and should spread out their risk by using a larger group of bulls. Avoiding these bulls entirely is a bad idea, even for risk-averse producers, because their genetic merit is high relative to their semen price, as shown in Figure 2.

Figure 2. January 2011 PTA for Lifetime Net Merit versus semen price for Holstein bulls with active status based on progeny testing (left) and genomic status based on DNA testing (right).





Development of Inexpensive, Low-Density Genotyping Platforms

Because the cost of the BovineSNP50 BeadChip has largely limited its application to males and elite females, attention has focused on development of inexpensive alternatives that can capture the majority of the gain for a fraction of the price. Initially, we attempted to select the most important SNPs based on magnitude of their estimated effects (Weigel et al., 2009). Using August 2003 progeny test PTAs for Lifetime Net Merit of 3,305 Holstein bulls born from 1952 to 1998, we evaluated the ability of various subsets of SNPs to predict April 2008 progeny test PTAs for 1,398 Holstein bulls born from 1999 to 2002. Subsets were created by sorting the original 32,518 SNPs by the absolute values of their estimated effects and choosing the top 300, 500, 750, 1,000, 1,250, 1,500, or 2,000 SNPs. For reference purposes, subsets of 300, 500, 750, 1,000, 1,250, 1,500, or 2,000 equally spaced SNPs were also created. Correlations between these genomic predictions and corresponding PTAs from progeny testing are shown below, in Table 2.

Table 2. Correlations between progeny test PTAs for Lifetime Net Merit and genomic predictions from various subsets of SNPs in a population of 1,398 Holstein bulls, where SNPs were chosen based on spacing or size of estimated effect (Weigel et al., 2009).

Number of SNP Markers Genotyped	SNPs with Largest Effects	Equally Spaced SNPs
300	0.428	0.253
500	0.485	0.333
750	0.519	0.435
1,000	0.537	0.422
1,250	0.554	0.477
1,500	0.559	0.518
2,000	0.567	0.539
32,518	0.612	

The reference model with 32,518 SNPs provided a correlation of 0.612, whereas correlations between progeny test PTAs and genomic predictions derived from 300 to 2,000 selected SNPs ranged from 0.428 to 0.567. Correlations for sets of selected SNPs were consistently greater than for sets of equally spaced SNPs. In a related study, Vazquez et al. (2010) noted that low-density chips containing SNPs with the largest estimated effects for Lifetime Net Merit would provide greater predictive ability for production traits than for fitness traits. Furthermore, low-density assays composed of selected SNPs would be breed-specific and trait-specific. For these reasons, we determined that it would be more efficient to genotype a slightly larger set of equally spaced SNPs that would facilitate imputation of missing high-density genotypes, as suggested by Habier et al. (2009), rather than focus on a few hundred selected SNPs with large effects.

To determine if imputation of high-density (i.e., BovineSNP50 BeadChip) genotypes from subsets of a few hundred or a few thousand equally spaced SNPs was feasible, we used a population of 2,656 Jersey bulls and 490 Jersey cows and heifers that had been genotyped for 43,385 SNPs. This population was divided into a reference panel, consisting of 2,542 animals born from 1953 to 2006, and a study sample, consisting of 604 animals born from 2007 to 2009. For animals in the study sample, genotypes were "masked" (i.e., hidden) for a randomly chosen 20, 60, 80, 90, 95, 98, or 99% of SNP markers. Three chromosomes were considered (BTA1,

BTA15, and BTA28), but results are shown only for BTA15, which contained 1,377 SNP markers. After masking 20 to 99% of the SNPs, the number of SNPs available for imputing missing genotypes ranged from 14 to 1,102. Many algorithms have been developed for constructing haplotypes and imputing genotypes in humans, and in this study we used the method of Scheet and Stephens (2006), which was implemented via fastPHASE 1.2 software, and the method of Howie et al. (2009), which was implemented via IMPUTE 2.0 software. The proportion of masked SNP genotypes that were imputed correctly is shown in Table 3.

Table 3. Proportion of SNP genotypes that were imputed in a sample of 604 Jersey cattle, using a reference panel of 2,542 Jersey cattle, according to method of imputation and percentage of SNPs that were actually genotyped (Weigel et al., 2010b).

Percentage of SNP Markers Genotyped	Method 1 (fastPHASE 1.2)	Method 2 (IMPUTE 2.0)
1%	0.701	0.730
2%	0.726	0.780
5%	0.780	0.890
10%	0.874	0.924
20%	0.951	0.932
40%	0.984	0.935
80%	0.992	0.930

The proportion imputed correctly ranged from 0.66 to 0.73 when only 1% or 2% of genotypes were unmasked in the study sample, versus 0.75 to 0.89 when 5 to 10% of genotypes were unmasked, as would be the case for a medium-density panel with 2,000 to 4,000 SNPs. This suggested that a low-density chip with approximately 3,000 equally spaced SNPs would be adequate for imputing high-density genotypes from reference animals of the same breed.

Next, we sought to determine the impact of imputing (more specifically, the impact of imputing errors) on the accuracy of genomic predictions for economically important traits in dairy cattle. Genotypes of 1,762 Jersey sires, with 42,552 SNP markers apiece, were used in conjunction with progeny test PTAs for milk yield, protein percentage, and daughter pregnancy rate. A group of 1,446 sires with ≥ 10 milking daughters in May 2006 were used as the reference panel, and the accuracy of genomic PTAs based on imputed genotypes was evaluated using 316 sires with 0 milking daughters in May 2006 and ≥ 10 milking daughters in April 2009. Next, we created equally spaced subsets in which all but 366, 741, 1,468, or 2,942 of the original SNP genotypes were masked. Masked genotypes were imputed using the method of Howie et al. (2009), implemented via IMPUTE 2.0 software. After imputation, genomic predictions for milk yield, protein percentage, and daughter pregnancy rate were computed, and these were compared with the traditional PTAs of these bulls resulting from progeny testing. Results are shown in Table 4.

Table 4. Correlations between progeny test PTAs for milk yield, protein percentage, and daughter pregnancy rate and genomic predictions for these traits based on 366, 741, 1,468, 2,942, or 42,552 SNP markers, with imputation of missing genotypes, in a population of 316 Jersey bulls (Weigel et al., 2010a).

Number of SNP Markers Genotyped	Milk Yield	Protein Percentage	Daughter Pregnancy Rate
366	0.367	0.468	0.470
741	0.525	0.546	0.572
1,468	0.649	0.676	0.619
2,942	0.673	0.740	0.642
42,552	0.673	0.770	0.674

As shown in Table 4, a low-density genotyping chip consisting of approximately 3,000 equally spaced SNPs (i.e., the so-called "3K chip") can provide genomic predictions for milk yield, protein percentage, and daughter pregnancy rate that are roughly 95% as accurate as predictions from the BovineSNP50 BeadChip, for a small fraction of the price.

Cost-Effective Strategies for Genotyping Females on Commercial Dairy Farms

To investigate whether low-density genotyping of females on commercial dairy farms would be cost effective, and to determine the conditions under which a producer could maximize the benefits of this technology, a simulation study was carried out. We created 100 dairy herds, each comprised of 1,850 animals; these included 850 replacement heifers (450 heifer calves and 400 yearling heifers) and 1,000 milking cows (350 in first lactation, 250 in second lactation, 170 in third lactation, 120 in fourth lactation, 70 in fifth lactation, and 40 in sixth lactation). Each animal's genetic potential for Lifetime Net Merit was simulated, using an average of $45 and a standard deviation of $146; these values correspond to the current mean and standard deviation for sire-identified, milk-recorded Holsteins in the US national genetic evaluation system (http://aipl.arsusda.gov/eval/summary/pctl.cfm). Genetic improvement over time was taken into account by adjusting the average PTA by $26 per year, according to age of the animal. Reliability of genetic predictions varied, according to the availability (or lack thereof) of pedigree information, performance (milk-recording) data, and low-density (3K) DNA test results for a given animal, as shown below.

Table 5. Assumed reliability values for predictions of Lifetime Net Merit based on pedigree, performance, and low-density genotyping data ("Traditional" = no DNA testing, "Genomic" = DNA testing with 3K chip) for simulated animals in each age group.

Age Group	Ancestry Unknown		Sire-Identified		Full Pedigree	
	Traditional	Genomic	Traditional	Genomic	Traditional	Genomic
Heifer calves	0.00	0.50	0.20	0.57	0.34	0.67
Yearling Heifers	0.00	0.52	0.21	0.59	0.35	0.68
1st Lactation Cows	0.18	0.56	0.40	0.63	0.52	0.71
2nd Lactation Cows	0.22	0.59	0.44	0.66	0.55	0.73
3rd Lactation Cows	0.25	0.62	0.46	0.68	0.57	0.74
4th Lactation Cows	0.27	0.64	0.48	0.69	0.58	0.74
5th Lactation Cows	0.29	0.65	0.49	0.70	0.59	0.75
6th Lactation Cows	0.30	0.65	0.50	0.70	0.60	0.75

After generating true and estimated breeding values for these animals, where accuracy of the estimated breeding values varied according to age, extent of known ancestry, and presence or

absence of genomic testing information, we carried out selection and culling decisions within in each herd. Producers selected the top 10, 20, 30, . . ., 90% of animals within each age group based on the aforementioned estimates of genetic merit, and the remaining animals were culled. Next, the average breeding value for Lifetime Net Merit of animals that were selected using pedigree plus genomic information was compared with that of animals that were selected from the same age group using pedigree information only. The average gain in genetic merit due to DNA testing was then compared with the cost of the test, which was assumed to be $35 per animal. This cost was prorated over the number of animals that were selected from a given age group, such that the break-even gain in breeding value was $350, 175, 117, 88, 70, 58, 50, 44, or 39 when the top 10, 20, 30, 40, 50, 60, 70, 80, or 90% of animals were selected, respectively. The fraction of genetic merit that was passed along to future generations was also considered, assuming that each female generated her own replacement, and that one-half, one-quarter, and one-eighth of her genetic superiority or inferiority would be passed along to her daughter, granddaughter, and great-granddaughter, respectively. When future generations were considered with a discount rate of 5% per year, the net present value of the break-even gain in breeding value was $206, 103, 69, 52, 41, 34, 29, 26, or 23, respectively, depending on the proportion of animals selected. Lastly, strategies were considered in which the producers pre-sorted animals based on pedigree information (if available) and then DNA tested the top 50% or bottom 50% of animals in each age group, rather than DNA testing the entire herd. Results are shown below.

Table 6. Average Lifetime Net Merit breeding values ($) for **heifer calves** selected based on genetic predictions from pedigree, performance, and low-density genotyping data (Trad = no DNA testing, All = DNA testing whole herd with 3K chip, Top = DNA testing top half of herd, Bot = DNA testing bottom half of herd) for simulated herds in this study. Cases in which testing costs are offset by gains in genetic merit in the current generation (underlined and bold) or in current plus future generations (underlined) are highlighted.

%	Unknown Ancestry				Sire-Identified				Full Pedigree			
Selected	Trad	All	Top	Bot	Trad	All	Top	Bot	Trad	All	Top	Bot
Top 10	245	**612**	**531**	389	474	628	630	503	550	664	667	563
Top 20	247	**537**	**443**	**361**	429	554	**540**	459	485	580	**577**	502
Top 30	245	**487**	**382**	**346**	395	501	**475**	427	444	523	**511**	462
Top 40	245	**445**	**344**	**334**	370	**458**	**419**	402	410	477	450	432
Top 50	246	**410**	**320**	**322**	350	**422**	381	382	381	436	404	405
Top 60	246	**378**	**302**	**312**	329	387	351	**364**	354	399	368	382
Top 70	246	**347**	**287**	**306**	311	355	324	**346**	329	364	338	**359**
Top 80	246	**318**	**274**	**296**	292	323	299	**320**	305	329	309	**329**
Top 90	246	**286**	261	**278**	272	289	275	289	279	293	280	293

As shown in Table 6, genomic testing of all heifer calves seems to be cost-effective if pedigree information is unavailable. This could be the case if replacements were purchased (or were about to be purchased) from a source that could not provide accompanying pedigree information, or if recording of ancestry had lapsed within a given herd. As expected, the value of genomic testing is lower in herds that routinely record sire identification, and lower yet in herds with several generations of pedigree data for every animal. Nonetheless, genomic testing of heifer calves may be cost-effective in such herds, particularly if animals are pre-sorted prior to testing.

Table 7. Average Lifetime Net Merit breeding values ($) for **yearling heifers** selected based on genetic predictions from pedigree, performance, and low-density genotyping data (Trad = no DNA testing, All = DNA testing whole herd with 3K chip, Top = DNA testing top half of herd, Bot = DNA testing bottom half of herd) for simulated herds in this study. Cases in which testing costs are offset by gains in genetic merit in the current generation (underlined and bold) or in current plus future generations (underlined) are highlighted.

%	Unknown Ancestry				Sire-Identified				Full Pedigree			
Selected	Trad	All	Top	Bot	Trad	All	Top	Bot	Trad	All	Top	Bot
Top 10	194	**569**	**489**	336	433	592	590	461	505	621	626	516
Top 20	193	**491**	**399**	**309**	385	510	**501**	413	439	534	**532**	455
Top 30	194	**440**	**334**	**293**	352	458	**435**	382	395	477	**464**	414
Top 40	197	**400**	**297**	**282**	328	412	**376**	357	362	429	403	383
Top 50	197	**365**	**272**	**273**	305	375	335	335	334	389	357	357
Top 60	196	**332**	**254**	**265**	283	340	303	**316**	307	351	321	335
Top 70	197	**301**	**239**	**256**	263	308	274	**298**	283	315	289	**311**
Top 80	197	**270**	**225**	**247**	242	274	250	**272**	257	280	260	**280**
Top 90	197	**237**	211	**229**	222	240	225	239	230	243	231	243

As shown in Table 7, testing yearling heifers can also be cost-effective, particularly if pedigree information is lacking, or if testing is targeted toward a group of animals that are "at risk" for selection or culling based on pedigree data. For example, a buyer who seeks to purchase the top 20% of heifers from a herd will find little value in testing animals that rank in the bottom half of the herd based on pedigree data, because few of these animals will rank among the top 20% after testing. Conversely, a producer who has used gender-selected semen and seeks to cull the bottom 30% of heifers based on genomic testing will find little value in testing animals that rank in the top half of the herd based on pedigree data, because most of them will be kept anyway.

Table 8. Average Lifetime Net Merit breeding values ($) for **first lactation cows** selected based on genetic predictions from pedigree, performance, and low-density genotyping data (Trad = no DNA testing, All = DNA testing whole herd with 3K chip, Top = DNA testing top half of herd, Bot = DNA testing bottom half of herd) for simulated herds in this study. Cases in which testing costs are offset by gains in genetic merit in the current generation (underlined and bold) or in current plus future generations (underlined) are highlighted.

%	Unknown Ancestry				Sire-Identified				Full Pedigree			
Selected	Trad	All	Top	Bot	Trad	All	Top	Bot	Trad	All	Top	Bot
Top 10	359	524	516	393	465	545	556	470	508	571	577	505
Top 20	317	447	**428**	353	403	466	469	411	435	484	489	437
Top 30	286	393	**366**	320	355	409	407	368	384	426	428	390
Top 40	262	**352**	**312**	296	317	365	349	333	343	379	369	352
Top 50	239	**315**	273	**275**	287	326	303	304	309	337	321	321
Top 60	220	**281**	242	**256**	259	290	267	279	277	299	282	293
Top 70	202	249	216	**237**	233	256	237	256	246	263	247	264
Top 80	184	217	193	**214**	206	221	208	224	215	227	215	229
Top 90	166	184	169	183	178	186	178	187	182	189	182	190

Table 9. Average Lifetime Net Merit breeding values ($) for **second lactation cows** selected based on genetic predictions from pedigree, performance, and low-density genotyping data (Trad = no DNA testing, All = DNA testing whole herd with 3K chip, Top = DNA testing top half of herd, Bot = DNA testing bottom half of herd) for simulated herds in this study. Cases in which testing costs are offset by gains in genetic merit in the current generation (underlined and bold) or in current plus future generations (underlined) are highlighted.

%	Unknown Ancestry				Sire-Identified				Full Pedigree			
Selected	Trad	All	Top	Bot	Trad	All	Top	Bot	Trad	All	Top	Bot
Top 10	344	493	492	364	433	514	523	437	484	537	544	481
Top 20	293	413	**403**	320	366	432	437	372	400	446	453	403
Top 30	257	357	**336**	287	321	373	371	328	346	385	388	349
Top 40	228	314	**277**	259	283	325	312	294	303	336	329	310
Top 50	203	**274**	235	236	248	284	264	265	266	293	278	278
Top 60	181	238	202	**215**	218	246	225	240	233	254	238	249
Top 70	162	205	173	**195**	189	211	193	211	200	216	202	218
Top 80	141	171	147	**168**	161	175	162	177	168	180	168	181
Top 90	119	136	122	135	130	138	130	139	134	141	134	142

Table 10. Average Lifetime Net Merit breeding values ($) for **third lactation cows** selected based on genetic predictions from pedigree, performance, and low-density genotyping data (Trad = no DNA testing, All = DNA testing whole herd with 3K chip, Top = DNA testing top half of herd, Bot = DNA testing bottom half of herd) for simulated herds in this study. Cases in which testing costs are offset by gains in genetic merit in the current generation (underlined and bold) or in current plus future generations (underlined) are highlighted.

%	Unknown Ancestry				Sire-Identified				Full Pedigree			
Selected	Trad	All	Top	Bot	Trad	All	Top	Bot	Trad	All	Top	Bot
Top 10	288	438	438	308	382	459	467	385	422	474	481	421
Top 20	242	362	**352**	264	317	375	380	320	347	389	396	345
Top 30	207	303	**286**	231	270	316	319	275	296	330	333	297
Top 40	181	259	**226**	206	233	272	261	242	253	281	273	260
Top 50	155	221	184	183	199	230	212	213	214	238	224	226
Top 60	131	185	152	**164**	168	193	173	186	180	200	185	196
Top 70	112	152	123	**143**	137	157	140	158	148	163	149	164
Top 80	91	119	97	**116**	107	122	108	124	115	126	115	127
Top 90	67	83	69	83	76	85	77	86	81	87	81	87

As shown in Tables 8, 9, and 10, the value of testing young cows depends heavily on the availability (or lack thereof) of pedigree data. One or two lactation records on a young cow cannot provide an accurate assessment of her genetic value if her ancestry is unknown, and in this case there is an opportunity to add significant accuracy through genomic testing. On the other hand, the amount of additional information provided by genomic testing is relatively small for a pedigree-recorded cow that has lactation records of her own, and in this situation a producer should pre-sort the herd (perhaps more precisely than in this study, such as into thirds or quartiles) and test only those animals that are "on the bubble" with respect to a selection or

culling decision. Although the value of genomic testing is greater if pedigree information is lacking, we do not advocate the use of genomic testing as a substitute for recording of ancestry. In fact, one cannot pre-sort the herd with any degree of accuracy without knowledge of each animal's sire, and preferably its maternal grandsire as well. Therefore, producers who keep accurate records of ancestry can more effectively target animals for DNA testing, and in this manner they can reap greater benefits from the technology.

Table 11. Average Lifetime Net Merit breeding values ($) for **fourth lactation cows** selected based on genetic predictions from pedigree, performance, and low-density genotyping data (Trad = no DNA testing, All = DNA testing whole herd with 3K chip, Top = DNA testing top half of herd, Bot = DNA testing bottom half of herd) for simulated herds in this study. Cases in which testing costs are offset by gains in genetic merit in the current generation (underlined and bold) or in current plus future generations (underlined) are highlighted.

%	Unknown Ancestry				Sire-Identified				Full Pedigree			
Selected	Trad	All	Top	Bot	Trad	All	Top	Bot	Trad	All	Top	Bot
Top 10	246	387	391	267	334	413	421	336	371	427	433	371
Top 20	197	311	**305**	215	266	324	332	267	293	336	341	293
Top 30	160	256	**236**	185	220	267	267	224	243	276	279	245
Top 40	130	211	**176**	158	182	220	211	189	199	225	220	205
Top 50	108	171	135	135	149	179	163	160	162	184	170	171
Top 60	84	134	100	**113**	118	142	122	135	126	146	131	143
Top 70	61	100	71	**93**	86	105	88	107	95	110	97	111
Top 80	38	66	44	**64**	56	70	57	71	63	73	62	74
Top 90	15	31	18	31	25	32	25	34	28	34	28	35

Table 12. Average Lifetime Net Merit breeding values ($) for **fifth lactation cows** selected based on genetic predictions from pedigree, performance, and low-density genotyping data (Trad = no DNA testing, All = DNA testing whole herd with 3K chip, Top = DNA testing top half of herd, Bot = DNA testing bottom half of herd) for simulated herds in this study. Cases in which testing costs are offset by gains in genetic merit in the current generation (underlined and bold) or in current plus future generations (underlined) are highlighted.

%	Unknown Ancestry				Sire-Identified				Full Pedigree			
Selected	Trad	All	Top	Bot	Trad	All	Top	Bot	Trad	All	Top	Bot
Top 10	208	334	333	226	288	350	359	289	318	371	374	318
Top 20	147	253	**246**	170	220	267	274	220	241	282	288	240
Top 30	108	202	**184**	135	170	212	213	175	185	221	226	188
Top 40	80	159	**127**	107	129	167	155	140	145	175	170	148
Top 50	56	121	80	83	96	128	107	110	110	133	121	118
Top 60	29	85	48	**62**	65	88	70	84	77	95	81	91
Top 70	8	51	20	**41**	35	54	37	54	44	59	45	60
Top 80	-12	16	-7	**13**	6	18	7	20	11	22	11	24
Top 90	-35	-20	-33	-20	-25	-20	-26	-19	-23	-17	-24	-16

Table 13. Average Lifetime Net Merit breeding values ($) for **sixth lactation cows** selected based on genetic predictions from pedigree, performance, and low-density genotyping data (Trad = no DNA testing, All = DNA testing whole herd with 3K chip, Top = DNA testing top half of herd, Bot = DNA testing bottom half of herd) for simulated herds in this study. Cases in which testing costs are offset by gains in genetic merit in the current generation (underlined and bold) or in current plus future generations (underlined) are highlighted.

%	Unknown Ancestry				Sire-Identified				Full Pedigree			
Selected	Trad	All	Top	Bot	Trad	All	Top	Bot	Trad	All	Top	Bot
Top 10	161	288	285	173	223	299	304	226	261	322	330	263
Top 20	109	205	195	134	158	218	221	158	184	231	235	185
Top 30	63	150	**130**	91	117	157	158	119	135	165	168	135
Top 40	37	104	75	57	76	109	101	86	94	117	113	100
Top 50	7	66	30	36	40	71	57	54	55	78	66	65
Top 60	-17	31	-3	**13**	11	35	17	28	24	41	26	37
Top 70	-41	-3	-32	**-9**	-19	0	-16	-1	-9	5	-7	6
Top 80	-63	-37	-58	**-39**	-49	-34	-47	-34	-40	-31	-40	-30
Top 90	-88	-73	-86	-73	-80	-71	-79	-71	-75	-70	-75	-69

As shown in Tables 11, 12, and 13, the value of testing older cows within a herd is less than that of testing younger cows, and substantially less than that of testing yearling heifers and calves. Many animals have already culled themselves from the herd prior to fourth or fifth lactation, through poor performance, impaired health, or infertility, and therefore additional opportunities for culling are limited. Furthermore, using older animals to produce additional replacements, such as through embryo transfer or the use of gender-selected semen, will not be particularly beneficial, because these animals have fallen victim to genetic trend and are not genetically competitive with their daughters' and granddaughters' generations.

Conclusions

In summary, it is clear that genomic information can enhance the accuracy of genetic evaluations for bulls, cows, heifers, and calves. Breeding companies are now marketing hundreds of young bulls based solely on genomic information. These bulls have higher average genetic merit than older bulls that have completed progeny testing, but reliability values are lower. Using a single genome-tested bull very heavily is a significant risk, but ignoring these young bulls as a group has a heavy opportunity cost. To date, price has largely limited genotyping to males and elite females. However, the recent development of low-density assays that facilitate imputation of high-density genotypes from a reference population of AI sires allows users to capture the majority of benefits for a fraction of the price. This may lead to widespread adoption of genomic testing of cows, heifers, and calves on commercial farms, particularly in herds that lack pedigree information or herds that can effectively pre-sort animals based on pedigree data. Potential applications include selection among heifer calves or springing heifers on farms that have used gender-selected semen, screening of heifers or cows prior to purchase by herds that are expanding, evaluation of potentially elite heifers and cows that could provide added revenue through sale of breeding stock, and eventually value-added services such as genome-enhanced mate selection and genome-guided management protocols.

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