

# Selection Changes in the United States Due to Genomics

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## Abstract

Recent changes in U.S. breeding programs that resulted from the implementation of genomic evaluation were documented. In 2013, over 146 000 females and 20 000 males were genotyped in the United States. Mean number of U.S. bulls that entered artificial insemination (AI) service from 2008 to 2013 was 2 033. From 2010 to 2013, mean age of sires when AI bulls were born decreased from 7.2 to 3.6 years, and mean age of dams decreased from 3.9 to 3.2 years. Reductions for mean ages of paternal and maternal grandparents were similar to those reflected in (respective) parents; largest decreases were for paternal grandsires (from 14.0 to 9.6 years) and for paternal granddams (from 11.6 to 7.3 years). For bulls that entered AI service over the same 5 years, the percentage that resulted from embryo transfer increased from 76 to 89. For bulls entering AI from 2008 to 2013, genetic gains for milk, fat, and protein yields and the three lifetime merit indexes were around twice the gains for bulls entering AI from 2005 to 2008; comparable later genetic gain difference for productive life was slightly higher. For potential future genetic changes based on breeding records, comparable gains were 50% for milk yield and 60% for fat and protein yields. The use of genomic predictions has accelerated genetic improvement for most currently evaluated traits.

**Key words:** genomics, selection, artificial insemination, genotype, genetic improvement, breeding

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## Introduction

Commercial genotyping of dairy cattle was initiated in the United States in late 2007 (Wiggans *et al.*, 2011b). Genomics has revolutionized the way breeding programs are operated. The objective of this study was to document changes in selection practices through examination of available resources and their effects on parent choices for replacement animals and on genetic improvement.

## Materials and Methods

Information stored in the Council on Dairy Cattle Breeding's national dairy database was used to examine changes in selection practice in the United States that were attributed to the onset of genotyping and genomic evaluation. The number of genotyped U.S. animals was documented by breed and sex across time as were mean ancestor ages for bulls entering artificial insemination (AI) service. Means of

predicted transmitting abilities (PTAs) by year entered AI were calculated for Holstein bulls using April 2014 evaluations. Future changes in PTAs were projected by examining breeding records.

## Results & Discussion

### *Genotyped Animals*

The numbers of genotyped U.S. males and females have grown steadily since 2007 (Table 1). For genotyped Holsteins, number of females increased from 2 740 in 2008 to 125 314 in 2013; number of males increased from 8 810 to 17 417. For genotyped Jerseys, corresponding increases were from 90 to 20 206 for females and 1 123 to 2 829 for males; for genotyped Brown Swiss, increases were from 3 to 632 for females and from 62 to 170 for males. Genotyping for other breeds was limited.

**Table 1.** Numbers of genotyped U.S. dairy cattle by breed, sex, and year.

Breed	Sex	2007	2008	2009	2010	2011	2012	2013
Brown Swiss	Female	0	3	58	42	508	416	632
	Male	0	62	762	150	112	238	170
Holstein	Female	77	2 740	4 445	14 212	37 091	81 382	125 314
	Male	2 389	8 810	7 083	6 786	9 668	11 699	17 417
Jersey	Female	0	90	532	3 201	7 427	12 640	20 206
	Male	1	1 123	1 290	757	1 287	1 598	2 829

### Ages

The number of bulls that entered AI service varied from 2005 through 2013 (Table 2), but no general decline was evident after the initiation of genomic evaluation in 2009 (Wiggans *et al.*, 2011b); mean number of U.S. bulls that entered artificial insemination (AI) service from 2008 to 2013 was 2 033. The percentage of bulls entering AI service coded as progeny test from 2008 to 2013 declined from 96 to 58, while the percentage coded as genomic bulls increased from 3 to 42 (not shown). For the same 5 years, the percentage of bulls entering AI service that resulted from embryo transfer increased from 76 to 89.

Mean age of bulls at entry into AI service remained largely unchanged at ~16.3 months, but ancestor ages changed drastically, especially since 2010. The most notable declines in age since 2010 were for sires (from 7.2 to 3.6 years), paternal grandsires (from 14.0 to 9.6 years), and paternal granddams (from 11.6 to 7.3 years); mean age of dams decreased from 3.9 to 3.2 years.

### Holstein Genetic Improvement

The increase per year in PTAs from 2008 to 2013 was around twice the rate from 2005 to 2008 for milk, fat, and protein yields and the three lifetime merit indexes (Table 3). Later annual PTA increases were almost 3 times the earlier rate for productive life.

The foundation for future genetic change determined from Holstein breeding records provides a direct indication of potential change (Table 4). Annual increases in PTAs from 2008 to 2013 were 50% higher for milk yield and 60% higher for fat and protein yields than those from 2005 to 2008 in contrast to increases in Table 3. Although rates of genetic progress appear to have increased in recent years, those rates are dependent on having accurate genomic predictions. Earlier PTAs based on genomic information have been shown to be overestimated (VanRaden *et al.*, 2009), and evaluation methods have been changed to reduce that bias (Wiggans *et al.*, 2011a, 2012).

**Table 2.** Mean ages of dairy bulls at entry into artificial insemination (AI) service<sup>1</sup> by year and mean ages of their ancestors at bull's birth.

Year	Bulls		Mean ancestor age (years)					
	Number	Mean age (months)	Sire	Dam	Paternal grandsire	Paternal granddam	Maternal grandsire	Maternal granddam
2005	2 142	16.5	6.8	4.5	13.5	10.7	11.1	8.6
2006	2 076	16.6	6.9	4.4	13.6	11.3	11.1	8.5
2007	2 213	16.6	6.7	4.3	13.3	11.4	11.1	8.6
2008	2 095	16.7	6.8	4.2	13.1	10.8	11.1	8.5
2009	2 065	16.7	7.4	3.9	13.6	11.3	10.7	7.8
2010	1 917	15.9	7.2	3.9	14.0	11.6	10.7	7.8
2011	2 058	15.8	5.9	4.0	12.7	9.8	10.9	7.8
2012	2 130	16.4	4.8	3.7	11.4	8.6	10.8	7.3
2013	1 931	15.9	3.6	3.2	9.6	7.3	9.5	6.7

<sup>1</sup> Ayrshire, Browns Swiss, Guernsey, Holstein, Jersey, Milking Shorthorn, and Red and White bulls that entered AI service at <30 months of age.

**Table 3.** Numbers of Holstein bulls and their mean predicted transmitting abilities (PTAs), and genetic-economic indexes in April 2014 by year of entry into artificial-insemination service.

Statistic <sup>1</sup>	2005	2006	2007	2008	2009	2010	2011	2012	2013
Bulls, no.	1 818	1 755	1 910	1 797	1 766	1 613	1 731	1 811	1 593
PTA milk, kg	144	175	180	233	249	286	335	466	533
PTA fat, kg	6	8	9	10	14	16	18	21	27
PTA fat, %	0.00	0.01	0.02	0.02	0.04	0.05	0.05	0.04	0.06
PTA protein, kg	5	7	7	8	9	10	13	17	20
PTA protein, %	0.01	0.01	0.01	0.01	0.01	0.02	0.03	0.03	0.03
PTA SCS	2.99	2.94	2.91	2.92	2.88	2.85	2.81	2.80	2.75
PTA PL, months	-0.2	0.3	0.4	0.6	1.6	2.3	2.9	3.6	4.2
PTA DPR, %	-0.4	-0.4	-0.2	-0.1	0.2	0.2	0.5	0.5	0.8
PTA HCR, %	-0.2	-0.3	0.0	0.0	0.3	0.5	0.6	0.7	1.0
PTA CCR, %	-1.3	-1.3	-1.1	-1.0	-0.4	-0.2	0.2	0.4	1.0
Net merit, \$	73	133	161	195	281	335	426	511	618
Fluid merit, \$	66	119	146	182	260	312	388	472	571
Cheese merit, \$	84	149	177	210	305	361	467	553	668

<sup>1</sup>SCS = somatic cell score, PL = productive life, DPR = daughter pregnancy rate, HCR = heifer conception rate, and CCR = cow conception rate.

**Table 4.** Numbers of Holstein breeding records and mean predicted transmitting abilities (PTAs) and net merit in April 2014 for potential offspring by breeding year.

Statistic <sup>1</sup>	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013
Breedings, millions	0.72	0.74	0.84	1.02	1.10	1.11	1.25	1.29	1.32	1.33
PTA milk, kg	-2	41	76	102	128	161	195	229	284	341
PTA fat, kg	-0.5	0.9	2.7	4	4.9	6.9	8.7	10.5	12.5	15.6
PTA protein, kg	-0.2	1.1	2.4	3.2	3.9	5.2	6.4	7.6	9.4	11.5
PTA PL, months	-0.13	-0.15	-0.14	-0.05	0.03	0.14	0.21	0.26	0.37	0.4
PTA DPR, %	-0.09	0.03	0.12	0.33	0.56	0.94	1.3	1.59	2.03	2.44
Net merit, \$	-14	17	49	82	111	160	207	249	305	367

<sup>1</sup>PL = productive life and DPR = daughter pregnancy rate.

## Conclusions

Industry acceptance of genomic predictions has resulted in shorter generation intervals as evidenced by declines in ancestor ages for bulls entering AI. The use of genomic predictions has accelerated genetic improvement for most currently evaluated traits.

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