Changes to evaluation system (April 2008)

Genomic prediction

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Genomic predictions of genetic merit are being released for the first time. Those predictions are based on genotypes derived from blood samples (or other DNA) provided by animal owners through arrangements made by participating artificial-insemination (AI) organizations. The DNA was extracted from the samples in most cases by GeneSeek (Lincoln, NE). The extracted DNA was then placed on a chip developed by Illumina (San Diego, CA), USDA's Bovine Functional Genomics Laboratory (Beltsville, MD), and other research partners. That chip provides genotypes on more than 50,000 single nucleotide polymorphisms (SNPs) evenly distributed across all 30 chromosomes; of those SNPs, nearly 40,000 are informative for Holsteins. The genotypes document which genes each animal inherited, and that completely new source of information can be included in genetic evaluations. Predicted transmitting abilities (PTAs) have used pedigrees to calculate probabilities that relatives share genes. With genotypes, the actual genes that are shared can be determined.

The DNA of 5,285 proven Holstein bulls contributed by members of the National Association of Animal Breeders (Columbia, MO), Semex Alliance (Guelph, ON, Canada), and some other projects was used in estimating genetic effects for each SNP. The DNA of 75 cows with records was also included. Each animal's PTA or parent average (PA) for each trait as well as its net merit index was then adjusted for the sum of the estimated genetic effects. The primary focus was to calculate genomic evaluations for 623 young bulls and 29 heifers nominated by the participating AI organizations. Evaluations of the nominated animals (including the 75 cows) were distributed to the U.S. owners (see example mailer) and to the organizations that paid for genotyping to aid in selection decisions. The AI organizations that contributed to the research have a 5-year period of exclusive rights to obtain genomic evaluations of males. Evaluations of females will be available to anyone who provides a genotype through a cooperating organization.

Reliability of the young bulls averaged 36% for net merit PA but increased to 76% when genomic information was included. The theoretical reliabilities reported for this first evaluation averaged 9% higher than true reliabilities in research tests, and future adjustments to the reported genomic reliabilities are needed. Genomic evaluations of proven bulls had significantly higher theoretical and true reliabilities than traditional evaluations for nearly all traits. For young bulls, genomic PTAs for some traits averaged a little lower than PAs because upward biases in PAs were being corrected. For example, genomic net merit averaged $367 compared with $427 for traditional PA; genomic PTA for protein averaged 32 pounds compared with 39 pounds for traditional PA. The following table below provides more complete statistics:

	PTA/PA			Standard deviation			Reliability (%)	
Trait	**Genomic**	**Traditional**	**Difference[1]**	**Genomic**	**Traditional**	**Difference[2]**	**Genomic**	**Traditional**
Net merit ($)	367	427	**−60**	136	107	**95**	71	36
Milk (pounds)	968	1,207	**−239**	523	373	**425**	75	39
Fat (pounds)	42	52	**−10**	20	16	**15**	75	39
Protein (pounds)	32	39	**−7**	14	10	**11**	75	39
Productive life (months)	2.1	2.4	**−0.3**	1.8	1.5	**1.2**	65	31
Somatic cell score	2.89	2.89	**0.00**	0.15	0.11	**0.12**	70	34
Daughter pregnancy rate (%)	−0.2	−0.4	**0.2**	1.2	1.0	**0.8**	64	30
Final score	2.33	2.54	**−0.21**	0.69	0.57	**0.46**	70	36
Sire calving ease (%)	7.6	7.5	**0.1**	1.4	1.1	**1.0**	67	33
Daughter calving ease (%)	7.1	7.1	**0.0**	1.1	0.9	**1.0**	63	28

[1]Genomic PTA minus traditional PA.
[2]Standard deviation of difference between genomic PTA and traditional PA.

Two different evaluations predict the merit of an animal's daughters and sons separately. The difference is the sum of genetic effects on the X chromosome. The standard deviation of the difference between daughter and son merit is about one-tenth of the genetic standard deviation for most traits.

Genomic predictions should not be used in advertising. More research and education is needed before they can replace official PTAs, and methods to incorporate genomic information into evaluations of relatives that have not been genotyped are being developed. Statistical methods and results from both simulated and real genomic data have been reported by

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