Update on Genomic Calculations and Evaluations

There has been a great deal of discussion and interest regarding the April genetic evaluation. Following is some information that may be helpful in understanding what contributed to some of the changes.

Last year, USDA informed the industry that a large number of families had been genotyped, and from that information, the genotypes of their dams could be derived (or imputed) with 97 percent accuracy. This news was well-received by the industry, as it meant that more animals would receive a genomic prediction with no additional genotyping costs. This would also help usher in a lower cost genotyping tool using 3,000 SNPs (Single Nucleotide Polymorphisms). USDA was encouraged to pursue the use of these genotypes, derived by imputation, in the genomic predictions.

However, an unresolved problem was bias in the genomic predictions. USDA believed that the genomic predictions were too high on young animals because the Traditional Parent Averages were too high. The problem was mostly in the dam's PTAs. They wanted to lower the heritability in an effort to control the bias.

In the interim, more cows got genotyped and the bias problem grew. Evaluations on proven bulls were being questioned more often, as AIPL received many complaints from the industry about biases in genomic evaluations for bulls that had large proportions of genotyped daughters. More research by USDA lead to a new procedure that adjusted the cow PTAs by scaling the difference between the cow's PTA and her Parent Average (PA).

This led the USDA to introduce the rescaling cow PTAs and imputing dam's genotypes.

Two important changes were proposed:

1. Rescale cow PTAs - scaling down the difference between the cow's PTA and her PA applied to genomic animals only.
2. Impute dam's genotype for cows with five or more genomically-tested progeny – these cows would now receive a genomic prediction for the first time.

Based upon the April evaluations, the impact of these changes on the 1,471 imputed cows were:

1. Adjustment - Rescale of cow PTAs
   - Average change -136.7 NM$
   - 2 percent went up, 98 percent went down
2. Imputation of genomic predictions
   - Average change -37.5 NM$
   - 39 percent went up, 61 percent went down
3. Combined impact
   - Average change -174.2 NM$
   - 5 percent went up, 95 percent went down

The rescaling of cow PTAs had the larger impact, adjusting 98 percent of the dams down. Calculating genomic predictions from imputed genotypes had a more neutral impact with 61 percent of the cows going down and 39 percent of them going up.

The combined effect of both changes resulted in 95 percent of the imputed cows to go down and 5 percent to go up.

Here are two actual examples of cows that were impacted by the changes:

	January	April		
	PTA Milk	USDA Adjustment Rescale of PTA	Imputation & genomic prediction	Final PTA Milk
Cow A	+728	Brought her down -509	Brought her up +791	+1030
Cow B	+1576	Brought her down -380	Brought her down -484	+712

Though some animals saw large changes, it's important to remember that these changes have lead to more accurate genomic predictions:

- Over-prediction of young animals is less of a problem. For example, the genomic young sires now average 58 NM$ less in April than they did in January.
- Genomic predictions on young animals are much more in agreement with their Parent Averages.
- New results have been validated by using the 2006 genetic evaluations to predict the new 2010 genetic evaluations.
- Accuracy of predictions has increased, resulting in a gain of 3 percent reliability for yield traits.

In the end, the overall accuracy of genetic evaluations has been improved. However, it is recognized that, as an industry, we could have done a better job of informing dairy producers of those changes before they went into effect, and how those changes might impact animals in their herd.