

Multi-breed Genetic Evaluation powered by BOLT

Are the New BOLT-Derived EPDs More Accurate Than Previous Cornell EPDs?

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The ASA and International Genetic Solution (IGS) partners invested in a new and improved genetic evaluation software called BOLT to replace the Cornell EPD evaluation system. Among other benefits, this enables the use of Single-step methods for incorporating genomic information into the National Cattle Evaluation instead of the blending approach. In the Single-step process, the DNA marker genotypes are directly incorporated into the genetic evaluation along with the phenotypes (performance data) and the pedigree. As a result, the genomic data has an impact not only on the genotyped individual, but also on all the relatives of that genotyped individual. This allows for the genomic information to improve the accuracy of non-genotyped relatives.

The Multi-breed Genetic Evaluation powered by BOLT squeezes more information from the DNA markers by allowing for certain DNA markers to have a larger influence on predicting the genetic merit of an animal than other DNA markers while some DNA markers to have no effects on trait(s) of interest. This model is closer to what we expect based on biology where some parts of an

animal's genome (or genes) play more important roles than other parts of its genome (or genes). This is unique to the IGS Single-step method compared to other organizations where the DNA marker information is used to adjust relationships among the individuals.

Are the BOLT EPDs more accurate than the Cornell derived EPDs in the real world? To answer this question, we performed a validation study where we ran a data set (pedigree, performance, genomics) through both genetic evaluation software (BOLT and Cornell) to compare the accuracies of the EPDs produced. To enable a fair comparison, we removed the performance records of animals born in 2015 and later from the evaluation in both systems to be used as progeny performance records for validation purposes. Table 1 shows the correlations between EPDs and progeny performance of non-genotyped sires evaluated in both systems that have progeny born in 2015 or later with recorded birth, weaning, and yearling weights. As shown, the BOLT EPDs are more accurate than Cornell EPDs as the correlations are higher for BOLT EPDs with sires' progeny performances.

Table 1 - The correlations between BOLT vs. Cornell EPDs with progeny performance of non-genotyped sires for birth, weaning and yearling weights.

Trait	N of Sires	BOLT	Cornell
Birth weight	29,154	0.34	0.27
Weaning weight	21,571	0.29	0.19
Yearling weight	10,849	0.26	0.20

To have a better sense of improvement in accuracies, we ranked sires based on either BOLT or Cornell EPDs for birth, weaning and yearling weights. Then, we compared the progeny performance of the top 1% vs bottom 1% ranked sires for each trait in each evaluation system. The results are shown in Table 2.

Table 2 - The average progeny performance of non-genotyped sires ranked based on either BOLT or Cornell EPDs.

Trait	N of sires	BOLT			Cornell			BOLT vs Cornell
		Top 1%	Bottom 1%	Difference	Top 1%	Bottom 1%	Difference	Top 1%
BW	29,151	74.2	95.9	+21.7	76.0	92.8	+16.8	+3.1
WW	21,571	655.3	546.2	+109.1	638.5	558.6	+79.9	+16.8
YW	10,849	1,151.5	915.8	+235.7	1,111.3	895.6	+215.7	+40.2

As you can see, the BOLT EPDs ranked sires more accurately than EPDs from the Cornell software, where progenies of top 1% ranked sires based on the BOLT EPDs are +3.1, +16.8 and +40.2 lb heavier at birth, weaning and yearling. These results are exciting, and show that our investment in new technology will lead to more accurate EPDs. ♦