Updates to Growth Trait Predictions

By the International Genetic Solutions Science Team

The genetic evaluation is constantly evolving with updates to models as new science is discovered and new technologies are available. One area under recent scrutiny is the prediction of growth traits (birth, weaning, and yearling weights, and milk). The International Genetic Solutions (IGS) Genetic Evaluation Science Team is implementing the following five areas of improvement for the prediction of growth traits.

1. A new definition of contemporary groups based on the age of the dam.

Regardless of how users designate contemporary groups (CG), all calves born from first-calf dams will be placed into a separate CG from calves out of mature cows. Given the vast majority of producers actually manage this age group separately, it is reasonable to define their calves as their own CG. Handling these as separate CG will reduce the environmental noise caused by different management strategies and biological constraints for this age group.

2. Milk modeling updates.

The magnitude, and even direction, of the correlation between weaning weight direct and milk, has been long debated in scientific circles. In fact, there is a wide range of estimates that exist in the scientific literature. Given that, the science team developed a model that assumes milk and weaning weight direct are independent (i.e., genetic correlation of 0). In addition, with some of the other proposed updates, it was discovered that the evaluation solved more effectively when genomics were removed for Milk EPDs. In light of this discovery, the IGS Milk EPD will not use genomic information for the time being.

3. Different variances for different sexes.

Males usually have a higher growth potential than females simply due to gender. As a consequence, the variation associated with their weights also tends to be greater. This difference in the amount of variation between the sexes are set to a male scale in the up-dated growth trait predictions.

4. New DNA Marker subset.

As the number of genotyped animals has increased, so has our ability to estimate marker effects and identify subsets that are more predictive. Relative to growth traits, a new (and larger) subset of markers has been identified to add more accuracy to EPD.

5. Accounting for different birth weight collection methods.

When we began looking into growth trait data, we discovered that not all birth weights followed expected amounts of variation. Some of the examples of reduced variation included weights rounded to the nearest 5 pounds, reduced variation when hoof tapes were used, and likely-fabricated data with little to no variation. Some of these data are useful, but they are clearly on a different scale and need to be treated appropriately. Dr. Bruce Golden developed a way to use machine learning to recognize unique features of each class of birth weight observation and predict how it was obtained. By accounting for the various categories, the genetic evaluation is still able to use submitted records that fall out of biological expectations for most scenarios, while more accurately accounting for different practices of collecting the weights.

Results of Updates to Growth Model

With these proposed changes, a considerable amount of work went into testing if the new models improved growth trait predictions. One of the most common procedures for evaluating updates to EPD systems is to exclude a certain portion of the phenotypes available, run the evaluation, and compare the correlation of the EPD from two systems to the phenotypes that were removed from the evaluation (higher correlation is better). For these updates, this procedure was used where all animals born after 2018 were excluded from the evaluation system and then comparisons between the current growth trait EPDs and the updated EPDs were made to this phenotypic information. The results for each of the analyses are presented in the following table.

Pearson correlation between parental average EPDs and excluded phenotypes from animals in the IGS genetic evaluation that were born in 2018 or later.

Trait	Updated Evaluation	Previous Evaluation
Birth Weight	0.52	0.50
Weaning Weight	0.38	0.34
Yearling Weight	0.45	0.37

The results in the table above show the evaluation updates had higher correlations to phenotypes than the previous growth trait models. This equates to more precise EPDs for Birth, Weaning, and Yearling Weight.

An additional trait that is evaluated with the growth analysis is the Milk EPD. A Milk EPD represents the genetic difference in calf weaning weight based on the maternal environment provided by the dam. Due to the nature of this trait being the maternal component of weaning weight, a different validation strategy must be used to evaluate the updated predictions. To evaluate the updated Milk predictions an expected weaning weight for the excluded animals was formed using the following equation:

Predicted Weaning Weight = Calf WW EBV + Dam's Milk EBV

This predicted weaning weight was then correlated with the excluded weaning weight phenotypes. Again, the updated predictions of Milk had higher correlations compared to the previous Milk EPDs (0.42 vs. 0.39, respectively). These results show that the updated predictions more precisely predict the weaning weight of an animal than the currently published evaluation.

Breeders may notice reranking of animals with the release of the growth trait updates. While the change may be unsettling, the end results by every measure have shown an improvement in the precision of the growth trait predictions. **ST**