



Kansas City- Listed below are some points of interest released by IGS regarding the publication of single-step EPD evaluations, powered by the new BOLT software.

Here are the notable changes in the evaluation:

Movement of EPDs and reranking: EPDs and indexes will change. These changes will be more dramatic for younger, lower accuracy cattle. The IGS team has tested the changes and proven the new EPDs result in superior predictions of genetic merit.

Shrinking of EPD range: You will notice a reduction in the range of EPDs for most traits. The IGS evaluation team tested the statistical veracity of the reduction and it has proven to be in line with expectations based on the genetic variation in the population.

Improved use of genomics: With the switch to the BOLT software, IGS will use single-step genomic evaluation on all EPDs. Single-step uses DNA markers, pedigree information, and phenotypic data simultaneously in the prediction of EPDs. Previously, molecular breeding values (MBVs) were calculated from the genomic information and those MBVs were blended in a separate procedure into the EPD predictions. The single-step method squeezes more information from the DNA markers than the previous approach allowed. Additionally, with single-step, the genomic information will not only enhance each EPD for the genotyped animals but also will be used in the EPD estimates of relatives.

It is well established that DNA markers vary greatly in their effect on traits - ranging from large to virtually no impact. To leverage this biological fact in a statistically advantageous manner, the BOLT single-step method only uses markers that have a meaningful impact on the traits of interest, while ignoring those that have little to no effect. Research has shown that by using this approach, BOLT reduces statistical "noise" and thereby increases the accuracy of the EPD prediction compared to other single-step methods. It is important to note, continued collection of phenotypic records remains a vital part of genetic predictions. DNA testing will never replace the need to record and submit phenotypes.

More accurate accuracy: In the previous IGS evaluation platform, and all others in existence other than BOLT, the calculation of the accuracy associated with each EPD is achieved through "approximation" methods. It has long been known these methods are a less than optimal approach to the calculation of accuracy - tending to overestimate accuracy. By employing unique computing strategies that leverage both software and hardware efficiencies, BOLT performs what was previously unthinkable - utilizing a sampling methodology to calculate what is essentially true accuracy. Unlike approximated accuracies, BOLT-derived accuracies will result in predicted movements associated with possible change holding true over time. This is not the case with the previous IGS software or any other system currently in existence.

For more information about the IGS Multi-breed Genetic Evaluation powered by BOLT, go to www.internationalgeneticsolutions.com, or contact the ASA office (816-599-7777).