

The Value of Improving Accuracy of Yearling Bulls

Matt Spangler, University of Nebraska-Lincoln

The accuracy associated with EPDs increase as more information becomes available. Initially EPDs are derived from the average of animals' parents (pedigree estimate). Once an animal has a record themselves the accuracy of the EPD increases and continues to do so as the animal has recorded progeny. This can take a long time and for some economically relevant traits (ERTs) it is not possible for animals to have a record themselves or the record may occur very late in life (i.e. stayability). The benefit of DNA-tests lies in the fact that they can be done at birth and thus have the potential to increase the accuracy of genetic predictions on young animals. That being said, the magnitude of the benefit of this is determined by the genetic correlation between DNA test results and the trait of interest.

Example: Assume that a DNA test has a genetic correlation of 0.8 with the trait of interest. This would equate to a BIF accuracy of 0.40. For traits that are hard to measure or measured late in life this would be very beneficial. Seedstock producers could identify superior animals earlier in life and commercial producers who purchase unproven sires could reduce the risk associated with low accuracy values. However, if the genetic correlation between the molecular test and the trait of interest is low (0.1) then the value of using only the genetic test score for the purposes of selection is dramatically decreased, especially in the context of having available EPDs for the trait of interest. The greatest benefit in accuracy should come from the integration of DNA tests scores along with phenotypic records in the calculation of EPDs.

What is the benefit of higher accuracy values on young sires? For the seedstock producer it enables the selection of truly superior animals earlier in life and potentially decreases the number of animals to place on test. It also allows seedstock producers to supply clientele with a product that has less risk of change associated with it. The benefit to commercial producers lies in the ability to buy yearling bulls with more certainty surrounding their EPDs.

Example: Assume a commercial producer wants to purchase a calving ease bull for use on heifers. If a bull does not have a record of calving ease himself, the BIF accuracy might be 0.20. Assume that the possible change* associated with this accuracy level is 6 and that his published EPD is +5 (breed average in this case). In this situation, we would be 68% confident that this bull's "true" EPD for calving ease is between -1 and +11 realizing that for calving ease a larger number is more desirable since it is interpreted as the percentage of unassisted births. However, if the accuracy were higher (0.5) this would mean a small possible change value (4) so we would then be 68% confident that his true EPD would be between +1 and +9. By increasing the accuracy we are increasing the correlation between the true and predicted value of a bull's EPD. Consequently, as accuracy increases it becomes easier to identify truly superior (or inferior animals).

Assume that two yearling bulls both have the same calving ease EPD of +5 with an accuracy of 0.2. From this we can be 95% confident that the true EPD of both bulls is between -7 and +17. There is value in being able to determine if one, or both, bulls is actually much worse than his yearling EPD would suggest. If these two bulls had accuracy values of 0.5 then we would have a better idea of their true genetic potential and could possibly eliminate the inferior animal. With the inclusion of additional information, such as a marker panel, we might find out that the predictions are very different with one bull having a -5 calving ease EPD and the other a +10. This is a difference of 15, or one bull would be likely to have 15% more assisted births than the other.

The traits that will benefit the most from the addition of DNA information in genetic predictions are those that are lowly heritable, difficult or expensive to measure, measured late in life, and those that are sex-specific. Combining phenotypic and molecular data, particularly for the categories listed above, can lead for faster genetic change. The factors that impact the rate of genetic change are the accuracy of selection, the genetic standard deviation, the selection intensity, and the generation interval. Generation interval is defined as the average parental age when the offspring are born. Typically this is six years of age in beef cattle. Genetic change per year can be derived by:

$$\frac{[(\text{Accuracy of Selection}) * (\text{Selection Intensity}) * (\text{Genetic Standard Deviation})]}{\text{Generation Interval}}$$

It is clear that if generation interval were to decrease then the rate of genetic change would increase. For seedstock producers, the ability to use a yearling sire heavily due to increased confidence in his EPD could reduce generation interval and thus lead to faster genetic progress.

The benefits of including molecular information in the calculation of EPDs for yearling bulls will depend on the marker panel itself. First the panel must be independently validated and proven to be significantly associated (statistically) with the trait of interest. Secondly, the more genetic variation that is explained by the trait the larger the increase in accuracy. Marker panel results should be thought of as another phenotype that can be included in the genetic prediction as being correlated to the trait of interest. With this in mind, the addition of this new phenotype adds to the amount of information and consequently provides an increase in accuracy proportional to the amount of variation explained by the panel.

There is also an advantage that is more challenging to quantify, marketing. Early adopters, those who have panel information sent to breed associations for inclusion in genetic evaluations, may have a competitive advantage over other seedstock producers who do not. This assumes that bull buyers are willing to pay more for yearling bulls with higher accuracy values.