Indicating Success

BY THE NUMBERS

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As winter-spring calving season is on the downhill slide, producers are already looking at their 2021 calves trying to get an indication of the successors this fall.

Size, stature, muscling, birth weight and health status are early indicators as to which calves will be kept and others that will be culled.

Over the next year, performance measures like weaning and yearling weights, ultrasound scan measurements, foot scores, scrotal measurements, and docility scores will be collected on the calf crop to support this decision-making process. With each data point, meticulously culling the calf crop will take place until final calls are made.

Throughout the selection process,

the population of individuals used to make the next culling decision shrinks. Figure 1 represents the number of birth, weaning and yearling weights recorded in Fiscal Year 2020. As time goes on, the number of performance weights submitted for each category shrinks.

When using this information in the genetic evaluation to predict expected progeny differences (EPDs), it is important to avoid analyzing a single trait in a vacuum by itself. Rather, use multiple-trait models where appropriate.



Figure 1: Number of individuals weights submitted for birth, weaning and yearling weights in Fiscal Year 2020. A multiple-trait model allows for the prediction of several traits at once and is especially useful when those traits have varying levels of reporting, as in the case with our weight traits. Using a multiple-trait model allows for all three weights to be utilized for the predictions of birth weight (BW), weaning weight (WW) and yearling weight (YW) EPDs, avoiding preselection bias.

Preselection bias

Preselection bias can cause problems if not correctly accounted for. At weaning time, animals may be culled for lack of performance and sold before yearling weights are collected. If that selection bias is not accounted for, yearling contemporary group differences will be skewed.

With the low-performers at weaning removed, the midlevelperformers at weaning who made the cut now look like the poorest performers at yearling. If the models ran in their own individual vacuums, there would be no indication the yearlings which weighed the least actually beat out a subset of their cohorts at weaning time.

A similar case is made in the carcass weight evaluation. Currently,

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some of the data flowing into the carcass evaluation is made up of carcass records from males not kept as breeding bulls. Some of these culled males are owned through the feedlot and that carcass data if fed back to the genetic evaluation.

Using postweaning gain in a multiple-trait carcass model allows for the avoidance of preselection bias. If all the culled males, who were steered and sent to the feedlot, are the low-performers, this could lead to inaccurately assessing the carcass weight predictions on the parents of those animals. Accounting for the fact they were indeed lower performers in their larger weaning groups avoids this risk.

Hard to measure

Multiple-trait models with the use of indicator traits are also useful when traits are expensive or hard to measure. Take, for instance, carcass data. Members do not have the ability to capture individual carcass measurements on breeding animals, but the ability does exist to capture ultrasound scan measurements to get an indication of the carcass characteristics of the animal.

By having indicator traits of percent intramuscular fat (IMF), ultrasound rib and rump fat, and ultrasound ribeye area, the genetic evaluation can get an indication of the individual carcass merit of the live animal.

Feed efficiency, which compares the feed intake and relative weight output of an animal, is another costly measurement. Systems to collect individual intake data are expensive, and some operations may not have the ability to collect this data.

However, by using a multipletrait model, weight which is readily collected by a large portion of the membership can be used as an indicator of feed intake. Why? Because it has been shown larger animals tend to eat more, so even if individual intake measurements are not present, weight is used as an indicator of feed intake.

While these types of predictions increase the rate of genetic change, they also help producers avoid unintended consequences. For instance, think of birth weight as an indicator of calving ease. Before models were built that could handle the evaluation of threshold traits like calving ease, birth weights, a much easier continuous trait to analyze, gave producers an indication of a breeding animal's genetic potential for calving ease.

The mature cow weight evaluation also uses indicator traits for this purpose. While more than 100,000 yearling weights are sent in every year, the number of mature cow weights being submitted is far less.

The good news is yearling weight is a good indicator of how large an animal will be at maturity. Having actual mature cow weights would be more informative, but yearling performance provides an indication of how large those animals will be later on in life, equipping producers with a more accurate tool to predict a parent's genetic potential for mature size.

Correlation

The informativeness of an indicator trait depends on the correlation, or strength of relationship, between the indicator trait and the direct trait of interest.

Correlations range from -1 to +1 and provide an indication of whether two traits are controlled by the same genes. Traits with zero correlation are not controlled by the same genes and share no relationship to one another, so fitting two traits with a zero correlation is not useful. A positive correlation indicates traits move in the same direction.

Birth weight is used as an indicator trait for calving ease. The relationship among these traits is -0.65, which is a strong negative correlation — meaning as birth weight goes down, calving ease goes up and vice versa. Ultrasound IMF has a +0.71 correlation with marbling score, so as ultrasound IMF increases, the degree of marbling increases.

What does that mean for genetic progress? Well, obviously being able to measure and select on the direct trait of emphasis is going to allow for faster genetic progress. However, by avoiding the use of indicator traits that explain a portion of the variation in the trait of interest would dramatically slow the genetic progress of the population, especially where data collection of the direct trait of interest is scarce or unavailable.

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Editor's note: For questions, contact the AGI customer service team at 816-383-5100.