

Why does this update need to take place?

As more animals are genotyped, updating core is routine maintenance that needs to take place to ensure maximum prediction accuracy and efficient evaluations. A core that fully represents the genotyped population is key to ensure our genetic evaluation is accurately assessing the genetic merit of individual animals. Core maintenance also increases the efficiency of the genetic evaluation by reducing computing time, which is essential to keeping on a weekly schedule for Angus's genetic evaluation.

What animals are included in the core?

Core 21 is a representative sample of the genotyped population which best captures the total variation of the genomic relationship matrix (GRM), or the relationships determined among animals using genomic results, which optimizes the evaluation.

How do you decide which genotyped animals are used in the genetic evaluation?

All genotyped animals are included and used in the weekly genetic evaluation. To successfully run Angus's genomic evaluation, the relationship matrix must be inverted. Because the Angus database holds nearly 1 million genotypes and modern computing power is not capable of directly inverting a GRM of this size, Core 21 is directly inverted and then combined with all other parts to calculate the inverse of the GRM for all animals. As such, Core 21 is a representative sample of the genotyped population that captures the variation in genomic relationships

How many are utilized in the core? How is that decided?

Over 20,000 animals are utilized in the core, which is a function of the effective population size and genome length of the Angus population. Effective population size and genome length are similar across all domesticated animal species, so whether you are talking about beef, pork, or poultry, a similar core size is effectively used to capture the total variation in the GRM.

How often will the core be updated going forward?

Core 21 was the first routine maintenance to take place on the genetic evaluation's GRM since the implementation of Single Step in 2017. Moving forward, the AGI team will continue to track new genotypes entering the evaluation and how they continue to affect the overall evaluation. While a set timeline is yet to be determined, AGI predicts this routine maintenance will happen more regularly in the future, perhaps every two years.

How did moderate to high accuracy animals move?

Although changes in high accuracy animals were seldom, some changes in high accuracy animals did take place. These types of changes were generally related to high use sires that were born after 2017 that have had many genotyped progenies added to the evaluation since that time.

How are ungenotyped animals used in the genetic evaluation?

Both genotyped and ungenotyped animals are used in the genetic evaluation. Through the Single Step evaluation, genotyped and ungenotyped animals are linked through the pedigree + genomic relationship matrix. Therefore, ungenotyped animals also saw some change in EPD.

My \$Values changed, were those changes due to the economic assumptions or the core update?

While both updates were made, most of the changes seen in \$Values released on May 28 were the result of core maintenance. Because the individual EPDs which feed into the \$Values changed, \$Values also changed. Updates to the economic assumptions had a lesser effect on \$Values.

How often are \$Value indexes updated?

Economic assumptions included in \$Values are updated annually and utilize a 7-year rolling average. The 2021 economic assumptions are based on prices from 2014-2020. The American Angus Association and Angus Genetics Inc. partner with CattleFax to gather these yearly adjustments.

Did additional updates take place on \$AxH or \$AxJ?

The Angus-on-Dairy indexes went through the same update process that happened with all other indexes. However, because both indexes incorporate a penalty for lack of muscling and \$AxH includes a penalty for too much height, animals that crossed these penalty thresholds as a result of the core update experienced significant change. As a result, these indexes experienced larger minimum and maximum value changes than those seen in \$B, \$M and \$C, even though correlations of \$AxH and \$AxJ with prior values were over 0.9.

Why did my genomic scores change?

Genomic scores are updated on a yearly basis as they reflect how an animal ranks in the genomic tested population. Therefore, as the population grows, genomic scores will change. With that, genomic scores are a by-product of the genetic evaluation, so as EPDs are updated, genomic scores will be updated as well. Genomic scores have no influence on the EPDs themselves.