

## GENOMIC SELECTION FOR REPRODUCTIVE TRAITS

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To provide more context to the discussion of genomic selection for reproductive traits, it may be useful to review two more general questions first, “What exactly is Genomic Selection?” and “How is it better than traditional selection methods?” To begin with, it is important to understand that most of the traits of economic importance to livestock production are influenced by both genetic and environmental variation. Furthermore, the genetic portion of variation for these traits is not inherited in simple fashion because the traits are controlled by many genes. Because of these characteristics, the identification of genetically superior individuals can be challenging. Reproductive traits are some of the most difficult traits to improve for the above reasons. This challenge can be demonstrated by examining what happens in a population of animals under selection as you go from one generation to the next. For simplicity, let’s look at an example of a commonly measured trait, weaning weight (WW), and assume that increased WW is associated with increased economic value. Before we do this, we first need to define two terms, selection differential (sometimes called “reach”) and selection response (called “gain”).

For our example, producer Smith weighs all of his calves at weaning and finds that the average weight is 550# with a range of 450# to 650#. Because he sells his calves as feeders at weaning, he would like to increase his weaning weights as much as possible. To do this, he selects his higher weaning weight replacement bulls and heifers. They have an average weaning weight of 600#, 50# heavier than his current average (e.g., reach = 50#). At this point, it is relevant to remember that producer Smith will not see the result of his selection for two years because he has to develop these replacements for eight additional months to breeding, another nine months to calving and seven more months to record his improvement in weaning weights. Finally, the anticipated weaning weight data are collected and the end result is an average WW of 564# (e.g., gain = 14#).

What went wrong? Why didn’t producer Smith capture all of his targeted performance? The primary reason is because his selection was based on individual phenotype only. Recall that the phenotype for many of these traits is controlled by both genetics and environment. Indeed, we can use this example to estimate what proportion of the population variation is due to either genetics or environment. In this case, the realized heritability (i.e., the variation due to genetics) can be calculated by dividing the “gain” by the “reach” (e.g.,  $14/50 = 0.28$  or 28%). This means that only 28% of the variation seen in WW is due to genetics. In contrast, this suggests that 72% of the variation is due to environment. In other words, even though the higher performing animals were selected for breeding, their higher performance was not necessarily due to higher genetic merit and results in the inaccurate selection of individuals.

So, how can we more accurately identify animals with higher genetic merit? Certainly, the incorporation of Expected Progeny Differences (EPDs) in animal breeding has improved genetic

progress significantly over the past 50-60 years that they have been actively used. This is because we can more accurately identify those high merit animals based on not only their individual performance, but the performance of their relatives. We have even further increased genetic progress because we can use tools such as EPDs to accurately identify higher merit animals earlier in the production cycle, thereby reducing generation interval (recall it took producer Smith two years to see his results). Even so, achieving the highest accuracy estimation of genetic merit can require many phenotypic records (i.e., to “prove” a bull’s genetic merit, many phenotypic records on his offspring are required) even if the heritability of a trait is moderately high.

This is where genomic selection has improved our ability to accurately identify those animals with the desired genetic merit. Genomic selection uses DNA markers that have been associated with variation in the measured phenotypes to assist with making these predictions. In addition, the DNA genotypes are also used to more accurately estimate the relationship between individuals. To date, there is very strong evidence that genomic selection is having a very significant positive impact on genetic progress within all the animal industries where it has been implemented (reviewed by Rexroad, et al., 2019).

So, what is it that makes reproductive traits some of the most challenging to improve genetically? Firstly, if you estimate the heritability for many of the measures we associate with reproduction, they are quite low (e.g., 10-15%), meaning that 85% to 90% of the variation we see in reproductive performance is due to environment. Just thinking about this briefly, it is probably not difficult to imagine the significant impact management (environment) can have on a herd’s reproductive success. Not very encouraging given that in our WW example above the heritability was 2-3 times higher. The exception for reproductive traits is scrotal circumference that has an estimated heritability of 35%-50%. Secondly, and to make things even more difficult, the phenotypes that we measure are only indirect indicators of reproductive merit (i.e., does a heifer get pregnant or a cow stay in the herd year after year). The truth is that direct indicators of reproductive merit have been extremely difficult to define scientifically and/or they are difficult or too expensive to routinely measure. Even so, the advantages of genomic selection, as stated above, are best applied to these difficult traits.

So what does all this mean for your breeding programs?

- Greater emphasis should be placed on matching other performance criteria to the management available in your operation, examples:
  - Don’t use high growth sires if the management of their daughters isn’t sufficient to support their reproductive development (heifer pregnancy)
  - Don’t select for high milk production if the nutritional resources aren’t available for a cow to recover and rebreed following calving (stayability)
- Genomic predictions for the currently measured traits are the best available predictors of reproductive merit, but should be used as a secondary selection criterion, examples:
  - Although traits such as heifer pregnancy and stayability are only indirect measures of reproductive merit, they may provide improvement over the long-term
  - Increased scrotal circumference is associated with positive fertility characteristics of semen that may indirectly enhance fertility, but has no genetic relationship to female fertility (i.e., daughter fertility)

Rexroad C, Vallet J, Matukumalli LK, Reecy J, Bickhart D, Blackburn H, Boggess M, Cheng H, Clutter A, Cockett N, Ernst C, Fulton JE, Liu J, Lunney J, Neibergs H, Purcell C, Smith TPL, Sonstegard T, Taylor J, Telugu B, Eenennaam AV, Tassell CPV, Wells K. 2019. Genome to Phenome: Improving Animal Health, Production, and Well-Being - A New USDA Blueprint for Animal Genome Research 2018-2027. *Front Genet.* 2019 May 16;10:327. doi: 10.3389/fgene.2019.00327.