

## Maximizing the Value of Phenotypic Data in Genetic Evaluations

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Optimizing animal genetic improvement begins by understanding the genetic differences available within the population (Wilton et al, 2013). Although differences in beef cattle genetic potential are most often expressed as Expected Progeny Differences, or EPDs, the foundation of describing these differences begins at the herd level with the collection of phenotypic data. Because the relative differences in phenotypes and not the actual phenotypes are utilized to calculate EPDs, it is imperative that breeders understand how to generate accurate, meaningful comparisons of genetic merit that will improve their understanding of the genetic potential of their herd, contribute to meaningful selection decisions, and result in genetic improvement.

At the herd level, the most critical component of genetic evaluation is the contemporary group, or animals that have been subjected to the same environmental influences throughout their life. Secondary to contemporary grouping is the distribution of progeny within the contemporary group or the number of progeny per sire represented. Because progeny distribution impacts the number of comparisons available for genetic prediction, contemporary grouping actually begins long before any calves are born. Contemporary group management begins with the development of a mating plan that will optimize progeny distribution within contemporary groups by creating sire groups of calves that are approximately equal in size and as large as possible within each sex. This is critical because contemporary groups only get smaller with age and as animals leave the contemporary group selection bias can take place.

Properly formed contemporary groups are the backbone of national cattle evaluation programs but can be a source of error if managed inappropriately. Some common issues with contemporary groups are:

1. **Size**—Properly formed contemporary groups should consist of 10 or more head of the same sex and 30 or more head are preferred. Fewer animals in a contemporary group result in a greater probability of error in determining the group mean. Because EPDs are calculated using contemporary group deviations (ratios), determining the mean as accurately as possible is critical. It is important to note that no phenotypic measurements collected are exact. Each has a certain level of measurement error. Larger contemporary groups also minimize the effect of measurement error. If small contemporary groups (< 10 head) cannot be avoided, supplementing phenotypic data with genomic testing is recommended.
2. **Sire Distribution**—Developing a mating plan to optimize sire distribution can be difficult but there are obvious issues to avoid. When a contemporary group consists of progeny of a single sire, no meaningful comparisons are generated for the sire. At least two sires should be represented in a contemporary group and at least one sire should be a reference sire. By

including a reference sire, breeders can ensure that the bull has been used in other herds and contemporary groups and has a reasonable level of accuracy associated with his EPDs; however, small to mid-size breeders often utilize too many sires and fail to generate sire groups of sufficient size. Having one or two progeny of a sire does not generate a meaningful contribution to the breeder's knowledge of the sire or how to utilize him in subsequent breeding seasons.

Another common error relative to sire distribution is using a sire exclusively on a particular age group or sire group of females. This most commonly occurs with sires used exclusively on heifers. Although using "heifer bulls" on large groups of mature cows is not advisable due to the reduction in performance and muscle expression, using a sire across the age spectrum represented in the herd is most appropriate. Even though pre-weaning performance is adjusted for age of dam, bias can occur that may temporarily skew a sire's EPDs. Additionally, evaluation of longevity traits like stayability and sustained cow fertility may utilize age class as a way to form contemporary groups in the cow herd. Having a single sire represented in an age class of females will reduce the value of these data.

- 3. Single Contemporaries**—When a contemporary group consists of only one animal, there are no comparisons that can be made. As such, phenotypic data on single contemporaries is of little value and is not used in national cattle evaluations. Genomic testing of single contemporaries is most appropriate. Even so, it is important to report animals as separate contemporary groups or as single contemporaries when management and/or environment has deviated from that of the larger group. For example, a calf whose dam became stifled during the breeding season and had to receive individual treatment.
- 4. Selection Bias**—As animals mature and selection decisions are made, contemporary group composition changes. This typically occurs post-weaning as some bull and heifer calves are selected for further development while others are culled. By doing so, selection bias is created in the phenotypes collected later in life. It is understood that submitting data on only a portion of the contemporary group creates bias and incorrect ranking of animals relative to group average; however, post-selection bias on yearling traits is often overlooked. Take yearling ultrasound data for an example, most breeders collect yearling ultrasound data on bulls because it is requested by buyers but fail to collect these data on yearling heifers even though a larger portion of heifers are retained post-weaning. Yearling bulls are a selected population representing the calves with the greatest pre-weaning performance (growth, muscle expression, etc.); however, yearling heifers have received less selection pressure and are more likely to be a representative cross section of the herd relative to sire and age of dam. Unless contemporary groups are quite large, collecting yearling ultrasound data on heifers is much more valuable for the individual breeder's knowledge of sires utilized and provides another trait that can be used to select replacement females.

- 5. Measurement Error**—Breeders should strive to collect as accurate phenotypic data as possible while understanding that no measurement is perfect—a certain amount of error is associated with each phenotype collected. It's no one's fault; it's a function of dealing with a living, breathing biological system. Phenotypes are a point-in-time estimate of the trait, and depending upon the methods utilized, can have varying levels of accuracy but are never perfect. Therefore, the primary goal of the breeder should be minimizing measurement error in collected phenotypes.

The most critical aspect of minimizing measurement error is consistency, which ranges from consistency in process to consistency in individuals collecting the data. If changes in personnel or process are needed, they should only occur between contemporary groups. The same individual and same process should be used for an entire contemporary group no matter the phenotype being collected. Secondary to consistency in reducing measurement error is collecting multiple measurements on the same animal. When multiple data points collected in a consistent manner can be aggregated, measurement error is most-often reduced. To apply this practice, collect phenotypes on two consecutive days and take the average of the two measurements. This is particularly important with body weights because body weights are highly variable and can change significantly due to gut fill. The date of the second measurement will be the reported measurement date (BIF Guidelines 9<sup>th</sup> Edition). Remember, it is not the actual measurement that matters but the relative difference among the measurements that are important.

Although phenotypic data have long been the foundation of genetic evaluation programs, genomic testing combined with advanced prediction methods have greatly expanded information available to breeders particularly early in an animal's life. Because the effect of genetic testing on prediction accuracy has often been expressed in phenotype equivalents, breeders may question the value of continuing to collect phenotypes when using genomic tests. While genomic data is a key component of advancing genetic evaluation programs, it is not a substitute for collecting phenotypic data. In fact, the two are complimentary to one another; phenotypic data inform and improve genomic predictions. With current prediction models, genomic testing progeny does not improve parent accuracy because it provides no additional information—only progeny phenotypes provide additional information and improve prediction accuracy. Therefore, collecting phenotypic data is and will remain a necessity for breeders.

Wilton, J. W., V. M. Quinton, and C. D. Quinton. *Optimizing Animal Genetic Improvement*. Centre for Genetic Improvement of Livestock, University of Guelph. 2013.

Guidelines for Uniform Beef Improvement Programs. Ninth Edition. 2018