

Beef Cattle Improvement in the Genomics Era

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Selection of cattle has been practiced for centuries using a variety of methods and tools. Early selection was based on visual observations and later on measured phenotypic traits. Development of statistical methods along with computational advances allowed handling of large data sets and the estimation of breeding values of cattle, known as Expected Progeny Differences (EPD). Widespread use of EPDs in the seedstock and commercial beef sectors resulted in great increases in the genetic propensity of beef cattle for a variety of traits including calving ease, growth and carcass composition.

Estimating EPDs for animals in a population is data-driven and the accuracy of an individual EPD is based on the amount of information available at the time when it is estimated. For this reason, young unproven bulls have EPDs with low accuracy, indicating lower reliability and high potential to change as additional data is collected on the bull. As more data become available, particularly progeny information, the accuracy of the bull's EPD increases, therefore greater reliability and smaller range within which the EPD can change with additional information. Given that commercial bull buyers could not wait for more information on the bull and the associated increase in accuracy, tools that could increase the accuracy of yearling bull EPD would be advantageous.

The sequencing of the cattle genome was followed by a revolution in genotyping offered by high-density SNP chips. The associated reduction in genotyping cost allows for large number of individuals to be genotyped across the entire genome and opportunity for the development of genomic selection as outlined by Meuwissen *et al.* (2001). The development of DNA tests for traits with information already available can enhance the accuracy of those genetic evaluations if the DNA information is seamlessly integrated into existing genetic prediction infrastructures and used to augment other sources of information. The increase in accuracy will be most pronounced in young animals with no recorded progeny, and, hence, has high value for selection of replacement animals. The magnitude of the increase in accuracy depends on available records on relatives, heritability and the portion of heritable variation accounted for by the tests (Thallman *et al.* 2009). Many traits of interest in selection programs, such as birthweight, weaning weight, ultrasound carcass scans or scrotal size can be measured on young animals before a selection decision is made. However, there are other traits which are measured later in life, expensive or difficult to record (i.e., carcass traits, meat quality or feed efficiency) and EPDs for these traits have low accuracy because individual performance or progeny records are not available.

The advantage of genomic selection over traditional methods is greatest where traditional methods are difficult to implement (Meuwissen and Goddard, 1996) – traits recorded late in life or after the selection candidate dies, traits difficult or expensive to record, traits expressed in only one sex. In genomic selection, a reference population is genotyped and recorded for the trait in order to estimate the effect of all SNPs on the high-density SNP chip. The selection candidates are then genotyped and using the estimated SNP effect from the reference population, the genomic EBV (GEBV) are estimated for selection candidates.

In beef cattle, it is necessary to generate training populations with a sufficient number of animals with high-density genotypes and key phenotypes, and the number of animals needed is larger for traits with low heritability. Even more importantly, for genomic selection to have an impact in the beef industry, accurate (i.e. reliable) GEBV across breeds or in multi-breed populations are required. GEBVs estimate from prediction equations derived in one breed have considerably lower accuracy of prediction when

applied to other breeds (de Roos *et al.* 2009) or in multi-breed beef populations (Weber *et al.* 2011). Therefore, what is currently available for the Angus breed has little value in other *Bos taurus* breeds and is even less likely to be useful in *Bos indicus* breeds. High accuracy genomic-enhanced EPDs will provide beef cattle breeders with the opportunity to increase the rate of gain by selecting their own bulls. Because the natural service will likely continue to dominate in the commercial field, the impact of genomics will likely be realized through increased accuracy in selecting young bulls and also in allowing targeted matching of genetics with production-marketing systems. To capitalize on this technology, the development of sufficiently large training populations, particularly on difficult or expensive to measure traits is needed.

References

de Roos APW, Hayes BJ, Goddard ME (2009) Reliability of genomic predictions across multiple populations. *Genetics* 183, 1545–1553.

Meuwissen THE, Hayes BJ, Goddard ME (2001) Prediction of total genetic value using genome-wide dense marker maps. *Genetics* 157, 1819–1829.

Meuwissen THE, Goddard ME (1996) The use of marker haplotypes in animal breeding schemes. *Genetics, Selection, Evolution*. 28, 161–176.

Thallman RM, Hanford KJ, Quaas RL, Kachman SD, Templeman RJ, Fernando RL, Kuehn LA, Pollak EJ (2009) Estimation of the proportion of genetic variation accounted for by DNA tests. In ‘Proceedings of the Beef Improvement Federation 41st annual research symposium and annual meeting’, 30 April–3 May 2009, Sacramento, CA. pp. 184–209.

Weber K, Bennett G, Keele J, Snelling W, Thallman RM, Van Eenennaam AL, Kuehn L (2011) Genomic selection in beef cattle: training and validation in multibreed populations. In ‘Proceedings plant and animal genome conference XIX’, San Diego, 2011. Poster P514.