Marker-Assisted EPD for Other Breeds: A Changing Paradigm

Matt Spangler, Ph.D.
University of Nebraska-Lincoln

Initially beef breed associations, particularly Angus, utilized genomic predictors (Molecular Breeding Values; MBV) that were provided by commercial companies (i.e. Merial Igenity, Pfizer Animal Genetics) whereby MBVs were provided to the breed association but genotypes were not. This is still the scenario for some breeds (American Angus Association; Table 1), however other breed associations have elected a different path to Marker-Assisted (or Genomically Enhanced) EPDs. This different path, in general, is to work without a commercial partner and instead send samples for genotyping directly to a lab (i.e. GeneSeek) and maintain access to the actual genotypes. These genotypes along with phenotypic information from genotyped animals are used to develop MBV. The training process, or process used to derive the 50K based prediction equations, is being performed by the National Beef Cattle Evaluation Consortium lead by Dr. Dorian Garrick at Iowa State University. This is drastically different than relying on products from commercial companies and many breeds feel this new path allows for greater flexibility. Some examples of breeds that have done this are the American Simmental Association (ASA) and American Hereford Association (AHA), although others are working towards this end (Table 2; Data provided by Dorian Garrick).

Table 1. Genetic correlations (rg) between traits and their genomic indicators used by the American Angus Association by company.

Trait	Igenity (Neogen) rg (384 SNP)	Pfizer rg (50K SNP)
Calving Ease Direct	0.47	0.33
Birth Weight	0.57	0.51
Weaning Weight	0.45	0.52
Yearling Weight	0.34	0.64
Dry Matter Intake	0.45	0.65
Yearling Height	0.38	0.63

Yearling Scrotal	0.35	0.65
Docility	0.29	0.60
Milk	0.24	0.32
Mature Weight	0.53	0.56
Mature Height	0.56	0.56
Carcass Marbling	0.65	0.57
Carcass Ribeye Area	0.58	0.60
Carcass Fat	0.50	0.56
Carcass Weight	0.54	0.48

Table 2. Genetic correlations of 50K derived MBV for several breeds developed by the National Beef Cattle Evaluation Consortium.

	Hereford n=800	Simmental n=2,800	Gelbvieh n=847	Gelbvieh + Angus (n=1,181)
BW	0.43	0.65	0.38	0.41
WW	0.32	0.52	0.31	0.34
YW	0.30	0.45	0.21	NC
MILK	0.22	0.34	0.36	0.34
FAT	0.40	0.29	NA	NA
REA	0.36	0.59	0.38	0.48
MARB	0.27	0.63	0.54	0.56
CED	0.43	0.45	NC	0.48
CEM	0.18	0.32	NC	NC
SC	0.28	NA	0.50	0.50

There are four basic ways of combining genomic and phenotypic information into a single selection tool (Marker or Genomic Enhanced EPD). The first method is to compute independent values, both EPD and MBV, and to then include both pieces of information in a selection index whereby each "trait" is weighted proportionally to the respective amount of genetic variation that they account for (this is done post EPD estimation by AHA). A second approach is through genomic relationships whereby marker information is used to fit a genomic relationship matrix (relationship among animals at each SNP locus) that is used to augment estimated relationships based on pedigree information. For this method it is necessary to know the actual SNP genotypes rather than having a marker score or MBV. This method is currently being used in dairy genetic evaluations and by some swine breeding companies. The first method deployed by the beef industry, and which is currently used by the AAA, is the correlated trait approach. MBV information is included in National Cattle Evaluation (NCE) as a correlated trait similarly to the way ultrasound information is utilized in a multiple trait model in the estimation of EBV for carcass traits. The final method is to treat MBV as if they were external EPD (EPD from an animal that is external to the population or breed). This method is currently being used by the American Simmental Association and allows for MBV to influence the accuracy of EPD differently, thus making use of the variation around the MBV estimates. This individual animal MBV prediction error variance (PEV) can vary depending on the relationship between the animal with the MBV and the training population.

Regardless of the method used, combining these sources of information, molecular tools and traditional EPD, has the potential to allow for the benefits of increased accuracy and increased rate of genetic change. The choice of a method for inclusion of genomic information into NCE is generally driven by the current NCE framework of each breed and the organization that ultimately runs the genetic evaluation. All methods have their benefits, be it simplicity (index or blending approach) or varying impacts on accuracy (external information approach).

Conclusions

Genomics and the corresponding Marker-Assisted or Genomic-Enhanced EPD, have become a reality. Within-breed genomic predictions based on medium density (i.e. 50K) genotypes have proven to add accuracy, particularly to young animals, for several traits. Cost undoubtedly impedes deployment of this technology, however recent advances show promise in dramatically decreasing the cost of genotyping. The crux of adoption will be getting commercial producers to see the value in, and thus pay for, increased EPD accuracy. There is a still a need to collect and routinely record phenotypic information by seedstock producers and commercial producers need to realize that EPD, and economic index values, are the currency of the realm for selection. Genomic technology only makes these tools stronger, it does not replace them.