

# SNPs, MVPs, and GE-EPDs - What are these things?

## Get on Board the Fast-Track Train to Improved Beef Cattle Selection

By Jennifer Scharpe, NALF director of PR and media

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Limousin breeders and their commercial customers benefit greatly from new breeding and selection tools. Tremendous advancements in beef cattle selection have been made in the last few decades. It's almost like riding on a train. Instead of stopping to pick up passengers, the train stops to pick up new technology that offers exciting opportunities for cattle breeders. Consider the stops that have been made so far along this track – artificial insemination, embryo transfer, national cattle evaluation (NCE) leading to the development of expected progeny differences (EPDs), cloning, and for the last two decades, genomic testing.

The introduction of genomic testing in beef cattle selection has led to the train picking up speed – so instead of riding a locomotive, we're now on a fast-track, high-speed train, with more stops that are closer together than any previous route on this ride. In a relatively short time span, genomic testing has brought revolutionary change to selection decisions. The 1990s brought tests for coat color, genetic defects, and parentage. The early 2000s brought tests for carcass traits. As researchers began to learn more about DNA, in 2007 large genomic panels were identified to have influence on multiple traits. This led to the first beef breed association, the American Angus Association®, introducing genomic-enhanced EPDs (GE-EPDs) in 2009. The North American Limousin Foundation launched their own GE-EPDs in the fall of 2015.

The more that is learned about DNA the more this technology will improve. Seedstock producers and their customers will greatly benefit from incorporating genomic technology with performance measurements of individual animals, their pedigree and progeny, into the national cattle evaluation.

### SNPs Unlock the Information

The promise of genomic-enhanced EPDs today relies on the SNPs – the panel of single-nucleotide polymorphisms (pronounced 'snips'). Basically, SNPs unlock the information about genetic influences on traits.

“Each SNP alone doesn't tell you much, but a panel of critically selected SNPs for multiple traits provides molecular breeding values that can be used in the calculation of EPDs,” says Sally Northcutt. “Already the EPD calculations use multiple sources of information. The genomic value becomes an additional piece of information.”

Dr. Matt Spangler, University of Nebraska, writes, “The U.S. beef industry has witnessed considerable evolution in terms of the genomic tests available in the market place. The tests that are currently being included in EPD calculations are comprised of either 30,000 (30K) SNP [low density] or 150,000 (150K) SNP [high density].”

The SNPs are the markers, meaning the location on the DNA where genes for identified traits exist. Estimates are that a beef genome contains three million SNPs.

“The more SNPs of interest, the better the prediction,” said Dr. Jack Whittier, Extension beef specialist, Colorado State University at the Range Beef Cow Symposium XXII.

The process of how SNPs are used can be explained by thinking of a light board. DNA is cut up and incubated on the SNP chip (i.e. individual lights on the board). When the chip lights up, matches have been identified. “Low density chips only light up a few SNPs. High density chips provide greater illumination,” says Whittier.

“The underlying question commonly asked by producers is ‘does it work?’” It is critical to understand that this is not a valid question, as

the true answer is not ‘yes’ or ‘no’. The important question to ask is ‘how well does it work?’, and the answer to that question is related to how much of the genetic variation the marker test explains,” added Spangler.

“Simply stated, the more genetic variance a test explains, the more impact it will have on your EPDs and accuracies for that trait,” says Northcutt.

SNPs lead to the development of molecular breeding values (MBVs). MBVs can then be included in the calculation of EPDs. Within the industry, MBVs are currently being used for moderately to highly heritable traits such as birth weight, weaning weight, yearling weight, ribeye area, and marbling. As more SNPs are identified, MBVs can be used for other traits including healthfulness, feed efficiency, and other difficult to measure traits.

It is important to note that SNPs won’t necessarily improve EPDs. The EPD values will increase or decrease depending on the MBVs. However, incorporating the data from the SNP chip will improve the accuracies of the EPDs for traits where MBVs have been incorporated into the calculations.

Spangler cautions some limitations with genomic-enhanced EPDs. “Current marker panels work best in the populations where training occurred, but will potentially decrease in predictive power as the target population becomes more genetically distant from the training population. The 50K based genomic predictions developed for Angus do not explain a substantial amount of variation even in a closely related breed like Red Angus. The same erosion in accuracy is likely to occur overtime as well (i.e. over generations if panels are not retrained).” **LW**