



# Cattle Producer's Handbook

Genetics Section

1043

## DNA-Based, Marker-Assisted Selection in Beef Cattle

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Genetic improvement through selection has been one of the most important contributors to the advancements in animal productivity in the past 50 years. Traditionally, selection in beef cattle has been based on estimating breeding value using expected progeny difference (EPDs). The EPDs are derived from the observable performance (or phenotype) of the animal and its relatives. EPDs statistically predict that animal's genetic potential for given traits (e.g., weaning weight). The accuracy of the estimate will increase over time as more information from progeny and relatives becomes available.

EPDs are the tools. They are not the plan. In order to effectively use EPDs, it is important to develop a breeding plan with specific goals and objectives (e.g., the most profitable selection criteria) for your herd or production system. Most of the economically relevant traits for cattle production (birth weight, weaning weight, growth, reproduction, milk production, carcass quality, etc.) are complex traits controlled by many genes and influenced by the production environment.

A gene is a segment of deoxyribonucleic acid (DNA) that is made up of pairs of four nucleotides abbreviated as "A", "C", "G", and "T" (see Fig. 1 on the next page). A gene dictates the production of a specific protein. It is possible for the sequence of the DNA that makes up a gene to differ between individuals. These DNA variations in a gene are called alleles, and they often result in differences in the amount or type of protein being produced by that gene among different individual animals.

The protein produced by different alleles may affect the expression of a given trait and influence the observed performance. When an animal has an EPD above the base year average for a certain trait, what that means is that the animal inherited a higher than average proportion of alleles that favorably affect the trait.

It should be noted that traditional selection methods inherently tend to increase the frequency of alleles that have major beneficial effects on selected traits. That is, EPDs as typically used, increase the number of favorable alleles without knowing which specific genes are involved. This contrasts with DNA-based selection where knowledge of which DNA sequences are associated with improvement in a given trait is required, and selection is focused on those known DNA "markers" to make genetic improvement in the trait.

Recently scientists have started to identify regions of DNA that influence production traits. They have used molecular techniques to find differences in the sequence of the nucleotide base pairs in these regions. Tests have been developed to identify these subtle differences in the DNA. This has allowed for the development of genetic markers that scientists can use to identify whether an animal is carrying a segment of DNA that is positively or negatively associated with the trait of interest.

Genetic markers in a given region of DNA may differ from each other by the sequence of only a single nucleotide base pair, such as a single A, C, G, or T (Fig. 1). Such differences are called single nucleotide polymorphisms or SNPs (referred to as "snips"). Genetic tests based on SNPs analyze DNA derived from an individual to determine the DNA sequence that is present at one specific location (nucleotide pair) in among the three billion nucleotide pairs that comprise the genome of the cow!

Genotyping is the term that is used to describe the process of using laboratory methods to determine the sequence of nucleotides in the DNA from an individual, usually at one particular gene or specific location in the genome.

Selecting an animal carrying the favorable form of a marker, or one that is associated with a positive impact