# High-Density SNP Genotypes for Predicting Genetic Merit of Beef Cattle

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**Summary and Implications**

Current selection strategies result in annual rates of genetic improvement less than one-quarter of the progress that is theoretically possible if merit could be accurately predicted by breeding age. Tens of thousands of single gene markers (called SNPs), spread throughout the genome, enable the ancestral inheritance of small chromosome fragments to be tracked. Genetic merit of new, perhaps unrelated cattle can be predicted by summing up the values of all the fragments they have inherited. Such predictions at young ages will facilitate faster rates of genetic gain, especially for traits that are difficult to measure.

**Introduction**

The genetic merit of beef cattle, reported as Expected Progeny Differences (EPD), are predicted from pedigree and performance records. The fact that chromosomes are paired, and one member of each pair is transmitted from parent to offspring, results in the expected merit of offspring being the average of the parents. However, recombination between homologous chromosomes and chance sampling of chromosomes at meiosis results in some offspring that are much better than parent average and others that are much worse. Identifying the outstanding individuals is not possible until they have produced their own performance records, or better still, generated a number of performance-recorded offspring. Accurate assessment of merit is therefore not possible until well beyond puberty, the ideal selection age to provide for rapid turnover of generations.

The ability to genotype cattle for 50,000 SNP markers for around $300 has made it possible to evaluate the genetic merit of thousands of chromosome fragments identified using the markers. Given an EPD for each chromosome fragment, an animal can readily be evaluated directly from knowledge of its SNP genotypes, even in the absence of information as to its parentage. The animal's EPD is simply the sum of the EPDs of the chromosome fragments.

**Materials and Methods**

Field and simulated data have been used to develop and implement methods for exploiting high-density SNP genotypes in beef cattle. The analysis of SNP genotypes involves two distinct steps. In the first step, historical records consisting of SNP genotypes and phenotypes (or SNP genotypes and EPDs) are analyzed in a process referred to as "training". This involves simultaneously identifying the chromosome fragments that contribute to the prediction of genetic merit, estimating the proportion of variation accounted for by that fragment and predicting its substitution effect. In the second step, genotypes of new animals are used to predict their genetic merit, given the results from the training.

The commercial system for high-density SNP genotyping became publicly available from Illumina in January 2008. Comparable systems will likely be available in sheep, pigs and chickens during 2009. Genotypes and phenotypes are becoming available from research herds and industry bulls, though breed associations and various research and commercial partnerships.

Preliminary research focuses on methods that can internally cross-validate results in order to quantify the predictive merit of these new procedures.

Interest is particularly focused at traits that are difficult to measure using conventional approaches, including carcass and meat quality traits, measures of healthfulness of beef, animal health and disease, female fertility, feed intake and efficiency.

**Discussion**

A USDA-NRI project funded for three years from 2009 will extend the analytical procedures, apply them to the analysis of animals recorded at the US Meat Animal Research Center (US-MARC), investigate combinations of flanking SNPs known as haplotypes, and make our analytical systems web accessible. That research involves collaborators at US-MARC and CalPoly, San Luis Obispo.

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