



# The Economics of Gene Testing Cattle

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## Introduction

There is a great deal of buzz in the cattle industry regarding genetic testing of bulls, beef cows, and even feeder calves. Several companies offer testing services, including MMI ([www.mmigenomics.com](http://www.mmigenomics.com)), Igenity ([www.igenity.com](http://www.igenity.com)) and Bovigen ([www.bovigen.com](http://www.bovigen.com)). Services include parentage testing and testing for markers associated with economically relevant traits. However, little unbiased information is available to producers regarding the value of genetic knowledge to their bottom line. This fact sheet discusses what little is known about the basic economics of gene testing. First is provided a primer on genetic markers to provide a biological basis for the economic discussion.

## A Basic Understanding of Genetics

Along with management and environment, genes determine the biology of an animal. Genes also determine, in part, the economics of animal agriculture. There are two general types of characteristics to be considered. A qualitative trait describes a trait that is either present or not. For example, a beef animal is either polled or not. So polled is called a qualitative trait. Similarly hide color in Angus cattle is a qualitative trait. A red beef animal carries two copies of the recessive red gene where a black-hided beef animal carries at most one copy. In general, management and environment do not affect qualitative traits.

Other characteristics are quantitative. They vary in a continuum from one animal to another. Traits such as marbling, tenderness, weight, and fat cover are quantitative traits and are affected by genetics, management and environment. These traits are typically influenced by numerous genes and this where gene testing comes in.

A gene is a strand of DNA. Genes are further divided into exons and introns. Exons and introns alternate along a gene. Each exon is followed by an intron (and vice versa). Introns act essentially as spacers between exons. Subdividing even further, both exons and introns are made of strings of nucleotides. When one of these nucleotides is replaced by another nucleotide, a genetic mutation has occurred. In the terminology of geneticists, a Single Nucleotide Polymorphism (SNP) is present. (The abbreviation SNP is pronounced as "snip.") An SNP can also occur due the insertion or deletion of a nucleotide.

To a layperson, the terminology can be confusing. It helps to think of a chromosome as a city, a gene as a city street,

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exons and introns as blocks on that street and nucleotides as specific houses in that block. So, given a chromosome (city), a gene (street), an exon (block) and a nucleotide (house), we can "drive" up to a given location and observe the specific type of nucleotide (house) present. Note, there is also genetic code located in between genes (i.e., rural houses), called microsatellites, that can also influence biology.

As the previous analogy implies, there are different types of houses (nucleotides) that can be found at a given location. Four different nucleotides, cytosine, guanine, adenine, and thymine, make up DNA. These acids are abbreviated with the letters C, G, A, and T.

While most SNPs have no association with changes in biology, some SNPs are important because they are associated with quantitative traits. Those SNPs that are associated with biological variability typically explain less than 5% of biological variability. So, for many economically relevant traits, we may need to look at dozens of SNPs to explain a significant portion of biological and economic variability between animals.

Geneticists also refer to "alleles." An allele is used to describe differences between gene pairs. For example, if at a given position a C-nucleotide is found on a gene and a T-nucleotide is found on its paired gene, we would refer to C-allele and T-allele to denote the differences between the gene pair. It is possible that the gene might have nucleotide differences in multiple locations. For example, a CT-allele and a GA-allele.

The allele pair is called a genotype. Animals with two different nucleotides are called heterozygous, for example a CT genotype. If the animal has the same nucleotide on the gene pair, it is called homozygous, for example, "homozygous T," or TT genotype. Also, note if more than one nucleotide or microsatellite is tested, the resulting information is called a haplotype.

Several genotyping/haplotyping testing services are available. These include parentage, hide color, polled, feed efficiency, tenderness, some reproductive traits, marbling, and several other carcass traits (Garrick and Van Eenennaam 2008). What is not well known at this time is the value to the producer of most of this genetic knowledge.

## Economics of Gene Testing

Economics of genetic information is still in its infancy and only a few economics studies have been published on

the value of gene testing. The two primary reasons are 1) the cost of collecting genetic information and 2) a lack of genetics training. However, two studies investigate the economic differences in fed cattle associated with an SNP in the leptin gene. One study considers the impact of that SNP on cow-calf profitability.

Leptin is a hormone secreted by white fat cells. SNPs in the leptin gene have been associated with fat deposition and metabolism. Lusk (2007) and DeVuyst et al. (2007) report the impact of one SNP on fed cattle returns (Tables 1 and 2). This SNP is due to a C to T switch at Exon 2, SNP 305. Prior research (Buchanan et al. 2002; Kononoff et al. 2005) report that the T-allele is associated with fatter beef carcasses than the C-allele. Using independent data sets and differing methodology, both find that profit-maximizing days-on-feed does is not altered by genetic knowledge. However, profits do vary by genotype. Fat genotype (TT) fed cattle are more profitable than lean genotype (CC) cattle. Depending on sex, price grids, and other factors, genotypic differences in profit range from \$14 to \$60 per head.

The same mutation has been investigated in milk production by Holstein cows and beef calf weaning weight. Buchanan et al. (2003) report that TT Holstein cows average 3.3 pounds per day more milk than CC Holstein cows during a 305-day lactation. DeVuyst et al. (2008) also report heavier calf weaning weights for TT and CT cows. The effect was significant in crossbred (mostly Angus cross) cows, but weaker in other breeds. There was a general tendency for TT cows to wean heavier calves than CC cows. However, small sample sizes hindered their ability to detect significant differences. Crossbred TT cows wean calves weighing 27 pounds more than calves weaned from crossbred CC cows. Mitchell et al. (2008) also find that TT and CT beef cows wean heavier calves than calves weaned from CC beef cows (Table 3).

Mitchell et al. (2008) considered the economic differences by genotype for cow-calf production. Their analysis found that TT and CT cows were more profitable than CC cows due to 1) higher calf weaning weights and 2) longer productive lives. Their study should be viewed as evidence, rather than definitive, since sample sizes were too small to test for breed by genotype interactions. Differences in profitability ranged from \$15 to \$39 per year depending on breed.

To summarize, little is known to date about profitability differences due to cattle genotypes. Only a few studies have explicitly considered genotype. All of those studies investigated mutations associated with the leptin gene (Table 4). Since these studies were initiated, a number of SNP panels can be tested for commercially. The economic content of these SNPs has not been evaluated by independent researchers.

**Table 2. Maximum profit per head for fed cattle by leptin genotype.**

Price	Genotype	Lot 1 (steers)	Lot 2 (heifers)	Lot 3 (heifers)
Low	CC	59	38	9
	CT	43	17	16
	TT	82	52	47
Medium	CC	125	101	70
	CT	109	79	75
	TT	153	117	106
High	CC	192	164	131
	CT	176	140	135
	TT	224	182	165

(DeVuyst et al. 2007)

**Table 3. Calving weaning weights by dam genotype.**

Genotype	Advantage over CC
CT	12.9 lbs
TT	14.3 lbs

(Source: Mitchell et al. 2008)

**Table 4. Differences in beef cow annual returns due to leptin genotype.**

Breed	CT – CC Returns	TT – CC Returns	TT – CT Returns
Shorthorn	21.29	NA	NA
Simmental	15.35	39.05*	23.70
Commercial X	24.11*	25.44*	1.33
Angus	29.72*	33.78*	4.51

\*Denotes statistical significance at  $p \leq 0.10$ .

(Source: Mitchell et al. 2008)

## The Future of Genetic Marker Selection and Markers

Since the economic valuation of genetic markers is just beginning, what markers should a producer select for? Current market conditions reward cow-calf producers for high weaning weights and black hide color, stockers for feed efficiency, and average daily gain, and feedlot operators for feed efficiency,

**Table 1. Maximum profit per head for fed cattle by leptin haplotype.** (Source: Lusk 2007)

	Haplotype						
	Type 1	Type 2	Type 3	Type 4	Type 5	Type 6	Type 7
Steers	297	302	261	296	273	286	270
Deviation from max	-5	0	-42	-6	-29	-16	-32
Heifers	241	254	208	235	222	224	202
Deviation from max	-13	0	-46	-20	-32	-30	-52

rate of gain, lean weight, marbling, and ribeye area. Markers have been identified that affect most of these traits. However, EPDs also predict these traits in progeny of registered bulls and cows. So, unless producers have agreements with buyers that require or reward collection and transfer of specific markers, it might not yet pay to collect this information for most producers.

It is interesting to note that there are potentially misaligned incentives between producers at different points in the supply chain and consumers. For example, cow-calf producers are paid largely on weight and not necessarily on feed efficiency and rate of gain—traits important to stockers and feed lot operators. Most concerning, there is no large scale program to reward producers for animals that yield tender cuts—one of the traits most valued by consumers. Quality grade, a subjective classification for marbling, is poorly correlated with tenderness. So, the beef industry lacks a method for rewarding producers that select for tenderness markers, even though those markers have great potential for increasing demand and hence profit for the entire industry. It is anticipated that new vertically-integrated markets will eventually open to exploit this high profit potential.

Some seedstock producers are using genetic test results as part of their marketing information at annual sales, but no studies have evaluated the market impact of using genetic information to supplement EPDs. If vertically integrated market channels develop for tenderness and other consumer-desired attributes in the near future, seed stock producers may want to select for these markers in their herds now. So when the channels are developed, they are in position to provide their customers—cow-calf producers—with these genetics.

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Issued in furtherance of Cooperative Extension work, acts of May 8 and June 30, 1914, in cooperation with the U.S. Department of Agriculture, Robert E. Whitson, Director of Cooperative Extension Service, Oklahoma State University, Stillwater, Oklahoma. This publication is printed and issued by Oklahoma State University as authorized by the Vice President, Dean, and Director of the Division of Agricultural Sciences and Natural Resources and has been prepared and distributed at a cost of 20 cents per copy. 1108 GH.