AN ECONOMIC ASSESSMENT OF GENETIC INFORMATION:

LEPTIN GENOTYPING OF BREEDING CATTLE

A Thesis
Submitted to the Graduate Faculty
of the
North Dakota State University
of Agriculture and Applied Science

By

Jay Douglas Mitchell

In Partial Fulfillment of the Requirements
for the Degree of
MASTER OF SCIENCE

Major Department:
Agribusiness and Applied Economics

October 2006

Fargo, North Dakota

North Dakota State University
Graduate School

Title

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The Supervisory Committee certifies that this *disquisition* complies with North Dakota State University's regulations and meets the accepted standards for the degree of

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ABSTRACT

Mitchell, Jay Douglas; M.S.; Department of Agribusiness and Applied Economics; College of Agriculture, Food Systems, and Natural Resources; North Dakota State University; October 2006. An Economic Assessment of Genetic Information: Leptin Genotyping of Breeding Cattle. Major Professor: Dr. Eric A. DeVuyst.

Recent studies show polymorphisms in the leptin gene significantly impact milk production in dairy cattle. If the leptin gene were to have a similar impact on beef cattle, calf weaning weights would be expected to increase from the increased milk production in the cows. Since weaning weight is a key component of profitability in a cow-calf operation, leptin genotyping may prove to have an economic impact in breeding cattle. However, no research has been done to link the economic impact of increased milk production to breeding cattle. Using 595 observations from genotyped cows spanning 11 years (1995-2005), calf weaning weight by genotype is estimated as a function of calf and dam characteristics and environmental effects. A MIXED procedure, utilizing data from 89 culled cows, is used to determine statistical differences in average cull age by genotype. A simulation model calculates mean annualized equivalent return by genotype and breed using the regression coefficients and residuals and 16 years of price data.

Results show that at least one T-allele in breeding cows increases calf weaning weight, average cull age, and annualized equivalent return compared to cows with homozygous C-alleles. These results indicate that there may be future premiums and discounts for breeding cattle based on genotype. Seedstock producers could potentially begin to segregate herds based upon genotype so that they could sell genotypic registered products. Cow-calf producers may also benefit from this knowledge by increasing the amount of TT genotype breeding cattle in their herd to maximize profits.

ACKNOWLEDGEMENTS

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CHAPTER 1. INTRODUCTION

Economists and animal scientists have recently begun investigating the economic benefits of genotyping beef cattle. Genotyping is the process of analyzing the particular genetic variations (polymorphisms) existing in an individual DNA sample. By genotyping cattle, producers hope to find certain genes or polymorphisms (i.e., naturally occurring mutations) of those genes that will help producers realize larger profits.

The leptin gene has been the focus of much recent research. Leptin is a hormone secreted by white adipose tissue (fat) and plays a role in the regulation of fat deposition, body weight, feed intake, immune function, and reproduction in cattle (Liefers et al., 2003; Buchanan et al., 2003). A single nucleotide polymorphism (SNP) within the leptin gene causes an allelic variation (cytosine [*C*] to thymine [*T*]), which has been found to be associated with increased leptin levels and fat deposition in cattle (Kononoff et al., 2005). This polymorphism results in cattle having one of three genotypes: *CC* (lean), *CT* (heterozygous), or *TT* (fat).

In a cow-calf operation, weaned calves are priced, in part, based on live weight and phenotypical features. The net price received for a feeder calf is based on the current market price and adjusted by a price slide. The price slide is used to increase the value of calves weighing less than a base weight of 750 pounds and to decrease the value of calves weighing more than 750 pounds. Buyers are willing to pay more per pound for lighter calves because they make profit on each pound of gain through finishing. In addition, premiums or discounts are applied to the market price based on phenotypical features such as hide color and frame size.

Calf weaning weight, a primary determinant of profit in a cow-calf operation, is largely influenced by the milk production of dams. Research shows that dairy cattle with the *TT* genotype produce significantly more milk than cattle with the *CC* genotype, thus making the *TT* polymorphism economically beneficial in the dairy industry (Buchanan et al., 2003). Brown et al. (2005) conclude that increased energy and protein intake in the preweaning period results in increased body growth rates of calves. Together these results suggest that the *TT* genotype in a dam may positively impact body growth rates of calves through an increased milk and protein production. This increased growth rate could result in heavier weaning weights, possibly increasing profit.

Research directly linking leptin genotyping to calf weaning weight is lacking. Another primary determinant of profit is called stayability. Stayability is a measure of how long a cow stays in the herd and is heavily influenced by rebreeding. The findings of Kunkle, Sand, and Rae (1994) show that body condition score (BCS) is directly related to the percentage of open cows and pregnancy rate. Leon et al. (2004) found leptin concentrations to be positively correlated to BCS. This indicates that *TT* genotype cattle, that produce higher concentrations of leptin, may tend to have a higher pregnancy rate, thus reducing their chances of being open and culled from the herd. By possibly having more calves than the other genotypes, the *TT* cows may be more valuable due to decreased depreciation costs. However, there is a lack of knowledge linking the leptin genotype in beef cows to stayability.

Problem Statement

The economic impact the leptin genotype has on milk production in dairy cattle, suggests the *TT* genotype beef cows will have an economic advantage over *CC* or *CT*

genotypes by producing heavier beef calves. Stokes, Farris, and Cartwright (1981) show that in a cow-calf operation, heavier milking cows generate higher revenues in comparison to medium and light milking cows, in addition to weaning calves at the lowest cost per pound. Research also suggests that the *TT* genotype may increase the average age at which the cow is culled (Kunkle, Sand, and Rae, 1994; Leon et al., 2004). Increasing the productive age of the cow, also called stayability, allows the producer to spread development and maintenance costs of the cow over more calf crops (Snelling, Golden, and Bourdon, 1995). This translates into large cost savings because Brown et al. (2005) claim that nearly 20% of a dairy farm's expenses can be attributed to the costs of raising replacement heifers. Therefore, in an attempt to determine if producers should select dams with the *TT* genotype to improve profits, some important questions need to be answered. First, do the polymorphisms of the leptin gene actually have an impact on the weaning weight of a calf in a beef cow herd? Second, does leptin genotype play a role in how long a beef cow stays in the herd? Third, if the homozygous *T* allele proves to be the economically superior allele, is its economic impact significant enough for cow-calf producers to benefit from breeding this genotype into their herds?

Objectives

The goal of this research is to determine if the economic value of a beef cow varies by leptin genotype. The hypothesized differences in values may be due to potential differences in average calf weaning weights and average stayability of cows. The specific objectives of this study are to

1) determine differences in calf weaning weight by dam genotype,

2) determine mean cull age by genotype, and

3) determine the value of beef cows by genotype and statistically compare across genotypes.

Methodology

To complete objective (1), data are collected from the beef herd at North Dakota State University. Blood samples were taken from breeding cows and genotype determined. A total of 595 observations are used in which a genotyped cow supported a calf until weaning. A regression model is estimated with calf weaning weight as a function of calf birth weight, dam breed, dam age, calf sex, dam genotype, calf age at weaning, and year. Significance of leptin genotypes are assessed by t-values on coefficients for genotype dummy variables.

Employing the data from objective (1), the MIXED procedure in SAS (SAS Institute Inc.) is used to complete objective (2). The data set contains the ages of 89 cows that were culled from the herd for various reasons. Stayability is used as the dependent variable, while the genotypes of the cows are fixed covariates. Statistical differences in the mean stayabilities between genotypes are determined using t-statistics.

To complete objective (3) a simulation model is developed. One cow representing each genotype and each breed is simulated 1000 times. Probabilities of cows from each genotype reaching ages from 2 to 16 are developed from the stayability distributions. Each genotype is then assigned a stayability based on the previously generated probabilities. Culled cows are sold at market prices from each of 16 years of historical cow price data at a weight of 544 kg. A replacement heifer weighing 340 kg of the same genotype and breed is then purchased to replace the culled cow. Replacement heifers are purchased at prices from each of 16 years of historical replacement heifer price data. The regression

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coefficients and residuals obtained from objective (1) are incorporated to estimate calf weaning weights with error for each of the cows. The weaned calves are priced similarly to the culled cows and replacement heifers; a price is selected from each year of the 16-year data set of feeder cattle prices. All 16 pricing scenarios are evaluated for each simulation, and for each cow in the simulation the same pricing year is used for the culled cow, replacement heifer, and weaned calves. A net present value (*NPV*) is computed for each cow that is simulated and recalculated for each of the 16 different pricing scenarios in each simulation. Using the *NPV* calculations, an annualized equivalent return (*AER*) is calculated for each pricing scenario. The *AER* from the 16 pricing scenarios in each simulation for each cow is used to calculate the average *AER* by breed and genotype. The statistical differences in average *AER* between each breed and genotype are determined by a z-test.

Summary

The remainder of this thesis is divided as follows. Chapter 2 reviews literature relevant to the biological impact of the leptin gene and the value of information regarding animal genetics. Chapter 3 describes of the methodology used to determine and compare the economic value of beef cows by genotype. Chapter 4 discusses the Results obtained from the methodology used. Chapter 5 discusses the Conclusions and Implications of the study.

CHAPTER 2. LITERATURE REVIEW

Biology

Leptin was initially discovered in 1950 in a research study of obesity (Kemp, 2003).

In this study mice were observed with recessive genetic obesity and labeled ob/ob mice

(Ingalls, Dickie, and Snell, 1950). The mice that exhibited this genetic mutation were

sterile and had over 50% body fat. However, the specific genetic mutation in these mice

was not revealed until 1994, when sufficient testing procedures became available. The new

technology allows researchers to show that an ob protein, now named leptin, reduces food

intake, eliminates obesity and increases reproductive performance when it is administered

to ob/ob mice (Houseknecht et al., 1998). Therefore the gene responsible for production of

the ob protein, leptin, is simply referred to as the leptin gene (Kemp, 2003).

Leptin is a protein hormone synthesized in white adipose tissue (fat) and is

transported to the hypothalamus via the bloodstream (Houseknecht et al., 1998). There the

leptin is read by receptor cells which inform the body about fat reserves, in response, the

brain alters food intake, energy expenditure, physical activity, and whole-body energy

balance (Houseknecht et al., 1998; Kononoff et al., 2005). Research shows that ob/ob mice

do not produce biologically active leptin. In other words, the leptin being produced is not

identified by the receptor cells. As a result, the appropriate response cannot be carried out

by the brain (Kemp, 2003). The cause behind this inability to produce biologically active

leptin is linked to an SNP in the leptin gene causing an allelic variation (cytosine [C] to

thymine [T]). The T allele is shown to be associated with higher leptin levels in adipose

tissue and increased fat deposition in cattle (Kononoff et al., 2005). Due to its involvement

in the regulation of several biologically important processes in the body, the leptin gene is

perhaps "one of the best physiological gauges for energy balance, body weight, and body fat content in mammals" (Nkrumah et al., 2005, p. 26).

The SNP in the leptin gene results in cattle having one of three genotypes, *TT* (homozygous thymine alleles), *CC* (homozygous cytosine alleles), or *CT* (heterozygous alleles). Kemp (2003) reports that cattle of the *TT* genotype are observed to have a high fat phenotype, while *CC* genotyped cattle have a lean appearance. In addition to affecting fat deposition in cattle, the genotype is also linked to milk production, reproduction rates, and body condition scores (Liefers et al., 2005; Buchanan et al., 2003; Kunkle, Sand, and Rae, 1994; Spitzer et al., 1995).

Milk Production

Research studies report positive correlations between leptin levels and milk production in dairy cattle (Liefers et al., 2005; Buchanan et al., 2003; Kulig, 2005). Much of the variation in milk yield in dairy cows can be attributed to a polymorphism on intron 2 of the leptin gene (Liefers et al., 2005). Body fat reserves play a considerable role in maintaining high milk production in early lactation and since the *TT* genotype is associated with increased fat deposition in beef cattle they may tend to milk heavier than the other genotypes. Buchanan et al. (2003) reinforces this idea by showing that the leptin *TT* genotype causes increased milk and protein yields in dairy cattle. Leifers et al. (2003) also finds that cows with higher leptin levels during pregnancy have higher percentages of fat and lactose during lactation, in agreement with the findings of Kulig (2005), showing significant positive correlations between leptin levels and fat content in edible commercial milk. However, no research has been done on the leptin gene's affect on milk production in beef cattle.

The effect on the weaning weight of calves in a cow-calf operation is greatly impacted by the milk production of the dam. Triplett, Neuendorff, and Randel (1995) claim that it is the primary factor for influencing the weaning weight of a calf. Buchanan and Stutts (2001) show that cows sired by bulls with a high milk expected progeny difference (EPD) had calves with higher growth rates and consequently heavier weaning weights than cows sired by bulls with a low milk EPD. Similar to the findings of Buchanan and Stutts, Marston et al. (1992) identify a positive relationship between milk EPD, actual milk production, and calf weaning weights. Buskirk et al. (1996) find a 20% decrease in milk production of a dam decreases the weaning weight of her calf by 16 kg. Arthur et al. (1997) demonstrate that greater than 50% of the variation in calf pre-weaning growth is attributed to its dam's milk yield and as a result the heaviest calves are weaned from the heaviest milking cows. In addition, Meyer, Carrick, and Donnelly (1994) identify a 0.60 correlation between calf gain to 205 days and milk intake. Another study shows that they wean heavier, and calves from heavier milking cows gain weight faster than lighter milking cows (Gerrish et al., 1996). Marston et al. (1992) demonstrate that preweaning calf growth and weaning weight are influenced by the total intake of milk fat and protein.

The economic benefit of heavy milking cows to cow-calf producers is shown in a study by Stokes, Farris, and Cartwright (1981). The heaviest milking cow herds wean calves at the lowest cost per pound. Since weaning weight of calves greatly influences net income, the milking ability of the cow herd plays a vital role in the efficiency of any cow-calf enterprise (Buchanan and Stutts, 2001). "Because a calf's weaning weight is influenced by the milk production of its dam, the ability to change the genetic potential of a herd for milk production could benefit cow-calf producers" (Marston et al., 1992, p. 3304).

Therefore, if beef cattle with the *TT* leptin genotype produce more milk like their dairy counterparts, cow-calf producers may be able to see an economic benefit from having *TT* dams to wean heavier calves in a shorter amount of time.

Rebreeding/Stayability

Body condition score (BCS) is a rating of the relative fatness or nutritional status of a cow. BCS uses a visual scale from 1 to 9, with 1 being the thinnest and 9 being the fattest cattle. Approximately an 80 lb weight change is associated with each unit change in BCS (Herd and Sprott, 1986). The body condition of cows is found to be closely related to the percentage of open cows, milk production, calf weaning weight, pregnancy rate, calving interval, calf age at weaning, and calf daily gain (Kunkle, Sand, and Rae, 1994). Spitzer et al. (1995) shows that as the BCS in dams is increased from 4 to 6, birth weights and weaning weights of calves also increase. Furthermore, a study done by Vargas et al. (1999) shows that pregnancy and calving rates directly correspond to BCS. In addition, Leon et al. (2004) confirms that concentrations of leptin are positively correlated with BCS. Similarily, Meikle et al. (2004), report leptin concentrations during late pregnancy and early lactation are higher in cows with a higher BCS. Cows with a BCS of 6 have a leptin concentration nine times higher than cows with a BCS of 1 (Leon et al., 2004).

Energy reserves are essential for a cow to meet the energy demands of pregnancy and lactation. Kulig et al. (2005) suggest that leptin may inform the hypothalamus about the energy reserves the cow has to support the pregnancy and lactation, thus permitting the cow to reproduce. Martin et al. (2005) suggests a threshold leptin requirement for cyclicity and pregnancy, as has been found in mice, may dictate the ability of a cow to reproduce. This implies *TT* cows, which produce higher concentrations of leptin due to their increased

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amounts of white adipose tissue, may quite possibly have a higher BCS and higher pregnancy rates and consequently heavier calves at weaning.

Body condition score is important because it is directly related to the profitability in a cow-calf operation due to its influence in calving intervals and rebreeding. The longer it takes a cow to rebreed the less profit the producer will receive due to increased production costs. After calving, cows with a greater BCS resume estrous cycles sooner than thin cows (Lents et al., 2005). Leon et al. (2004) find a drastic increase in calving interval when BCS is reduced from 5 to 3. Worse yet, if the cow does not rebreed at all when it should still be in its prime for weaning calves, the producer must cull the cow and incur the costs of either purchasing a new cow or backgrounding a replacement heifer. Harris and Freeman (1993, p. 876) claim that herd replacements are a major component of the economic value of genetic gain for cow longevity and "the largest component of the cost of herd replacements is the feed costs involved in rearing these replacements from calves to 2-yr-old heifers." Additionally, Brown et al. (2005) claim that nearly 20% of a dairy farm's expenses can be attributed to the costs of raising replacement heifers. Culling an open cow early in its productive life reduces the profit potential because the inability to spread the initial investment over a sufficient amount of years. Vast amounts of data have been collected by breed association such as the Red Angus Association of America (RAAA) and the American Simmental Association (ASA) to implement an expected progeny difference (EPD) that predicts stayability. Stayability is the amount of years a cow stays in production before being culled for various reasons, mainly the inability to rebreed. EPDs use performance information on a bull's offspring, along with his own performance records, the performance of his sire, dam, and other relatives to predict how future offspring will

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perform. The EPD used to predict stayability, developed by Dr. Warren Snelling, is called STAY. It predicts the probability that a cow entering the herd will stay in production though a specified age (Shafer, 2006). Producers generally specify an age between 2 and 8 because that is how long it typically takes to reach a break-even age, in which development and maintenance costs are recovered (Snelling, Golden, and Bourdon, 1995). Cow longevity or stayability is a primary component of producer profit and in terms of relative importance it dwarfs all other traits (Shafer, 2006).

Evidence of the effect of BCS on calving interval and rebreeding in conjunction with studies showing positive correlations between BCS and leptin levels in cattle, suggest cows with high leptin concentrations (*TT* genotype) are associated with a shorter calving interval and higher rebreeding percentages, thus increasing profit levels in cow-calf operations. Furthermore, since open cows are generally culled from the herd it draws the questions; does leptin genotype have any impact on cow longevity due to its influence on percentage of open cows and pregnancy rate and what is the economic impact of increasing herd longevity?

Economic Relevance

The recent technological advancements in genotyping cattle suggest a need to measure the value of information these genotypes provide. Hazel (1943, p. 477) defines the aggregate value of an animal as "the sum of its several genotypes, each genotype being weighted according to the relative economic value of that trait." Melton, Colette, and Willham (1994) estimate the value of improving a single genetic character of an existing breed or variety. The authors implement a technique to estimate the impact of variations of genetic characteristics on a dependent variable such as farm profit. Such analysis is

achieved by extending a general input characteristic model (ICM) to estimate economic values of genetic input traits. Melton, Collette, and Willham (1994, p. 478) state, "the ability to impute economic value to the individual characteristics contained in these genetic bundles should provide important indications of relative characteristic values for either traditional animal and plant breeders or genetic engineers."

Harris and Freeman (1993) study the use of economic weights for milk yield traits and herd life. They use a linear programming model to derive the economic weights for milk yield traits and herd life under various economic conditions and production quotas. The economic weights may then be used to develop selection indexes to allow dairy producers to maximize economic improvement in their herds. The economic weights used in the selection indexes represent marginal economic values for each additional genetic trait. Producers may then be able to use an index that estimates an animal's aggregate genotype as a breeding objective (Harris and Freeman, 1993).

Lambert, DeVuyst, and Moss (2006) assess the expected value of genetic information in cattle feeding. They assume profit maximization and estimate the cost a producer would be willing to pay for information about genetics that may directly or indirectly impact expected profits. The results show that, when only the initial weight of the animal is known, knowledge about the genotype has a positive effect on the revenue distribution. In addition, they found that, when marketing date is the only management input, expected net revenues differ when cattle are separated based on genotype. However, weakness in the study is apparent when genetic information becomes insignificant when days on feed, the main management input, is included in the model. They conclude that CC cattle, due to significant improvements in carcass values, are associated with higher

expected gains than the other two genotypes. This indicates that buyers and sellers of feeder cattle may benefit from genetic information.

A similar study performed by Bullinger et al. (2006) estimates the value of genetic information and determines if genetic information affects optimal marketing dates of fed cattle. An unconstrained profit maximization model in which the sum of profits is a function of days on feed is utilized to determine the value of the leptin genotype and the optimal marketing dates. Due to little differences in optimal days on feed, their results show the leptin genotype to be of little value in terms of making marketing date decisions. However, similar to the study done by Lambert, DeVuyst, and Moss (2006), they mention the leptin genotype may be important in valuing feeder cattle. Yet their results contradict that of the previous study by showing the *TT* genotype to be more profitable than the other genotypes.

These contradictory results are an indication of how little the cattle industry and agricultural economists know about the leptin gene and its economic implications. Many years before Hazel (1943, p. 476) described the difficulties faced in valuing genetic traits of animals: "In practice several or many traits influence an animal's practical value, although they do so in varying degrees. The information regarding different traits may vary widely, some coming from an animal's relatives and some from the animal's own performance for traits which are expressed once or repeatedly during its lifetime." Recent technological advancements are increasing the ability to identify specific genotypes and their traits. As more and more knowledge about bovine genetics becomes available, application of that knowledge may be used to assist the cattle industry in producing a more consistent, cost-efficient, and valuable product.

Recent literature showing the impact of the leptin genotype on milk production in dairy cattle suggests valuable economic implications may lie in the knowledge of genetic information in cow-calf herds in the beef industry. If beef cows with the *TT* genotype have increased milk production like dairy cows with the *TT* genotype, they may be able to wean heavier calves. In addition, if the hypothesis holds true that *TT* beef cows may stay in the herd longer, consequently weaning more calves and decreasing depreciation costs, they may prove to be more valuable than cows of other genotypes. This information may then be used by producers as a breeding objective to decrease variability in their herd and to increase profit. However no research has been done to test the economic impact of the leptin gene in beef cattle on calf weaning weights or cow stayability. This thesis attempts to fill that gap in the research.

CHAPTER 3. METHODS

A regression model, estimated with ordinary least squares, relates calf weaning weight as a function of both calf and dam characteristics and environmental variables. These variables consist of: calf age at weaning, calf birth weight, calf sex (steer or heifer), dam age, dam genotype (CC, CT, or TT), dam breed (Angus, Simmental, Shorthorn, or commercial), and year (1995, ...,or 2005). The t-values for coefficients of genotype dummy variables are used to test the significance of the leptin genotype. Using the SAS system (SAS Institute Inc.) a MIXED procedure is used to determine mean cull age by genotype. Again, t-values are used to determine statistical differences in average cull age by genotype. Finally, a simulation model is developed to compute values of cows across genotypes and to statistically compare the values across genotypes.

Notation and Variables

The following notation are used throughout the remainder of this thesis.

i	subscript indicating calf identification $i \in \{1...595\}$
j	subscript indicating dam breed $j \in \{$Angus, Simmental, Shorthorn, commercial$\}$
k	subscript indicating dam genotype $k \in \{CC, CT, TT\}$
t	subscript indicating year $t \in \{1995...2004\}$
WW_i	weaning weight of the ith calf
AAW_i	age at weaning of the ith calf
BW_i	birth weight of the ith calf
CS_i	dummy variable $\in \{0,1\}$ where $CS_i = 0$ indicates i^{th} calf is a steer and $CS_i = 1$ indicates i^{th} calf is a heifer

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DA_i age of the dam when its ith calf is born

GT_{ik} a vector of dummy variables where $GT_{ik} = 1$ indicates dam genotype of ith calf

BRD_{ij} a vector of dummy variables where $BRD_{ij} = 1$ indicates dam breed of ith calf

YR_{it} a vector of dummy variables where $YR_{it} = 1$ indicates i^{th} calf birth year

Producers are assumed to maximize the annualized equivalent return (AER) of cows. Maximizing AER is equivalent to maximizing the present value of a stream of returns from an asset multiplied by an annuity factor. Since cow stayability may vary by genotype, cows from each genotype and breed are assumed to be replaced infinitely to provide a common time basis for economic comparison. The AER of an infinite series of profit from cows with stayability of s years is given as

$$(1) \qquad AER = \frac{r}{1-(1+r)^{-s}}\left[\left(\sum_{n=1}^{s}\frac{E[R_n]}{(1+r)^n}\right)+\frac{M_s}{(1+r)^s}\right],$$

where r is the discount rate, s is the terminal year or year the cow is culled, n is the current year, R_n is the return in year n, and M_s is the culled cow value in year s (Perrin, 1972). The term inside the brackets is the present value of a single cow producing for s years (Barry et al., 2000). The term outside the bracketed expression converts the NPV into an annuity that is extended over a common length of time, in this case, infinity. The expected return, R_n, is computed differently in the year of purchase, the first year of production, the productive years and the terminal year and is expressed as

$$(2) \qquad E[R_n]=\begin{cases} -M_o - DE_{RH} & if\ n=1 \\ P(WW)\cdot(WW\cdot 0.919\cdot 0.93)-DE_{CC}+(0.07\cdot P(B)\cdot 544.3) & if\ n=2 \\ P(WW)\cdot(WW\cdot 0.919\cdot 0.93)-DE_{CC} & if\ 2<n<s \\ P(C)\cdot 635\cdot 0.93 & if\ n=s \end{cases},$$

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where DE_{RH} is the direct expenses associated with a replacement heifer, DE_{CC} is the direct expenses associated with a cow-calf pair, $P(WW)$ is calf market price, $P(B)$ is beef price, $P(C)$ is culled cow price, and other variables are defined previously. The expected return the year the replacement heifer is purchased is negative because no calf is produced and only the costs of purchasing the replacement heifer and direct expenses associated with maintaining it are incurred. In the second year when heifers have their first calf, a 93% pregnancy rate (Hancock et al., 1994) and a 91.9% weaning rate (North Dakota Farm and Ranch Business Management Annual Report, 2005) are assumed.

The expected return in year two is equal to the price as a function of WW multiplied by the WW, the pregnancy rate, and the weaning rate minus the direct expenses of the cow-calf pair and plus the return from selling the 7% of heifers that are open. All open heifers are assumed to weigh 544.3 kg and be sold for market beef prices. During all productive years (when the cow weans a calf), the expected return is the same as in year two less the return from sold heifers. The pregnancy rate still applies to account for the open heifers that were culled prior to this point. Calf price is a function of WW due to the price slide. Weaning weight is a function of calf and dam characteristics and year effects. In the terminal year, the cow is assumed to be open, so no calf is produced. Therefore, in the terminal year the expected return is equal to the market price of a beef cow multiplied by the weight of the cow, which is assumed to be 635 kg, and again multiplied by the 93% pregnancy rate to account for the 7% of heifers that are culled for being open in the second year.

Age at weaning (AAW), birth weight (BW), and calf sex (CS), are variables representing calf characteristics. Age at weaning positively affects the WW of the calf. As

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the calf gets older, it continues to gain weight. It is up to the producer's discretion when to wean the calves before the value of increased WW begins to be outweighed by the daily maintenance costs. Weaning weight is generally adjusted by the AAW to get a 205-day adjusted WW so that calves may be compared over the same amount of time.

Much research shows that BW plays a role in the WW of a calf. Birth weight positively influences WW in most cases due to increased pre-weaning growth (Gaertner et al., 1992; Jeffery, Bergand, and Hardin, 1971). However, high BW may develop into an undesirable trait when it becomes so high that calving is impeded. Ritchie and Anderson (2004), show that calving difficulty increases by 0.7% to 2 % for every pound increase in BW. The death loss of calves born unassisted is 4 to 5 times lower than calves that need assistance (Corah, Dhuyvetter, and Simms, 1989).

It has long been known that CS has a large impact on the WW of a calf. Woods et al. (1990) report the average daily gain for heifers is about 0.06 kg less than steers. Therefore, steers will either wean at a heavier weight than heifers or be weaned at a younger age due to their higher pre-weaning growth rate.

Dam characteristics also play an important role in the WW of calves. The dam characteristics used in this study to estimate WW are: dam age (DA), dam genotype (GT), and dam breed (BRD). Dam age and BRD are known to affect WW based on previous research, however the affect GT has on the WW is hypothesized.

The WW of calves is also dependent on DA. During the first few years of calving dams generally struggle to maintain a sufficient BCS to support their calves until they reach their mature weight (Sanson and Coombs, 2000). After its second or third calf, the productivity of the dam, in terms of calf WW, generally increases for some period of time

due to increasing milk production (Baker and Boyd, 2003). During the latter years of productivity the dam's body begins to wear out and calf *WW* begins to decrease. This is usually due to decreased milking capability, tooth wear, and increased nutritional demands associated with heavier body weights.

Four different breeds of cattle are studied in this thesis: Black Angus, Simmental, Shorthorn, and commercial. The commercial breed is a crossbred of common beef breeds, but mainly Black Angus, Hereford, and Simmental. Phenotypical features vary widely across each of the breeds, such as frame score, weight, and color. Phenotype is a combination of genotype and environmental influences. Genetic variation is greater between breeds of cattle than within breeds. Weaning hip height, weaning condition score, *WW*, height ratio, late milk production, and change in milk production are all influenced by the breed of the dam (Kress et al., 1995). All of these phenotypical and genetic traits have an impact on *WW* which inevitably varies amongst breeds thus making *BRD* an important variable when estimating *WW*.

Based on previous research indicating higher milk production is associated with dairy cattle possessing the *TT* genotype, it is hypothesized that *WW* in beef cattle is influenced by polymorphisms in the leptin gene (Buchanan et al., 2003). Milk production has a major influence on calves and therefore "is considered one of the most important factors affecting the weaning weight of calves and the profitability of the cow-calf enterprise" (Erat and Buchanan, 2005, p. 1).

Besides calf and dam characteristics, environmental conditions influence *WW*. Weather in the spring determines the amount of forage available when cattle are sent to graze. Wet spring and summer conditions are generally associated with abundant forage

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resources thus increasing nutrition available to the cow which in turn increases calf pre-weaning performance.

Regression Model

To estimate *WW* and the affect *GT* have on it, a regression model is developed. The model, as previously mentioned, estimates *WW* as a function of calf, dam, and environmental characteristics. The regression model is a linear regression using ordinary least squares. Coefficients measure how much the variables impact *WW*. The statistical significance of each variable is determined using t-values.

The base animal used in the regression model is an Angus steer with a *CC* genotype. In addition, the base year used in the model is 2005. This year is selected because it is the most recent year and also based on data obtained from the North Dakota Agricultural Weather Network (accessed August 10, 2006). It appears to be reasonably representative. Consequently, dummy variables for Angus, steer, *CC* genotype, and 2005 are excluded from the regression estimation. Both *BW* and *DA* are found to have a quadratic affect on *WW*.

$$
\begin{aligned}
(3) \quad WW_i = {} & C_1 + C_2 AAW_i + C_3 BW_i + C_4 BW_i^2 + C_5 CS_i + C_6 DA_i + C_7 DA_i^2 \\
& + \sum C_k GT_{ik} + \sum C_j BRD_{ij} + \sum C_l YR_{il} + \varepsilon_i
\end{aligned}
$$

The regression model is tested for multiple potential problems. To test for homoscedasticity, the assumption of constant error variance, the White test is performed and concludes the null hypothesis of homoscedasticity is rejected at the 5% level. The heteroscedasticity present in the model is corrected using the White heteroskedasticity consistent covariance matrix estimator and the model is reestimated (EViews, 2004). Finally, a correlation matrix composed of the independent variables shows little evidence

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of multicollinearity. Low correlation values, in addition to coefficient values possessing

expected signs and significance levels indicate multicollinearity is not a problem.

Simulation Model

A simulation model is developed to determine economic values of beef cows across

genotypes and to statistically compare those economic values. A MIXED procedure is

utilized in SAS to determine if there are statistical differences in average stayability across

genotypes. If the results do not show any statistical differences in average stayability then

net present values (*NPV*) can be computed to value the cows as they all have the same

economic lifespan.

However, when comparing investments with different economic lives, an

annualized equivalent return (*AER*) should be used because it allows the investments to be

evaluated over a common time basis (Barry et al., 2000). Therefore, if the results from the

MIXED procedure show average stayability to differ statistically by genotype, an *AER* is

computed to value the cows. Stayability data come from 89 genotyped cows that were

culled from the NDSU beef herd for various reasons, most commonly because they were

open. The MIXED procedure uses stayability as the dependent variable and the three

genotypes as fixed covariates to test if the slopes of the regression lines of the three

genotypes are equal. Then, t-values are used to test for statistical differences in stayability

between genotypes.

The model simulates one cow from each breed and genotype 1,000 times over 16

different pricing scenarios. The pricing scenarios are derived from the previous 16 years of

data for culled cow, beef cow, replacement heifer, and feeder calf prices (North Dakota

Farm and Ranch Business Management Annual Reports, 1990-2005). A consumer price

index provided by the U.S. Bureau of Labor Statistics is utilized to convert nominal prices from 1990 to 2005 to real dollars, with 2005 being the base year (Accessed July 17, 2006). In each simulation in which all 16 pricing scenarios are computed, the same pricing year is utilized for beef cow, replacement heifer, and calf prices.

Using the stayability distributions from each genotype, a probability is generated to represent the probability of a cow of each genotype reaching each age from 2 to 16 years old. Stayabilities, dependant on their previously generated probability, are assigned to each genotype. This is done in each simulation to estimate the productive life of the cow. When a cow is culled, it is sold at each one of the 16 different price points at an assumed weight of 635 kg. Sold cows are replaced by purchasing a 340.2 kg replacement heifer of the same breed and genotype. Replacement heifers are also purchased at each of the 16 different price points. Assuming a 93% pregnancy rate in replacement heifers, the model culls 7% of the heifers in each simulation year for being open (Hancock et al., 1994). The culled heifers are then finished to an assumed weight of 544.3 kg and sold for beef prices.

Weaning weights for calves are derived by incorporating regression coefficients and residuals obtained from equation (1). Using the results from equation (1), the simulation model estimates weaning weight with error for each of the cows. A random error is drawn from regression residuals to simulate weaning weight for each calf that a cow produces. All of the weaned calves for each cow are sold for each of the 16 different prices. Under the assumption that only 91.9% of the cows that are bred will actually wean a calf, the model applies a weight of 91.9% to the total weaning weights of calves from each cow (North Dakota Farm and Ranch Business Management Annual Report, 2005).

A price slide is also incorporated into the model for pricing calves. Calves receive a $0.18 per kilogram premium or discount for each 45.36 kg they are under or over the base weight of 340.2 kg. Data collected from the North Dakota Farm and Ranch Business Management Annual Reports (1990-2005) are used to incorporate the direct expenses associated with cow-calf pairs and replacement heifers. The direct expenses are subtracted from the annual revenue of the cow or replacement heifer to calculate net revenue.

In each simulation, the *NPV* and *AER* for each breed and genotype are computed. Mathematically, the equation used to compute *NPV* is expressed as

$$(4) \qquad NPV = \sum_{n=0}^{x} \frac{E[R_n]}{(1+r)^n},$$

where $E[R_n]$ is the expected return for each year, n represents each productive year, and r is the discount rate (Barry et al., 2000). The discount rate is assumed to be 5% throughout this thesis. Once the *NPV* is computed for each pricing scenario for each cow, an average *NPV* by genotype is computed. The *AER* for each cow is then calculated using its corresponding *NPV* calculation.

In every simulation, the *AER* is computed for each cow in each of the price scenarios resulting in a distribution of 176,000 (16 prices x 11 cows x 1000 random draws) observations. An average *AER* is then computed for each genotype. The average *AER* is compared across genotypes using a *z*-test to determine statistical differences.

A *z*-test is used to detect statistical differences between two population means (Mendenhall, Beaver, and Beaver, 2003). Due to the large number of observations from the simulation model, the *z*-test provides an adequate statistical test attributable to the law of large numbers. A null hypothesis of no difference between means is tested. The formula for the *z*-test is expressed as follows:

$$(6) \quad z \approx \frac{(\bar{x}_1 - \bar{x}_2) - D_o}{\sqrt{\dfrac{s_1^2}{n_1} + \dfrac{s_2^2}{n_2}}},$$

where D_o represents the hypothesized difference, x_1 and x_2 are the sample means, s_1^2 and s_2^2 are the variances in each sample, and n_1 and n_2 are the sample sizes. In a two-tailed test, the absolute value of the z-statistic is used to determine the significance level at which the null hypothesis can be rejected. Generally, a z-statistic with an absolute value of 1.96 is considered to represent a statistical difference in which the null hypothesis can be rejected at the 5% level.

Data

Data were collected at 3 different time periods from 595 calves in the NDSU beef herd. Birth weight, *CS*, *DA*, *BRD*, and *YR* are all collected when the calf is born. When the calf is weaned, data are again collected to measure *WW* and *AAW*. Finally, when technological advancements gave way to new biological testing equipment, the entire herd was genotyped through the use of blood samples. Now each time a new cow enters the herd, it is genotyped and recorded. The data used in this thesis are summarized in Tables 1 and 2.

Table 1. Number of observations by dam breed, dam genotype, and calf sex

Breed	n	Genotype	n	Calf Sex	n
Angus	134	*CC*	241	Steer	264
Commercial	257	*CT*	250	Heifer	331
Shorthorn	80	*TT*	104		
Simmental	124				

Table 2. Summary statistics for dam age, age at weaning, birth weight, and weaning weight

	DA* (years)	AAW (days)	BW (kg)	WW (kg)
Mean	4.1429	207.5899	40.8032	243.5045
Median	3.0000	211.0000	40.3701	240.4064
Maximum	16.0000	255.0000	67.1324	383.2895
Minimum	2.0000	150.0000	21.3191	113.3993
Std. Dev.	2.3666	18.7102	6.6542	45.4624

* AAW = calf age at weaning; BW = calf birth weight; DA = dam age; and WW = calf weaning weight.

Table 3 shows the price data for beef cows, replacement heifers, and feeder calves. Due to the unavailability of annual average replacement heifer price data, replacement heifer prices are collected from a weekly report published by the USDA-North Dakota Department of Agricultural Market News (Accessed July 17, 2006). These data consist of weekly prices received at the Napoleon Livestock Auction in North Dakota for potloads of replacement heifers. The weekly reports dating from 2000 to 2006 are used to generate annual average replacement heifer prices. The prices from those seven years are converted to a percentage of annual average feeder calf prices for the same years. The percentage is used to compute annual average replacement heifer prices for each of the 16 years. The price data for beef cows and feeder calves is published in the North Dakota Farm and Ranch Business Management Annual Reports (1990-2005).

Annual average direct expense data for cow-calf pairs and replacement heifers is shown in Table 4. The estimated direct expenses for cow-calf pairs and replacement heifers are the annual statewide averages from 1990 to 2005 in North Dakota. The expense data comes from farms representing all four regions of North Dakota (Red River Valley, North Central, South Central, and Western Missouri Slope). The direct expenses for cow-calf pairs consist of feed, vitamin and mineral, veterinary, supply, fuel and oil, repair,

Table 3. Annual average market prices for beef cows, replacement heifers, and feeder calves*

Year	Beef Cow Price ($/kg)	Replacement Heifer Price ($/kg)	Feeder Calf Price ($/kg)
1990	1.12	-	1.43
1991	1.16	-	1.48
1992	1.13	-	1.43
1993	1.19	-	1.57
1994	1.10	-	1.43
1995	0.96	-	1.19
1996	0.86	-	0.96
1997	1.09	-	1.37
1998	1.13	-	1.43
1999	1.23	-	1.64
2000	1.40	1.63	1.96
2001	1.55	1.68	1.91
2002	1.45	1.69	1.82
2003	1.60	1.60	2.18
2004	1.91	1.98	2.62
2005	2.19	2.35	2.98

*All prices are in real dollars derived from the North Dakota Farm and Ranch Business Management Annual Reports (1990-2005).

custom hire, livestock lease, marketing, and operating interest expenses. All of these expenses represent annual average costs of maintaining both a cow and calf until weaning. The direct expenses used for replacement heifers are similar; however, livestock lease and marketing expenses are excluded and breeding expense is included. These expenses are incurred from the time of purchase until first calving, which occurs at approximately two years of age. Since replacement heifers do not generate revenue in their first year, their expenses represent a large portion of the total production costs each year. Thus, for the expenses and purchase costs of replacement heifers to be offset, they must remain in the herd and wean calves for certain number of years. This is why stayability plays such a large role in producer profit.

Table 4. Annual average direct expenses for cow-calf pairs and replacement heifers*

Year	Cow-Calf Pair ($)	Replacement Heifer ($)
1990	166.87	110.07
1991	175.25	156.31
1992	178.12	129.37
1993	184.54	138.40
1994	201.38	132.16
1995	200.40	139.58
1996	213.04	189.09
1997	225.38	211.62
1998	219.44	200.17
1999	231.34	163.30
2000	248.04	248.53
2001	254.29	122.07
2002	264.09	140.56
2003	283.72	144.30
2004	305.51	175.98
2005	331.78	177.87

*All expenses are in real dollars derived from the North Dakota Farm and Ranch Business Management Annual Reports (1990-2005).

Stayability data are drawn from the NDSU cow herd, where a total of 89 genotyped cows were culled from the herd over a 10-year period (1995-2005) for various reasons. A summary of the stayability data is shown in Table 5.

Table 5. Summary statistics for stayability by genotype

	TT*	CT	CC
Mean	6.1111	5.5667	4.0800
Median	5.0000	4.0000	3.0000
Maximum	12.0000	16.0000	9.0000
Minimum	2.0000	2.0000	2.0000
Std. Dev.	3.2189	3.6253	2.1366
Observations	9	30	50

* TT = dams with TT (fat) genotype; CT = dams with CT (heterozygous) genotype; and CC = dams with CC (lean) genotype.

CHAPTER 4. RESULTS

Regression Estimation

An ordinary least squares estimation is used to determine the affect of leptin genotype on WW. Results are presented in Table 6. Nearly all independent variables included in the model are significant except for the dummy variable representing the commercial breed and several year effects. It is not surprising that these variables are not significant. Angus, which is the base breed in the model, is one of the primary breeds in the crossbred commercial cows, explaining why the commercial breed variable is insignificant. Additionally, environmental conditions and management in several years were similar to 2005, the base year.

The significant variables in the estimation are: AAW, BW, BW^2, DA, DA^2, CT, TT, CS, $Short$, Sim, $YR99$, $YR00$, $YR01$, $YR02$, and $YR04$. The results show that cattle possessing at least one T allele appear to produce calves with heavier weaning weights. The cows with the CT genotype wean calves about 5.85 kg heavier than the cows with the CC genotype. Additionally, the cows with the TT genotype wean the heaviest calves, which are an estimated 6.36 kg heavier than the calves from CC cows. The dummy variable for the TT genotype has a higher coefficient than the CT dummy variable. However, it also has a higher standard error, due to fewer TT genotype observations. Finally a Wald test is performed on the genotype variables and it rejects the null hypothesis that CT and TT are jointly equal to zero.

As expected AAW has a large affect on WW. The estimation shows that each additional day prior to weaning increases WW by 1.08 kg. Birth weight and DA both have a quadratic effect on WW, meaning for each additional unit of BW and DA the WW is

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increasing at a decreasing rate. The dummy variable, *CS*, representing the sex of the calf, was also highly significant as expected. Similar to previous research, the model shows that

Table 6. Ordinary least squares regression results with weaning weight as the dependent variable

Variable	Coefficient	Std. Error	t-stat	p-value
C	-274.19	48.43	-5.66	<0.001
AAW	1.08	0.07	16.51	<0.001
BW	9.47	2.35	4.02	<0.001
BW²	-0.08	0.03	-2.86	0.005
DA	10.76	1.62	6.63	<0.001
DA²	-0.71	0.11	-6.47	<0.001
CT	5.85	2.85	2.05	0.041
TT	6.36	3.45	1.84	0.066
CS	13.71	2.46	5.56	<0.001
Com	1.34	3.27	0.41	0.681
Short	-9.14	5.03	-1.82	0.070
Sim	11.78	3.95	2.99	0.003
YR95	9.62	4.47	2.15	0.032
YR96	11.14	8.82	1.26	0.207
YR97	5.68	11.10	0.51	0.609
YR98	8.24	7.48	1.10	0.271
YR99	10.83	6.70	1.62	0.107
YR00	24.75	4.87	5.08	<0.001
YR01	-12.10	4.12	-2.94	0.004
YR02	-17.86	4.52	-3.95	<0.001
YR03	-4.36	4.10	-1.06	0.288
YR04	37.60	3.31	11.35	<0.001

R-squared	0.629370
Adjusted R-squared	0.615787
Log likelihood	-2819.531
Durbin-Watson stat	1.757632
F-statistic	46.33416
Prob(F-statistic)	0.000000

*AAW = calf age at weaning; *BW* = calf birth weight; *DA* = dam age; *CT* = dummy variable for *CT* genotype; *TT* = dummy variable for *TT* genotype; *CS* = dummy variable for calf sex; *Com* = dummy variable for commercial breed dam; *Short* = dummy variable for Shorthorn breed dam; *Sim* = dummy variable for Simmental breed dam; *YR95* = dummy variable for 1995; *YR96* = dummy variable for 1996; *YR97* = dummy variable for 1997; *YR98* = dummy variable for 1998; *YR99* = dummy variable for 1999; *YR00* = dummy variable for 2000; *YR01* = dummy variable for 2001; *YR02* = dummy variable for 2002; *YR03* = dummy variable for 2003; and *YR04* = dummy variable for 2004.

steers are approximately 13.7 kg heavier at weaning than heifers, due to a higher

preweaning growth rate in steers (Woods et al., 1990). The breed of the cow also plays a

role in the *WW* of the calf. Shorthorn cows in our study produce calves that are an

estimated 9.13 kg lighter than the base breed, Angus. A lighter *WW* from Shorthorn cows

may be due to a slow growth rate of Shorthorn cattle. Conversely, Simmental cows, a

large-framed, fast growing breed, wean calves 11.8 kg heavier than the Angus cows.

Weather data are taken from the North Dakota Agricultural Weather Network to

determine if the base year selected in the biological model is representative. The data

consists of monthly average temperatures and total monthly rainfall in Fargo, North Dakota

for the months of May, June, July, August, and September for each of the 10 years cattle

data was collected. The monthly data from each year is then used to calculate annual

averages. These specific months are selected because that is when the weather conditions

are most influential to forage production.

Of the five dummy variables representing years that are significant, three years have

positive coefficients and two have negative coefficients. The significance of the years

1999 and 2000 are associated with above average rainfall coupled with above average

temperatures, likely increasing forage production. The increased forage growth in 1999

and 2000 resulted in calves with weaning weights 11 kg and 24.75 kg, respectively, heavier

than 2005. In 2001, above average temperature and below average rainfall perhaps limited

forage production, thus calves were 12.08 kg lighter at weaning than in 2005. The cool,

dry weather in May of 2002, may be responsible for calves being 17.85 kg lighter in that

year. Finally, excellent conditions consisting of below average temperatures and above

average rainfall in 2004 are likely the reason calves weaned heavier in 2004 than any other

year. In 2004, they were 37.59 kg heavier than in 2005. The positive and negative

coefficients on the aforementioned years, in addition to the five insignificant years, indicate

the base year is reasonably representative. A Wald test is performed on the year variables

and rejects the null hypothesis that that the year variables are jointly insignificant.

A truly surprising part of the regression results is the R^2 value of 0.629. When

using biological data that are not from a controlled experiment, obtaining a high R^2 value is

challenging due to the changing environmental and biological factors impacting the study.

Results from the MIXED procedure (Table 7) show a significant difference in

average stayability between genotypes. Dams with the *CC* leptin genotype have the lowest

stayability with an average of 4.17 years. The possession of at least one *T* allele proved to

increase stayability significantly. Dams with the *CT* genotype have an average stayability

of 5.81 years. Compared to dams with the *CC* genotype that is a 1.64 year increase in

stayability, which is significant at a 2.1% level. The average stayability increases even

more when the dam has homogenous *T* alleles or the *TT* genotype. The dams with the *TT*

genotype have an average stayability of 6.11 years, which is an increase of 1.94 years over

CC genotype dams. This difference of 1.94 years is significant at a 6.8% level. Although

the difference in average stayability is greater between *CC* and *TT* than *CC* and *CT*, the

decreased significance level is due to fewer *TT* observations.

Simulation Results

The results from the simulation are reported in Tables 8 and 9. Estimations of the

mean *AER* for each genotype and breed suggest the possession of at least one *T* allele

increases the value of a cow in a cow-calf operation. Cows with the *CC* genotype for each

breed in the simulation have the lowest mean *AER*. These results can be attributed to the

lower weaning weights and lower stayabilities of *CC* genotype cows.

Table 7. MIXED procedure test for differences in longevity by genotype

GT	GT	Estimate	t-stat	p-value
CC	-	4.170	9.910	<0.001
CT	-	5.815	10.480	<0.001
TT	-	6.111	6.360	<0.001
CC	*CT*	-1.645	-2.360	0.021
CC	*TT*	-1.941	-1.850	0.068
CT	*TT*	-0.296	-0.270	0.790

*TT = dams with *TT* (fat) genotype; *CT* = dams with *CT* (heterozygous)
genotype; and *CC* = dams with *CC* (lean) genotype.

Table 8. Simulation results by breed and genotype

Breed	Genotype*	Mean *AER* ($)	Variance
Shorthorn	*CC*	59.79	3683.617
	CT	81.08	4016.137
Simmental	*CC*	51.66	3424.434
	CT	67.01	3525.954
	TT	90.71	3784.473
Commercial	*CC*	52.19	3467.242
	CT	76.30	3837.547
	TT	77.63	3313.207
Angus	*CC*	39.05	2995.779
	CT	68.77	3565.669
	TT	73.28	3163.943

*TT = dams with *TT* (fat) genotype; *CT* = dams with *CT*
(heterozygous) genotype; and *CC* = dams with *CC* (lean) genotype.

Shorthorn cows with the *CC* genotype have a mean *AER* of $59.79 which is lower

than the mean *AER* of $81.08 produced by Shorthorn cows of the *CT* genotype. This

difference of $21.28 is significant at the 13% level. There was no data on Shorthorn cows

with the *TT* genotype. The mean *AERs* of Simmental cows with *CC*, *CT*, and *TT* genotypes

are $51.66, $67.01, and $90.71, respectively. The difference of $15.35 between *CC* and *CT*

Simmental cows is significant at the 23% level, while the difference of $39.05 between *CC*

and *TT* Simmental cows is significant at a 1.2% level. Increasing the amount of *T* alleles

from 1 to 2 (*CT* to *TT*) in the Simmental cows increases the mean *AER* by $23.70 (p =

0.112).

Table 9. Statistical comparison of mean *AER* by breed and genotype

Breed	Genotype*		Z-statistic	p-value
Shorthorn	*CC*	*CT*	-1.5138	0.130
Simmental	*CC*	*CT*	-1.2054	0.230
	CC	*TT*	-2.5164	0.012
	CT	*TT*	-1.5981	0.112
Commercial	*CC*	*CT*	-1.8095	0.070
	CC	*TT*	-1.7626	0.080
	CT	*TT*	-0.0940	0.828
Angus	*CC*	*CT*	-2.4905	0.013
	CC	*TT*	-2.5916	0.010
	CT	*TT*	-0.3394	0.740

*TT = dams with *TT* (fat) genotype; *CT* = dams with *CT*
(heterozygous) genotype; and *CC* = dams with *CC* (lean) genotype.

Commercial cows again show that *T* alleles are economically important. The *CC*,

CT, and *TT* commercial cows have mean *AERs* of $52.19, $76.30, and $77.63, respectively.

Differences of $24.11 and $25.44 between the *CC* and *CT* and the *CC* and *TT* cows are

significant at 7% and 8% levels, while no significant difference is detected between the *CT*

and *TT* genotypes (p = 0.828).

The *T*-alleles appear to have the largest affect on Angus cows. The mean *AER* of an

Angus cow with the *CC* genotype is $39.05 compared to a mean *AER* of $68.77 from the

CT genotype and $73.28 from the *TT* genotype. The $29.72 difference between the *CC* and

CT genotypes is significant at the 1.3% level, while the $34.22 difference between the *CC*

and *TT* genotypes is significant at the 1% level. Again, as in the Simmental cows, the *CT*

and *TT* genotypes have no significant difference in mean *AER* (p = 0.740).

Sensitivity analyses are completed to determine the effects of *CA* and *BW* on the

mean *AER* of cows. In the first sensitivity analysis, stayabilities are taken from the same

distribution of probabilities for each genotype, so each genotype will have the same mean

CA. Results from the *CA* sensitivity analysis are shown in Tables 10 and 11. The statistical

comparisons in Table 11 show that *CA* is a key factor in the mean *AER* of cows. There are

no significant differences in mean *AER* when *CA* is the same across genotypes.

A similar sensitivity analysis is performed to determine the sensitivity of *AER* to

differences in *BW*. The *BWs* from each genotype of each breed are used to obtain an

average *BW* to be used for all the cows in the simulation. Results from the *BW* sensitivity

analysis are reported in Tables 12 and 13.

Table 10. Cull age sensitivity analysis results by breed and genotype

Breed	Genotype*	Mean *AER* ($)	Variance
Shorthorn	*CC*	67.76	3802.022
	CT	73.13	4028.521
Simmental	*CC*	59.48	3515.751
	CT	60.12	3543.380
	TT	71.72	3959.582
Commercial	*CC*	59.56	3550.642
	CT	68.70	3845.485
	TT	59.68	3521.084
Angus	*CC*	46.04	3067.674
	CT	61.14	3583.077
	TT	55.72	3363.370

*_TT_ = dams with *TT* (fat) genotype; *CT* = dams with *CT*
(heterozygous) genotype; and *CC* = dams with *CC* (lean) genotype.

Table 11. Statistical comparison of cull age sensitivity analysis results by breed and genotype

Breed	Genotype*		z-statistic	p-value
Shorthorn	CC	CT	-0.4245	0.674
Simmental	CC	CT	-0.0560	0.952
	CC	TT	-1.0131	0.312
	CT	TT	-0.9570	0.337
Commercial	CC	CT	-0.7652	0.441
	CC	TT	-0.0104	0.992
	CT	TT	0.7581	0.447
Angus	CC	CT	-1.4024	0.162
	CC	TT	-0.9317	0.352
	CT	TT	0.4831	0.631

*TT = dams with TT (fat) genotype; CT = dams with CT (heterozygous) genotype; and CC = dams with CC (lean) genotype.

Table 12. Birth weight sensitivity results analysis by breed and genotype

Breed	Genotype*	Mean AER ($)	Variance
Shorthorn	CC	15.82	2472.639
	CT	33.68	2544.664
Simmental	CC	52.64	3456.214
	CT	72.70	3726.461
	TT	84.63	3562.959
Commercial	CC	51.65	3449.855
	CT	71.92	3676.517
	TT	83.52	3513.223
Angus	CC	43.72	3128.737
	CT	63.14	3375.647
	TT	74.54	3203.840

*TT = dams with TT (fat) genotype; CT = dams with CT (heterozygous) genotype; and CC = dams with CC (lean) genotype.

Similar to the results from the base simulation, cows possessing at least one T allele appear to have a significantly higher AER. For all breeds, except Shorthorns in which no TT observations are available, TT cows have significantly higher $AERs$ than CC cows when BW is held constant. Cows with the CT genotype also had higher $AERs$ than CC cows,

although the differences are not as highly significant as in *TT* to *CC* comparison. Results

from the *BW* sensitivity show Shorthorn cows with the *CC* and *CT* genotypes have mean

AERs of $15.82 and $33.68, respectively. In comparison to the base simulation, the mean

AER of Shorthorn cows with the *CC* genotype decreases by $43.98 and the mean *AER* of

CT genotype cows decreases by $47.40, resulting in Shorthorn cows having the largest

decrease in mean *AER* of any breed when a common *BW* is used. Shorthorn cows have the

highest *BW* of any breed in the base simulation, thus reducing their *BW* in this sensitivity

likely resulted in lowering the *WW* of their calves which led to a decrease in their *AER*.

Table 13. Statistical comparison of birth weight sensitivity analysis
results by breed and genotype

Breed	Genotype*		Z-statistic	P-value
Shorthorn	*CC*	*CT*	-1.9423	0.052
Simmental	*CC*	*CT*	-1.5289	0.128
	CC	*TT*	-2.1303	0.033
	CT	*TT*	-0.8210	0.412
Commercial	*CC*	*CT*	-1.5559	0.121
	CC	*TT*	-2.1411	0.032
	CT	*TT*	-0.8092	0.424
Angus	*CC*	*CT*	-1.6339	0.103
	CC	*TT*	-2.2754	0.023
	CT	*TT*	-0.8699	0.384

*TT = dams with *TT* (fat) genotype; *CT* = dams with *CT*
(heterozygous) genotype; and *CC* = dams with *CC* (lean) genotype.

A final analysis is performed to determine the sensitivity mean of *AER* to *CA* and

BW differences. In the analysis, both CA and BW are identical across breeds and

genotypes. The results from this sensitivity analysis are shown in Tables 14 and 15. The

lack of significant differences across breeds and genotypes indicates *CA* and *BW* are key

components of the economic value of a cow.

Table 14. Birth weight/cull age sensitivity analysis results by breed and genotype

Breed	Genotype*	Mean *AER* ($)	Variance
Shorthorn	CC	21.97	2475.970
	CT	27.45	2621.875
Simmental	CC	60.50	3550.447
	CT	65.60	3735.689
	TT	66.17	3751.793
Commercial	CC	59.00	3531.703
	CT	64.48	3691.596
	TT	65.07	3709.224
Angus	CC	50.91	3213.162
	CT	55.72	3401.582
	TT	56.88	3401.000

*TT = dams with TT (fat) genotype; CT = dams with CT (heterozygous) genotype; and CC = dams with CC (lean) genotype.

Table 15. Statistical comparison of birth weight/cull age sensitivity analysis results by breed and genotype

Breed	Genotype*		Z-statistic	P-value
Shorthorn	CC	CT	-0.6654	0.509
Simmental	CC	CT	-0.4333	0.667
	CC	TT	-0.4806	0.631
	CT	TT	-0.0472	0.960
Commercial	CC	CT	-0.4701	0.638
	CC	TT	-0.5195	0.603
	CT	TT	-0.0495	0.960
Angus	CC	CT	-0.4501	0.653
	CC	TT	-0.5588	0.575
	CT	TT	-0.1057	0.912

*TT = dams with TT (fat) genotype; CT = dams with CT (heterozygous) genotype; and CC = dams with CC (lean) genotype.

CHAPTER 5. CONCLUSIONS AND IMPLICATIONS

This chapter summarizes the problem addressed, the objectives, the methodology, and the results. Finally, implications, limitations of this study, and suggestions about future research are presented.

Summary of Problem

Recent investigation reports dairy cows with the *TT* leptin genotype produce significantly more milk than *CC* cows (Buchanan et al., 2003). The *TT* genotype may be of economic value in cow-calf herds, since weaning weight, a major component of profit in a cow-calf operation, largely depends on dam milk production. Studies show cows with the *TT* leptin genotype produce larger amounts of protein hormone leptin, which is positively correlated to BCS (Leon et al., 2004; Kononoff et al., 2005). Furthermore, research indicates BCS increases stayability, weaning weight, and pregnancy rate (Kunkle, Sand, and Rae, 1994). Thus the *TT* genotype may be of additional economic benefit by reducing the amount of open cows being culled and as a result, increase cow stayability.

Summary of Objectives

The main objective of this study is to determine if the economic value of a beef cow varies by leptin genotype. In addition to prices and feed costs, the primary determinants of the economic value of a beef cow are calf weaning weight and stayability. Thus, differences in calf weaning weight and average stayability by genotype are estimated and used to compute economic values of the cows.

Summary of Methodology

Data composed of 595 observations of genotyped beef cows are used to develop a regression model to estimate *WW* by dam genotype. Calf weaning weight is estimated as a

function of calf and dam characteristics and environmental effects. Differences in average stayability by genotype are determined though the use of a MIXED procedure in SAS. A simulation model using regression coefficients and residuals and stayability data is developed to determine how the economic value of the cow is impacted by genotype. Annualized equivalent returns are calculated for 16 different price scenarios for cows of each breed and genotype. Averages of the *AERs* are compared across genotypes within breeds using a z-test to determine statistical differences in economic value by leptin genotype.

Summary of Results

The results indicate that possessing at least one *T* allele increases the economic value of a beef cow. With the exception of Shorthorn cattle, in which there were no *TT* observations, cows with the *TT* genotype have the highest mean *AER* for each breed. The differences in mean *AER* between *TT* and *CC* genotypes in Simmental, commercial, and Angus cows are significant at a 1.2%, 8%, and 1% levels, respectively. Statistical analysis indicates *TT* genotype cows have the lowest *BW* of any genotype. The low *BWs* of the *TT* cows may play a key role in the *CA* and economic value of the cows. As previously mentioned, high *BW* is associated with decreased calving ease. When cows need assistance in calving, calf death loss increases by 4 to 5 times that of unassisted cows (Corah, Dhuyvetter, and Simms, 1989). In addition, assisted calving increases the amount of open cows being culled due to rebreeding difficulties (Wang et al., 2001). Due to these undesirable circumstances associated with high *BW*, cows that require assistance when calving are often culled. Therefore, the increased stayability exhibited by the *TT* genotype cows in this study may be largely impacted by lower *BW*. Increasing stayability directly

impacts profit in a cow-calf operation, thus indicating why the *TT* cows have the highest

mean *AER* and *CC* cows have the lowest mean *AER* for all breeds in this study.

Implications

The implications from this study could potentially carry through all the way from

the seedstock producer to the processing plant. The results indicate that in the short term,

premiums and discounts may be applied to breeding stock based on genotype. Assuming

the results from this study hold true, seedstock producers may begin to segregate herds by

genotype to develop identity registered herds. With segregated herds, they could sell

registered semen, embryos, and breeding cattle containing the *TT* genotype for a premium

price without having to genotype their products. By genotyping seedstock breeding herds,

the costs of genotyping can be spread out over numerous generations of progeny. Cow-

calf producers may be willing to pay more for the *TT* genotype in an attempt to increase the

amount of *T* allele in the herd to maximize profit.

Study Limitations

The results of this study are limited by a small number of observations for

genotypes across breeds and by the management practice used on the herd in the study.

Although this study uses 595 observations, it is limited by the number of genotype

observations across breeds. No TT genotype Shorthorn cows were contained in the data

set. Assuming Shorthorn cows would follow the same pattern as the other breeds, in which

the *CC* cows were the least valuable and *TT* cows were the most valuable, the results may

have been even more conclusive in proving the *TT* genotype to be the most valuable. The

data on cow stayability is also limited in this study. Observations from only 89 culled cows

were used to determine cow stayability by genotype. Only nine of the 89 culled cow

observations represented cows with the *TT* genotype. Obviously more data may have led to different stayability results and greater confidence in those results.

The cow data used in this study comes from a cattle herd that is managed with research and teaching objectives in mind. The management practices of this cattle herd may vary widely from that of a commercial herd. Since much of the data used in the study is dependent on management, a similar study in a commercial herd may lead to different results.

Suggestions for Further Study

Further investigation into how leptin genotypes affect economic value of beef cows may be necessary due to the small number of observations of genotypes across breeds used in this study. Data from many more herds and breeds should be collected to provide more definitive results. Additional research may also need to use data from commercial cattle herds to obtain more representative results. Finally, further economic analysis using the real options valuation approach may provide a more accurate assessment of economic values and optimal transition time.

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APPENDIX A. GAMS CODE

```
*computes the value of leptin genotyping
*copyright North Dakota State University
*created by Eric A. DeVuyst and Jay Mitchell
*July 2006
*Includes genotype information

option limrow=0;
option limcol=0;
$offsymlist
$offsymxref
$offuellist
$offuelxref

SETS
 cow
   /c1*c11/
 parm  results from econometric estimation
     /c,age_at_wean, birth_kg, birth_kg2,dam_CC,dam_CT,dam_TT,
         sex_dummy,d_com,d_short,d_sim,d_ang,yr95*yr99,yr00*yr05,age,age2/
 genotype(parm) /dam_CC,dam_CT,dam_TT/
 breed(parm) /d_com, d_short, d_sim, d_ang/
 long longevity of cow /l1*l16/
 priceyr price repetitions /pr1*pr16/
 momentlong moments of longevity distribution /meanlong, varlong/
 err errors from econometric estimation /1*595/
 rep number of repetitions of simulation /r1*r1000/
 CT_cows /ct1*ct30/
 CC_cows /cc1*cc50/
 TT_cows /tt1*tt9/
;
ALIAS (long,long1), (genotype,geno1);
TABLE cdata(cow,breed,genotype)
        dam_CC dam_CT dam_TT
c1.d_short    1
c2.d_short           1
c3.d_Sim      1
c4.d_sim             1
c5.d_sim                    1
c6.d_com      1
c7.d_com             1
c8.d_com                    1
c9.d_ang      1
c10.d_ang            1
c11.d_ang                   1
```

;
TABLE cullfreq(long,genotype)

	dam_CC	dam_CT	dam_TT
l2	16	5	1
l3	10	6	0
l4	6	6	3
l5	6	2	1
l6	3	2	0
l7	3	0	2
l8	5	3	0
l9	1	2	0
l10	0	1	1
l11	0	0	0
l12	0	1	1
l13	0	1	0
l14	0	0	0
l15	0	0	0
l16	0	1	0

;
cullfreq(long,genotype)= cullfreq(long,genotype)
        /SUM(long1,cullfreq(long1,genotype));
PARAMETER prob(cow,long);
LOOP((cow,genotype,breed)$cdata(cow,breed,genotype),
 prob(cow,long)=cullfreq(long,genotype);
);
DISPLAY prob;
PARAMETER
cowdata(cow,parm);
LOOP((cow,genotype,breed)$cdata(cow,breed,genotype),
 cowdata(cow,genotype) = cdata(cow,breed,genotype);
 cowdata(cow,breed) = cdata(cow,breed,genotype);
);
PARAMETER parmvalues(parm) from eviews file eviews cows all years
 /
C   -274.1921
AGE_AT_WEAN   1.082230
BIRTH_KG   9.470149
BIRTH_KG2   -0.082518
AGE   10.75922
AGE2   -0.712558
DAM_CT   5.854521
DAM_TT   6.363315
SEX_DUMMY   13.70742
D_COM   1.342032
D_SHORT   -9.144817
D_SIM   11.78374

48

```
YR95        9.621286
YR96       11.13863
YR97        5.676869
YR98        8.244042
YR99       10.83361
YR00       24.75479
YR01      -12.10411
YR02      -17.86110
YR03       -4.356392
YR04       37.60120
/;


PARAMETER calfcrop(cow);
PARAMETER error(err) errors from econometric estimation
$include c:\research\cow-calf\errors.txt


$include c:\research\cow-calf\culls.txt
PARAMETER price(priceyr) calf price in real dollars per cwt
/
pr1       64.71
pr2       67.23
pr3       64.65
pr4       71.18
pr5       64.96
pr6       54.00
pr7       43.46
pr8       62.05
pr9       65.02
pr10      74.39
pr11      89.05
pr12      86.60
pr13      82.53
pr14      98.92
pr15     118.97
pr16     135.00
/
;


PARAMETERS cull(priceyr) cull cow price in real dollars per cwt
/pr1      34.00
 pr2      33.89
 pr3      33.12
 pr4      35.88
 pr5      32.48
 pr6      28.17
 pr7      24.74
```

```
pr8      28.68
pr9      29.63
pr10    31.56
pr11    35.00
pr12    37.00
pr13    33.44
pr14    41.93
pr15    50.78
pr16    54.30
/

;
price(priceyr) = price(priceyr)*2.2046/100;
cull(priceyr) = cull(priceyr)*2.2046/100;
PARAMETERS heifer_cost(priceyr)
/
pr1      110.07
pr2      156.31
pr3      129.37
pr4      138.40
pr5      132.16
pr6      139.58
pr7      189.09
pr8      211.62
pr9      200.17
pr10    163.30
pr11    248.53
pr12    122.07
pr13    140.56
pr14    144.30
pr15    175.98
pr16    177.87
/
cow_cost(priceyr)
/
pr1      166.87
pr2      175.25
pr3      178.12
pr4      184.54
pr5      201.38
pr6      200.40
pr7      213.04
pr8      225.38
pr9      219.44
pr10    231.34
pr11    248.04
```

```
pr12    254.29
pr13    264.09
pr14    283.72
pr15    305.51
pr16    331.78
/
beef(priceyr)
/
pr1     50.86123912
pr2     52.72258065
pr3     51.36431132
pr4     54.01177675
pr5     49.70353303
pr6     43.46482335
pr7     38.88356375
pr8     49.39093702
pr9     51.2452637
pr10    55.70394265
pr11    63.66021505
pr12    70.27777778
pr13    65.86200717
pr14    72.73323093
pr15    86.85724526
pr16    99.2
/
;
```

PARAMETERS
calfweight(cow,long,priceyr,rep,long1) calf weaning weight
value(cow,long,priceyr,rep,long1) calf value less price slide
npv(cow,priceyr,rep,long1) net present value of cow's calves
aer(cow,priceyr,rep,long) annualized equivalent return of cow
discount_rate /0.05/
sim_error simulation error for weights randomly drawn from error(err)
life(cow,priceyr,rep,long1) productive life
replacement(priceyr)
interest(cow,priceyr,rep,long1)
;
TABLE birth_wt(breed,genotype)

	dam_CC	dam_CT	dam_TT
d_Ang	79.23076923	86.90217391	81.79310345
d_Sim	89.63636364	85.81818182	96.21428571
d_Com	90.15	93.70408163	85.08474576
d_short	98.0483871	98.625	

;
birth_wt(breed,genotype) = SUM(geno1,birth_wt(breed,geno1))/3;

```
replacement(priceyr) = 0.82*price(priceyr);
LOOP((cow,genotype,breed)$(cowdata(cow,genotype) AND cowdata(cow,breed)),
 cowdata(cow,'birth_kg') = birth_wt(breed,genotype)/2.2046;
 cowdata(cow,'birth_kg2') = cowdata(cow,'birth_kg')**2;
);

cowdata(cow,'sex_dummy') = 0.443697;
cowdata(cow,'age_at_wean') = 205;
cowdata(cow,'c') = 1;
parmvalues(breed)=1;

LOOP(long1$(ORD(long1) GT 1),
 LOOP((rep,cow)$prob(cow,long1),
  LOOP(long$((ORD(long) GT 1) AND (ORD(long) LE ORD(long1))),
   life(cow,priceyr,rep,long1)=ORD(long1);
   sim_error = ROUND(UNIFORM(0.5,595.49999999),0);
   cowdata(cow,'age') = ORD(long);
   cowdata(cow,'age2') = ORD(long)**2;
   LOOP(err$(ORD(err) EQ sim_error),
    sim_error = error(err);
    LOOP(priceyr$price(priceyr),
     calfweight(cow,long,priceyr,rep,long1) = SUM(parm,cowdata(cow,parm)
                     *parmvalues(parm)) + sim_error;
* assumes 91.9% weaning rate and $0.08 price slide
     value(cow,long,priceyr,rep,long1)=0.919*calfweight(cow,long,priceyr,rep,long1)
            *(price(priceyr)
             + (-calfweight(cow,long,priceyr,rep,long1)+750/2.2046)*(.08*2.2046)/100);

* assumes 93% pregnancy rate as heifer. if open sold as beef.
     value(cow,long,priceyr,rep,long1)=  0.93*(value(cow,long,priceyr,rep,long1)
                     -cow_cost(priceyr));
     interest(cow,priceyr,rep,long1) = (replacement(priceyr)*340.2+heifer_cost(priceyr)
                -635*cull(priceyr))/2*0.07;
   );
  );
 );

);
 value(cow,'l1',priceyr,rep,long1)= -replacement(priceyr)*340.2
                -heifer_cost(priceyr);
*assumes 7% open hiefers sold at 1200 lbs of beef sold at beef prices
 value(cow,'l2',priceyr,rep,long1)= value(cow,'l2',priceyr,rep,long1) + 0.07*1200/100*
                beef(priceyr);
 LOOP((long,cow,rep,priceyr)$(ORD(long) EQ life(cow,priceyr,rep,long1)),
  value(cow,long,priceyr,rep,long1)
```

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```
                = value(cow,long,priceyr,rep,long1)+ 635*cull(priceyr);
);
value(cow,long,priceyr,rep,long1) = value(cow,long,priceyr,rep,long1)
                - interest(cow,priceyr,rep,long1);
npv(cow,priceyr,rep,long1) = SUM(long$(ORD(long) LE life(cow,priceyr,rep,long1)),
                value(cow,long,priceyr,rep,long1)
                /(1+discount_rate)**ORD(long));
aer(cow,priceyr,rep,long1)$life(cow,priceyr,rep,long1) = npv(cow,priceyr,rep,long1)
                /((1-1/((1+discount_rate)**life(cow,priceyr,rep,long1)))
                /discount_rate);
);


PARAMETERS
meanww(cow)      average weaning weights from simulation
meanret(cow)
avgret(genotype)
varret(cow)
varbygeno(genotype)
;

meanww(cow)
           = SUM((priceyr,rep,long,long1)
                $calfweight(cow,long,priceyr,rep,long1),
                calfweight(cow,long,priceyr,rep,long1)*prob(cow,long1)
                /(life(cow,priceyr,rep,long1)-1))
                /(CARD(priceyr)*CARD(rep));

meanret(cow)
           = SUM((priceyr,rep,long1),
                aer(cow,priceyr,rep,long1)*prob(cow,long1))
                /(CARD(priceyr)*CARD(rep));
avgret(genotype) = SUM((cow,priceyr,rep,long)
                $cowdata(cow,genotype),
                aer(cow,priceyr,rep,long)*prob(cow,long))
                /(CARD(priceyr)*CARD(rep));
varret(cow)= SUM((priceyr,rep,long),
                POWER(aer(cow,priceyr,rep,long)-meanret(cow),2)
                *prob(cow,long))/(CARD(rep)*CARD(priceyr));
varbygeno(genotype) = SUM((cow,priceyr,rep,long)
                $cowdata(cow,genotype),
                POWER(aer(cow,priceyr,rep,long)-avgret(genotype),2)
                *prob(cow,long));


DISPLAY  meanret, avgret, varret,varbygeno, meanww;
```