

The expected utility of genetic information in beef cattle production

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ABSTRACT

Scientific inquiry is increasing our knowledge of plant and animal genomics. The ability to specify heterogeneous production processes, to sort agricultural inputs by genotype, or to guide breeding programs to satisfy specific markets based on genetic expression may increase producer and consumer benefits. This research develops a decision analysis framework to assess the expected value of genetic information under risk aversion. Expected utilities are evaluated both with and without genetic trait information. Potential gains in the value of information can be quantified as research unravels the linkages between genetics and crop and animal performance and quality. An application to cattle feeding indicates potential gains to developing markets for specific animal genetic characteristics based on the amino acid sequence of the leptin gene.

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1. Introduction

The outcomes of biological processes are seldom certain. Yields vary from field to field. Crop quality varies by variety and growing conditions. Animal performance and value differ even among progeny of the same parents. While laboratory and controlled environments remove much of the output uncertainty arising from weather, spatial or temporal variability in the application of complementary inputs, and differences in management effort, production uncertainty may still exist due to the genetic complexity underlying biological processes. Variability in output yield and quality is increasingly being linked to specific genetic sequences of individual plants and animals.

Scientific discovery is slowly unraveling genetic complexity underlying production variability. Recent advances have led to genetic mappings for the human (Collins et al., 2003), rice (Goodman et al., 2002), corn (Pennisi, 2004) and chicken genomes (Hillier et al., 2004). As the ability to map the genetic characteristics of individual organisms increases, the amount of information retrievable increases and the cost of information procurement falls. Increasingly, genetic information is being linked to crop and animal performance and quality (DeVuyst et al., 2007; Lusk, 2007).

Important as the advances in genetics have been, research is only beginning to address the economic contribution of genetic information in agricultural production. Essential to determining the value of genetic information in agricultural production is identifying the influence of genotype on production. Considerable research has assessed the effects of genetic modification (Moschini

et al., 2000), yet these studies approach the problem as discrete decisions of process adoption rather than using genetic characteristics of the plant or animal to guide selection, production, marketing, or management decisions. Information theoretic approaches provide excellent insight into the value of additional information, yet yield little operational guidance on incorporating this information in decision making (Hennessy et al., 2004; Hennessy, 2007).

The objective of this paper is to estimate the value of feeder cattle genetic information. Carcass outcomes are characterized by a multivariate distribution of quality measures used in determining output value. Value distributions are estimated based on the adoption of optimal management controls both under naïve assumptions (i.e., levels of conditioning variables affecting outcome distributions are not known) and when controls are applied with knowledge of the conditioning variables. The value of the additional information is derived from differences in expected values under both risk neutrality and risk aversion.

The empirical application estimates parameters of a system of equations relating beef animal characteristics at feedlot placement to a multivariate vector of carcass traits. Statistically significant relationships are found between the amino acid sequence on the leptin-encoding gene of the individual animals and carcass traits. Using the estimated system, distributions of carcass characteristics are simulated, yielding a discontinuous empirical distribution of carcass net returns. Simulated draws from the net return distributions are assessed in an expected utility framework to compare certainty equivalents for the pooled population (the uninformed, naïve sample) and subsamples sorted by genetic characteristics. Two specific uses of the information are analyzed: (1) genetic information can be acquired and, conditional upon the information attained, optimal management controls can be selected; and (2)

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the biological input (i.e., the group of animals) is heterogeneous, and acquired information can affect selection of subgroups by genetic trait.

2. The value of information in agricultural systems

Analysts have applied decision theory to determine the value of information in several agricultural settings. Baquet et al. (1976) determined the value of weather forecasts in farmer planting decisions. The expected value of sample information embedded in frost forecasts was calculated as the compensating variation necessary to equate maximal expected utility resulting from optimal actions based on a farmer's prior probabilities with the expected utility achieved when optimal actions are chosen conditional upon received information. Babcock (1990) expanded the analysis to consider sectoral effects when the weather information is a public good, resulting in supply shifts when many farmers base decisions on the forecast information. Babcock's analysis supports the counter-intuitive conclusion that increased information can be welfare reducing when external effects, such as market prices, are negatively affected by individual responses to widely available information.

The value of information about the productive input itself has also received considerable attention. Ladd and Martin (1976) applied the input characteristics model to determine marginal implicit prices for a vector of quality traits for corn varieties. In a pointer to future developments, they proposed use of the method to guide future product line research. Lambert and Wilson (2003) pursued this suggestion in deriving values embodied in wheat varieties based on varietal differences in a multivariate set of desirable end-user product traits. Using a rich set of variety trial data, Lambert and Wilson derived distance function estimates relating a vector of agronomic (inputs) and end-user (outputs) characteristics, bundled by variety, to determine the values of different varieties from the perspective of the downstream processor. The information relayed by variety was found to provide value to the end user processor.

In an application to improve hog values, Ladd and Gibson (1978) used parametric programming to find the marginal value of genetic improvements related to three heritable traits (backfat, feed efficiency, and average daily gain). Ladd and Gibson claimed to be the first economists contributing to the determination of the economic values of heritable genetic traits, measures long used among plant and animal breeders to guide breeding programs. Subsequent research has identified optimal short-run feeding rations when milk component pricing is adopted, as well as possible longer-run responses to milk cow breeding programs to exploit pricing grids based on specific milk output traits (protein, butterfat, and fluid carrier production) (Buccola and Iizuka, 1997). In a precursor to the current research, DeVuyst et al. (2007) and Lusk (2007) both derive values of genetic markers related to the leptin gene in beef cattle based on a distribution of net returns derived from a multivariate grid pricing formula. Similar to the current research, pricing grids are based on carcass weights and on yield and quality grades. Genetic characteristics of the animals are found to be related to the three pricing components, and thus suggest cattle value may be related to genetic composition.

Hennessy et al. (2004) have recently made two major contributions in determining the value of information in agricultural production. The authors demonstrated the potential benefits of improved information about the genetic attributes of biological inputs arising from sorting and improved returns to product differentiation. The authors' second contribution was to demonstrate how the use of information *ex ante* can lead to heterogeneous production decisions based on input characteristics. In a clear

challenge providing a segue to the current research is the authors' statement concerning impediments to improvements in beef quality arising from the lack of information about the genetic traits of beef cattle.

Both of the considerations posed by Hennessy et al. (2004) are addressed in this research. The influence of genetic information on animal net returns is determined based on carcass data collected for 770 steers and heifers. If positive, collection of the genetic information may increase returns to feeding by sorting animals based on genotype, as well as allowing management controls to be adopted conditional upon the genetic traits of the animals. Research suggests livestock markets are responsive to phenotypic and lineage information (Chvosta et al., 2001; Jones et al., 2008; Dhuyvetter et al., 1996). If performance and product quality can be explained at least in part by genotype, signaling of genetic traits may affect prices throughout the beef production chain. Vanek et al. (2008) have recently shown how bull markets have recently incorporated ribeye area and intramuscular fat deposits, two measures known to be affected by the leptin gene, in determining bull sale prices.

The paper proceeds as follows. The next section builds upon Hennessy et al.'s depiction of increasing information affecting conditional distributions by developing a new model of expected utility maximization based on conditional probability density functions or, in the case of discrete outcomes, based on draws from an empirical probability distribution. Section three describes data used in the study and derives econometric estimates of system coefficients describing the multivariate distribution of carcass attributes. Results are next presented based on changing the only management control available in the data set (days on feed), as well as determining different values of the animals based on genotype. Ending comments summarize the results and indicate future directions for research in which production and marketing channels might be affected by increasing availability of information relating genotype to product performance and quality.

3. A model of the value of genetic information

Consider a control problem with a univariate outcome, $X \in \mathbb{R}^1$. $X = X(\Omega|a)$ is a random variable, conditional on discrete and mutually exclusive control actions $a = \{a_1, a_2, \dots, a_n\}$. Letting ω represent an event in Ω , we can write the distribution of outcome X given action a is selected as

$$F_{X|a}(x) = P((X|a) \leq x) = P(\{\omega : X(\omega|a) \leq x\}). \quad (1)$$

The density of X is $f_{X|a}(x)$ is therefore

$$F_{X|a}(b) = \int_{-\infty}^b f_{X|a}(x) dx. \quad (2)$$

Control costs are $c(a_i)$. The decision maker selects action a_i to maximize expected utility over outcome space $X(\Omega|a)$, where utility is assumed continuous, increasing, at least twice differentiable, and concave with respect to X

$$\text{Max}_a EU(X - c(a)) = \text{Max}_a \int_{-\infty}^{\infty} U(X(\omega, a) - c(a)) f_{X|a}(x) dx \quad (3)$$

Numerical solution of (3) may be obtained through direct solution of the expected utility maximization problem (Lambert and McCarl, 1985), given (1) random draws $x_{s|a}$ from an empirical distribution of $f_{X|a}(x)$, with (2) the probability of the draw, π_s , and (3) an assumed functional form of the utility function. The algorithm for calculating expected utilities is in the Appendix. For each action a_i

$$EU(X - c(a_i)) \approx \sum_s \pi_s U(x_{s|a_i} - c(a_i)) \quad (4)$$

equals the expected utility of the action. Use of the approximation instead of a strict equality indicates that random, discrete draws from a continuous density function are being used in the solution of the expected utility maximization problem. Optimality involves selecting the action yielding the greatest expected utility.

Problem (3) is the uninformed problem. In [Hennessy et al.'s \(2004\)](#) terminology, problem (3) is the baseline empty information set, in which little or no information regarding eventual characteristics of the product is available. Additional genotypic information, or any other information allowing sorting, is not available. The population underlying the density function $f_{X|a}(x)$ is likely, however, to be composed of subpopulations that could, with additional information, be sorted into more homogeneous groupings. The decision maker may then consider actions $A^k = \{a_i^k\}$ that are appropriate to each grouping k . The distribution of conditional outcomes, $F_{X|a}(x)$, may differ if x is drawn from population k . Additional information may allow decisions to be made conditional upon possibly sorting the heterogeneous population into k subgroups. Outcomes X may then be dependent upon the underlying population and the different management controls:

$$F_{X|a_i^k}(x) = P((X|a_i^k) \leq x) = P(\{\omega^k : X(\omega^k|a_i^k) \leq x\}) \quad (5)$$

With knowledge of k , the decision maker seeks to maximize expected utility by selecting a_i^k from the set of possible actions. He will select actions appropriate to each subpopulation to maximize

$$\text{Max}_a EU(X - \delta - \sum_k c(a^k)) \approx \text{Max}_a \sum_k \rho^k \int_{-\infty}^{\infty} U(X(\omega, a_i^k) - \delta - \sum_k c(a^k)) f_{X|a_i^k}(x) dx \quad (6)$$

where ρ^k is the proportion of the sample from population k and δ is the cost of acquiring the signal allowing sorting.

Similar to the conditions characterizing optimality for the pooled population, determination of the optimal set of actions $\{A^k\}$ will result from numerical solution of

$$EU(X - \delta - c(a_i^k)) \approx \sum_k \rho^k \sum_s \pi_s^k U(X_s^k - \delta - c(a_i^k)). \quad (7)$$

Given independence among the controls and the distributions of outcomes, solving (7) is equivalent to maximizing expected utility for each subpopulation. Of course, the processor may decide to only procure inputs from subpopulation k . This may place a higher premium on this subpopulation, yet downstream market impacts may adjust to equalize returns among subpopulations. Although the model is easily modified to allow, for example, $p^1 = 1$ and $p^j = 0$ for $j = 2, \dots, n$, market effects require an additional component to the research that is the focus of a current research project.

The expected value of the additional information (EVI) allowing segregation into k groups will be the increase in value (either expected returns or expected utility) resulting from using the information, net of acquisition costs, over the value derived from decisions not using the additional information, or

$$\begin{aligned} EU(X - c(a_i) + EVI) &= \int_{-\infty}^{\infty} U(X(\omega, a_i) - c(a_i) + EVI) f_{X|a_i}(x) dx \\ &\approx \sum_k \rho^k \int_{-\infty}^{\infty} U\left(X(\omega, a_i^k) - \delta - \sum_k c(a_i^k)\right) \\ &\quad \times (f_{X|a_i^k}(x)) dx \approx EU\left(X - \delta - \sum_k c(a_i^k)\right). \end{aligned} \quad (8)$$

Defining the certainty equivalent as the monetary outcome yielding the same level of utility as expected utility evaluated over a distribution of outcomes, or $EU(X) = U(CE_X)$, both evaluated over

distribution X . EVI will equal the certainty equivalent difference between the uninformed problem and the solution when additional information is available and used, or

$$EVI = CE^{\Omega_1} - CE^{\Omega_0}, \quad (9)$$

where information sets are distinguished by subscripts 0 or 1.

4. Data, estimation, and model solution

Two years (2003 and 2004) of data on placement and final carcass characteristics were combined from 770 steers and heifers in South Dakota. The first year's data covering 180 steers was combined with observations from an additional 192 steers and 398 heifers placed in year two. The animals were fed in a commercial feedlot; consequently, experimental design was limited and the only control variable was number of days on feed. Days on feed ranged from 160 to 208 days. Steers comprised 48 percent of the sample. In addition to initial placement weight, animals were evaluated for body characteristics that presumably affect feedlot performance and carcass characteristics. Specifically, data were collected on initial ribeye area (REA) and backfat (BF). Recent experiments conducted by animal scientists suggest the amino acid sequence on the leptin gene affects production of the leptin hormone. Leptin in turn affects animal metabolism, feed uptake, fat deposition, and, consequently, the weight, yield, and quality characteristics of the animal at slaughter ([Houseknecht et al., 1998](#)). Research has associated single nucleotide polymorphisms associated with homozygous cytosine amino acid sequences (a CC combination on the receptor sites of the allele) with leaner body composition, and animals having a homozygous genotype of the thymine amino acid (or TT animals) tend to deposit greater layers of fat. Therefore, blood was drawn at placement to obtain information on the amino acid sequence of each animal. Genetic tests revealed that 15(27)% of the steers (heifers) were homozygous CC ("lean" coding), 54(50)% were heterozygous CT, and 32(23)% of the steers (heifers) were TT ("fat" coding). Summary statistics for the 770 animals are in [Table 1](#).

When carcass pricing is based on a quality grid, slaughter animal value is determined by three quality measures: hot carcass weight (HCW), yield grade, and quality grade. Yield grade is determined by ending values of backfat and ribeye area, in addition to kidney, pelvic, and heart fat deposition and hot carcass weight. Quality grade is determined primarily by intramuscular fat, or the marbling score (MS).

Similar to [DeVuyst et al. \(2007\)](#) and [Lusk \(2007\)](#), a system of equations relating animal characteristics at placement to ending values of hot carcass weight ($\ln HCW$), backfat ($\ln BF_T$), ribeye area ($\ln REA_T$), and marbling score ($\ln MS_T$) was estimated:

$$\begin{aligned} \ln HCW_i &= \gamma_1 + \gamma_2 CT_i + \gamma_3 TT_i + \gamma_4 SEX_i + \gamma_5 \ln DOF_i \\ &\quad + \gamma_6 (\ln DOF_i)^2 + \gamma_7 \ln W_{0i} + \varepsilon_{1i} \end{aligned} \quad (10)$$

$$\begin{aligned} \ln BF_{Ti} &= (\alpha_1 + \alpha_2 CT_i + \alpha_3 TT_i + \alpha_4 SEX_i) \times \ln \widehat{HCW}_i \\ &\quad + \alpha_5 \ln BF_{0i} + \varepsilon_{2i} \end{aligned} \quad (11)$$

$$\begin{aligned} \ln REA_{Ti} &= (\beta_1 + \beta_2 CT_i + \beta_3 TT_i + \beta_4 SEX_i) \times \ln \widehat{HCW}_i \\ &\quad + \alpha_5 \ln REA_{0i} + \varepsilon_{3i} \end{aligned} \quad (12)$$

$$\begin{aligned} \ln MS_{Ti} &= \delta_1 + \delta_2 CT_i + \delta_3 TT_i + \delta_4 SEX_i + \delta_5 \ln BF_{0i} \\ &\quad + \delta_6 \ln REA_{0i} + \delta_7 \ln \widehat{HCW}_i + \varepsilon_{4i} \end{aligned} \quad (13)$$

Exogenous dummy variables are genotype (CT and TT equal one for the heterozygous CT or homozygous TT genotypes) and gender (equals one for heifers). DOF is a continuous variable for days on feed. Parameter estimates are reported in [Table 2](#). Errors across animals were assumed to be independent ($E(\varepsilon_{ji}\varepsilon_{jk}) = 0, i \neq k$), but

Table 1

Sample summary statistics (standard deviations reported in parentheses where applicable).

	Steers			Heifers		
	CC	CT	TT	CC	CT	TT
Animals	55	199	118	109	198	91
Beginning weight	602.15 (70.82)	603.67 (66.21)	603.11 (68.25)	590.85 (77.17)	589.13 (88.65)	615.10 (102.28)
Hot carcass weight	790.93 (59.66)	783.31 (57.00)	781.82 (58.33)	716.94 (56.32)	720.04 (66.80)	730.66 (61.55)
Yield grade 1 (%)	9	5	4	20	18	7
Yield grade 2 (%)	38	31	23	48	46	35
Yield grade 3 (%)	45	51	53	28	30	48
Yield grade 4 (%)	7	13	19	4	6	10
Yield grade 5 (%)	0	1	1	0	0	0
Standard (%)	4	1	1	2	1	0
Select (%)	20	22	25	28	24	13
Choice (%)	56	55	44	48	47	52
High choice ^a (%)	16	21	26	21	25	32
Prime (%)	4	2	3	2	2	3
Net revenue (based on 2007 prices and costs)	203.45 (72.48)	176.10 (81.99)	169.03 (84.34)	138.54 (96.96)	148.47 (87.83)	142.58 (81.34)

^a “High choice” refers to carcasses having marbling scores between 500 and 699.

Table 2

Full Information Maximum Likelihood (FIML) parameter estimates.

Equation	Variable	Coefficient (standard error)
$LnHCW$ $R^2 = 0.4770$	Intercept	−29.30363** (8.04022)
	CT	0.00132 (0.00569)
	TT	0.00279 (0.00644)
	SEX	−0.06825** (0.00479)
	$LnDOF$	12.33913** (3.08587)
	$LnDOF^2$	0.46653* (0.01723)
	LnW_o	−1.15355** (0.29574)
$LnBF_T$ $R^2 = 0.2565$	Intercept	−0.00972 (0.00763)
	CT	0.00809* (0.00403)
	TT	0.01834** (0.00456)
	SEX	−0.01148** (0.00334)
	$LnBF_o$	0.28113** (0.01684)
$LnREA_T$ $R^2 = 0.2565$	Intercept	0.33258** (0.00647)
	CT	−0.00178 (0.00145)
	TT	−0.00707** (0.00164)
	SEX	0.01317** (0.00113)
	$LnMS_T$	5.55769** (0.52249)
$LnMS_T$ $R^2 = 0.0820$	Intercept	0.01145 (0.01711)
	CT	0.04293* (0.01940)
	TT	−0.00845 (0.01600)
	SEX	0.05715** (0.01200)
	$LnBF_o$	−0.13805** (0.03828)
	$LnREA_o$	0.14194 (0.08164)
	$LnHCW$	

Asterisks indicate significance at the 5% (*) and the 1% (**) levels.

cross-equation errors were assumed to be correlated. Consequently, full information maximum likelihood procedures were used in GAUSSX v 7.0.

Point estimates of the traits determining carcass value (HCW, BF, REA, and MS) for 600 pound feeder steers were obtained from the system of equations conditional upon the genetic marker being CC, CT, or TT. Randomness was simulated by generating a vector of 100,000 multivariate normal random numbers and premultiplying by the lower-triangular Cholesky decomposition of the error covariance matrix of the estimated system to retain correlations among the carcass traits (Clements et al., 1971). Since experimental treatments were limited, the only control variable in the experiment was the number of days on feed. Optimal days on feed for the pooled sample and for the sorted groups were determined using a grid search. For the pooled sample, 21.3% of the draws were

generated assuming the animal was CC, 51.6% under an assumption of the CT genotype, and 27.1% of the draws assumed the TT genotype, the same distribution as the sample of combined animals included in the experiment. For the sorted groups, 100,000 replicates of each genotype, CC, CT, and TT, were drawn.

Net returns were calculated using average 2007 prices for feeder steers, a combined feed and yardage cost of \$1.46 per day, and an interest rate of 6% on capital and operating costs. Revenues were based on average 2007 fed animal prices, adjusted by quality and grade discounts and premiums. Quality and grade adjustments were the same as used in DeVuyst et al.

Costs do not include genetic testing costs. Similar to the DeVuyst et al. and the Lusk 2007 papers, the values ascribed to sorting by genotype fall short of the per animal testing costs for the leptin-encoding gene. At the time when these data were collected, commercial testing costs were \$35–\$50 per animal. Costs have since fallen, and the genotype information provided has also increased as testing technology improves. Our approach of estimating the value of the genetic information provides an upper limit on testing costs. Should the expected value be greater than the testing costs, per animal testing may be justified. Alternatively, if per animal testing costs exceed the value of the information, per animal tests should not be conducted, or alternative sampling techniques to derive likely animal genotype may be desirable. Strategies may include marketing of breeding animals based on genotype or possibly incorporating genetic uniformity through cloning of breeding stock.

The optimization model is presented in Appendix. The optimization problem was solved in GAUSS using grid search procedures over the only control variable, days on feed. Multiple control variables would render the grid search approach unwieldy, and may thus require simplification of the conditioning equations (e.g., specification of linear relationships between product trait and conditioning variables) and using continuous functions relating price adjustments to multiple quality traits, thus allowing direct solution via nonlinear programming algorithms.

Random vectors of hot carcass weight, backfat, ribeye area, and marbling score are simulated based on the coefficients of the system in (10)–(13), conditional upon both variables and draws from the multivariate distribution of errors. Yield and quality grade are calculated for each random draw, and resulting price premiums or discounts are added to the price per pound on a hot carcass weight basis. Feeder and yardage costs, including a capital cost adjustment, are subtracted from the gross carcass value. Utility under each draw was determined using a negative exponential, constant absolute risk aversion utility function, $U_s = 1 - \exp(-\delta W_s)$, where W_s is net revenue under state of nature s and δ is the risk aversion parameter, initially set equal to 0.005. The objective function of the problem equaled the expected utility evaluated over 100,000 outcomes of U_s .

5. Results

5.1. System estimation

Parameter estimates from the estimated system are presented in Table 2. Seventeen of the 24 coefficients were different than zero with significance levels less than five percent. Of special interest was the significance of the genotype dummy variables in the four equations. Dummy variables for CT and for TT were both significant and positive in the equation for backfat. Presence of the TT genotype significantly and negatively affected ribeye area compared to the CC genotype. The CT gene had a negative, though insignificantly different than zero, effect on ribeye area. The TT genotype yielded a significantly positive influence on the

marbling score equation, consistent with the TT gene being characterized as the “fat” gene. Neither the CT nor the TT gene exerted significantly different impacts on hot carcass weight. Although not statistically significant at normally acceptable levels of significance, the influence of the CT and TT genotype on hot carcass weight was positive, which will affect carcass characteristics in the model simulations.

5.2. Sorting and choice of control based on input characteristics

The feeder seeks the expected utility maximizing number of days on feed for each animal. Results of varying days on feed on expected net returns and on expected utility are presented in Table 3 for steers. Optimal days on feed did not vary greatly. For the pooled, uninformed sample, 186 days on feed was optimal using both the expected revenue and the expected utility criterion. Based on both the expected net returns and the expected utility criteria, optimal days on feed were reduced by one, to 185, for the sorted CC, CT, and the TT groupings.

These results are clear. Sorting by genotype in order to apply controls specific to a sorted subgroup is not warranted based on the results for this group of animals and when the only control is days on feed. These results should not of course be generalized to other settings. Further research may sort animals by genotype at placement, alter rations, and estimate feed conversion efficiencies as functions of genotype. In addition, alternative marketing strategies based on animal genotype may improve profitability

(e.g., selling TT animals on a weight basis rather than a quality and yield grid).

5.3. Sorting and heterogeneous product markets

The primary hypothesis underlying this research is that genetic information yields information about product quality. Consistent with DeVuyst et al. (2007) and with Lusk (2007), our results confirm the role of the leptin gene in affecting carcass quality. The statistical significance of the coefficients on the genotype dummy variables confirms the effects of genotype on backfat, ribeye area, and, in the case of the TT polymorphism, on marbling score. An illustration of the outcome measures, conditional on genetic trait, are shown in Figs. 1–3 for animals held on feed for 185 days. Frequency diagrams for hot carcass weight, yield, and quality grade for the three separate genotypes indicate differences in value exist depending upon genotype and marketing strategy (i.e., choice of a grade and quality grid for pricing carcasses rather than a mere weight basis). Price premiums are paid for yield grades of 1 or 2 and for carcasses grading high choice or prime. Discounts are levied for yield grades of 4 or 5 or for quality falling below choice. Yield grade distribution, Fig. 1 shows the CC and CT animals yielded grades 1 or 2 at a higher proportion than did the homozygous TT animals. This is consistent with the TT animals being the “fat” animals, resulting in less higher value meat per pound of carcass. Conversely, the “fat” TT animals tended to grade higher on the quality grid

Table 3

Expected net returns and certainty equivalents of days on feed (boxes indicate optimal days on feed for the animal groupings and outcome measures).

DoF	Expected Returns				Certainty Equivalent			
	Pooled	CC	CT	TT	Pooled	CC	CT	TT
160	\$149.73	\$153.94	\$151.26	\$144.07	\$135.75	\$140.22	\$137.23	\$129.81
165	\$159.99	\$164.44	\$160.95	\$153.81	\$145.34	\$150.14	\$146.52	\$138.91
170	\$168.03	\$172.28	\$169.59	\$161.88	\$152.83	\$157.69	\$154.71	\$146.46
175	\$173.11	\$178.62	\$175.28	\$166.72	\$157.68	\$163.47	\$159.78	\$150.82
180	\$176.55	\$181.98	\$178.85	\$169.49	\$160.72	\$166.52	\$163.19	\$153.14
181	\$176.66	\$182.11	\$179.09	\$170.17	\$160.82	\$166.55	\$163.18	\$153.81
182	\$177.42	\$182.73	\$179.43	\$170.13	\$161.38	\$167.11	\$163.61	\$153.65
183	\$177.96	\$183.28	\$179.13	\$170.04	\$161.90	\$167.79	\$163.23	\$153.71
184	\$177.64	\$183.38	\$179.55	\$170.24	\$161.55	\$167.74	\$163.68	\$153.69
185	\$177.82	\$183.65	\$179.69	\$170.48	\$161.74	\$167.97	\$163.68	\$153.93
186	\$178.15	\$183.40	\$179.49	\$170.13	\$161.78	\$167.57	\$163.35	\$153.44
187	\$177.91	\$183.63	\$179.30	\$170.04	\$161.51	\$167.82	\$163.19	\$153.36
188	\$177.74	\$183.58	\$179.36	\$169.36	\$161.48	\$167.70	\$163.07	\$152.44
189	\$177.33	\$183.07	\$179.27	\$170.01	\$160.81	\$167.21	\$163.12	\$153.19
190	\$177.05	\$182.90	\$178.85	\$168.95	\$160.54	\$166.90	\$162.53	\$152.15
195	\$174.77	\$180.35	\$175.59	\$166.79	\$158.14	\$164.19	\$159.12	\$149.74

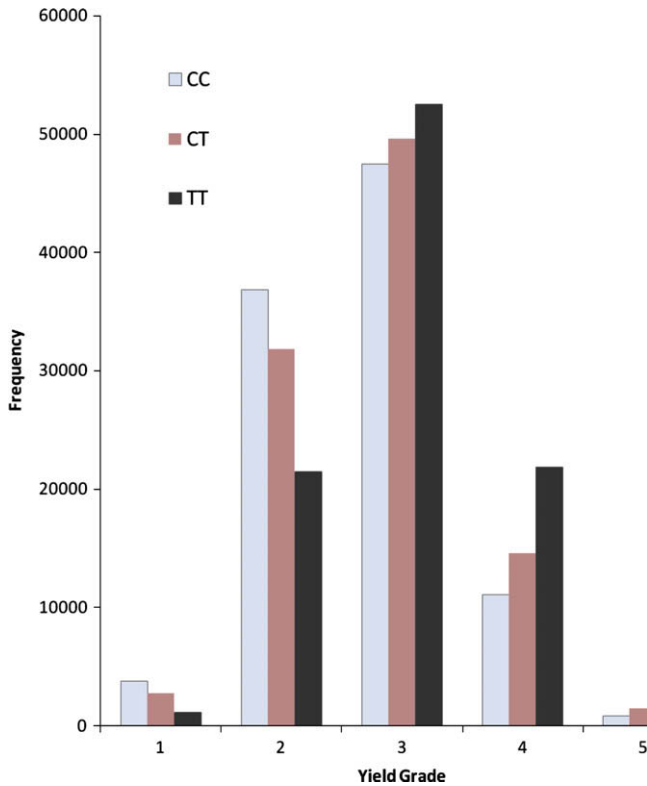


Fig. 1. Frequency distribution of animals by yield grade.

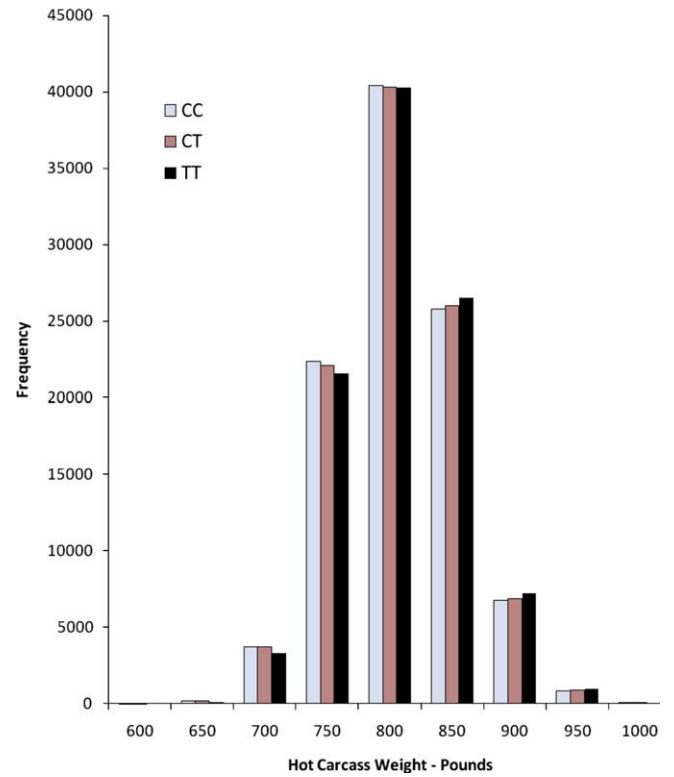


Fig. 3. Frequency distribution of animals by hot carcass weight.

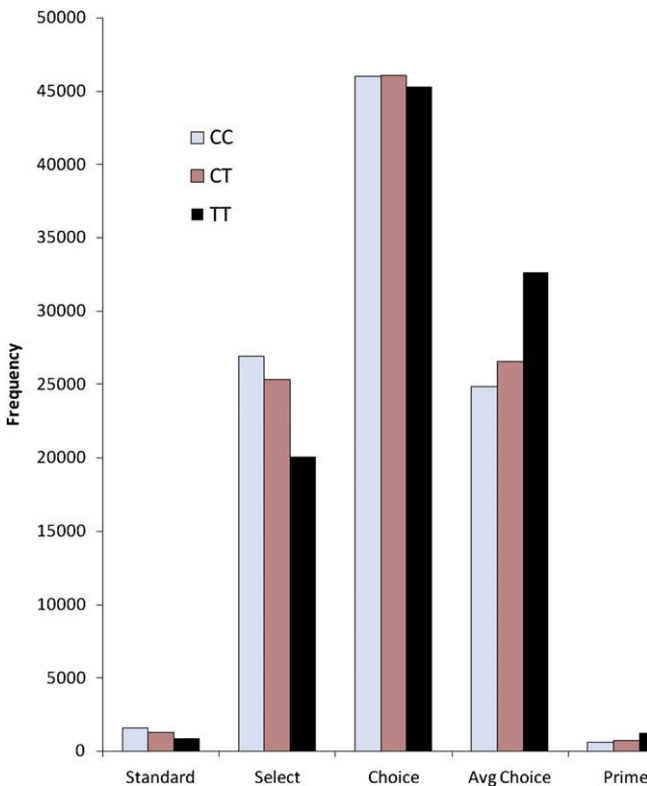


Fig. 2. Frequency distribution of animals by quality grade.

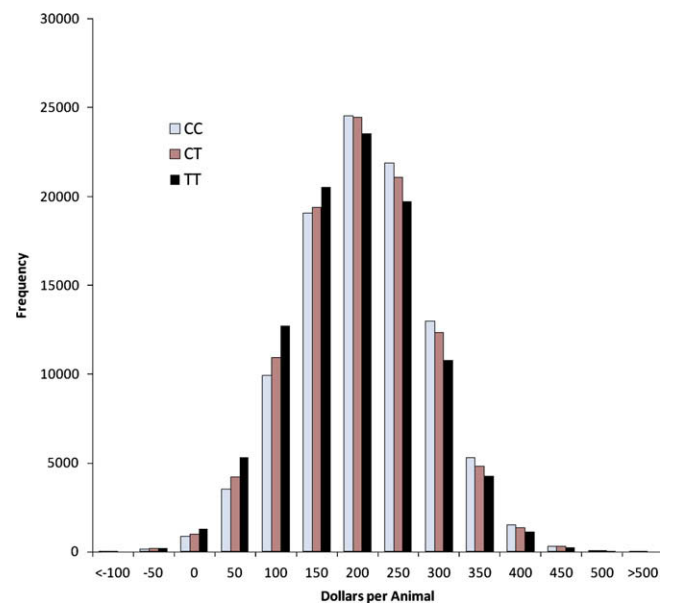


Fig. 4. Frequency distribution of animals by net revenues.

(Fig. 2). Quality is based on marbling score. The greater the marbling score, the higher the grade. Thus, the “fat” TT animals produce more high choice and prime carcasses. The leptin gene also

appears to influence hot carcass weights, shown in Fig. 3. The “lean” CC animals have lower hot carcass weights, and are thus priced lower based just on a price per pound basis. However, the CC animals gain from the yield grade premium available on the pricing grid. The higher premium for CC animals on the yield grade basis is offset by the lower returns relative to the CT and TT animals based on quality scores.

The net effect of the trade-offs among hot carcass weight, yield grade, and quality grade are combined in the simulated distribu-

tions of net returns per animal (Fig. 4). Differences in the conditional distributions of weight and grade appear to affect revenue. Although yield and quality grades offset one another in comparisons of the homozygous CC and TT animals, net revenues tend to be skewed slightly to the right for the CC and the CT animals compared to the TT animals. Of more pertinent interest is whether these differences are economically important based on a behavioral assumption of either expected profit or expected utility maximization.

Similar to the findings of DeVuyst et al. (2007) and Lusk (2007), carcass values depended upon the amino acid sequence of the leptin-encoding gene. Average per head expected net returns to the pooled group of CC, CT, and TT animals are \$178.15. If sorted by genotype, expected net returns to a CC animal are \$5.50 higher and are \$1.54 higher for a CT animal than they are to the average from the pooled group. Expected returns to a TT animal are \$7.67 less than the average from the pooled group. Under risk neutrality, expected net returns to the CC animals were \$3.97 higher than maximum returns to CT animals and \$13.17 higher than returns to TT animals. CT animals earned an expected net return \$9.21 higher than the TT animals.

Under the base level of risk aversion, the certainty equivalent of the CC and the CT animals are \$6.07 and \$1.78 higher, respectively, than the pooled group. The certainty equivalent for the TT animals is \$7.97 below the pooled certainty equivalent. The certainty equivalent of the CC animals relative to the CT animals is \$4.29 greater and is \$14.04 higher than the certainty equivalent of the TT animals. Instead of the \$9.21 expected return difference between CT and TT animals, the certainty equivalent difference is \$9.75.

These results suggest two conclusions. First, the economic value of animals does vary by carcass characteristics such as ribeye area and backfat, and these characteristics are affected by polymorphisms of the leptin-encoding gene. Second, leptin gene information does not greatly affect the relative values of the carcass characteristics under risk aversion. The distributional assumptions underlying the model result in locational shifts of the animal revenue distributions (i.e., mean values shift for the three genotypes), but the shapes of the distributions do not change when returns are calculated for the CC, CT, or TT animals. However, our procedures might be expanded to derive density functions that are conditional upon genotype, thus allowing the effects of distributional moments higher than just the mean to affect sorting and management decisions under risk.

5.4. Influence of risk attitudes on value of information

Although the quantitative differences between genotype changed between the risk neutral and the risk averse solutions given a risk aversion coefficient of 0.005, the qualitative results changed little. Slight differences were observed in the optimal days on feed, and the differences in value between genotype increased slightly when risk was considered.

The decision model easily accommodates differing assumptions about risk behavior. Methods proposed in McCarl and Bessler (1989) suggest an upper bound on the absolute risk aversion coefficient of 0.058. The absolute risk aversion should be less than $2E(\text{Revenue})/\sigma_{\text{Revenue}}^2$, or approximately 0.058 for the average expected revenue and variance of revenue in the current simulations. Our base absolute risk aversion coefficient of 0.005 corresponds to a moderate level of relative risk aversion (approximately 0.9 when wealth is defined as expected per animal revenue) based on the guidelines in Anderson and Dillon (1992). Anderson and Dillon characterize actors as hardly risk averse at all when relative risk aversion equals 0.5 through very risk averse when relative risk aversion is 4.0.

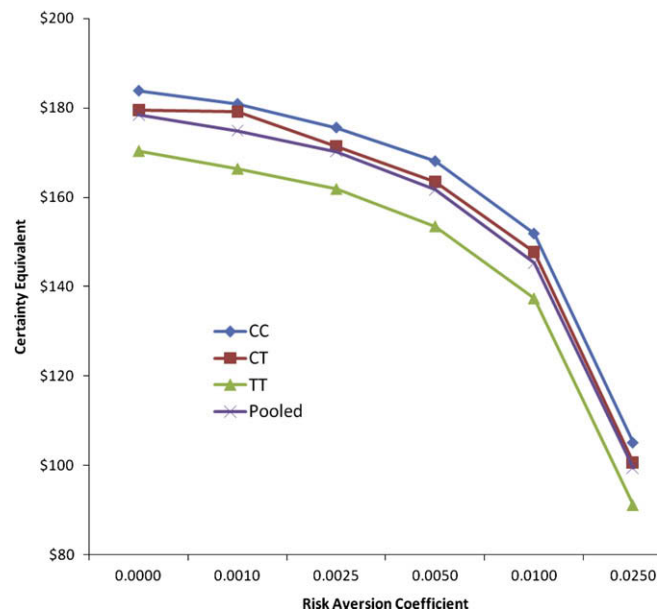


Fig. 5. Certainty equivalents by genotype and risk aversion coefficient.

The risk aversion coefficient of the negative exponential utility function can be changed, or alternative formulations of the utility function can be used. As an illustration, certainty equivalents were generated under alternative values of the risk aversion coefficient. Results are presented in Fig. 5. Under increasing risk aversion, it is expected that risk premiums increase and certainty equivalents fall. However, differences in certainty equivalents among the different genotypes did not change significantly. For example, the difference in certainty equivalents between CC and TT animals was \$13.74 for a risk aversion coefficient of 0.001 (little risk aversion) and was \$13.65 for a coefficient of 0.025 (large aversion to risk). However, the management control, days on feed, decreased as risk aversion increased. Under the most risk averse scenario, in which the coefficient equaled 0.025, days on feed were 177, 178, and 177 for the CC, the CT, and the TT animals, respectively. Days on feed under the level of risk aversion corresponding to 0.025 were thus nine (and eight in the case of CT) days fewer than under expected revenue maximization and eight (and seven) days fewer than under the base scenario of a risk aversion parameter of 0.005 (Table 3). The dispersion of net returns increases as animals are held on feed for longer periods, so the more risk averse decision maker will market animals earlier to reduce net return dispersion and thus to maximize expected utility.

5.5. What is the value of genetic information?

The objective of this paper is to determine the value of genetic information. One measure of the value of information is the change in expected outcomes conditional upon any new information. In the current research, a sample of 770 feeder steers and heifers was fed between 160 and 208 days. A multivariate density function of hot carcass weight, backfat, ribeye area, and marbling score was derived conditional upon both a single management decision, days on feed, and genotype. Choice of the optimal number of days on feed changed little when knowledge of the amino acid sequence was included as a conditioning variable. Based on the experimental protocol, knowledge of the amino acid sequence on the leptin gene in beef cattle had little value when days on feed is the only management control. In this case, knowledge of the genetic trait *ex ante* did not lead to heterogeneous production decisions, one of the

potential benefits identified in Hennessey et al. arising from increasing knowledge of an animal's genotype.

However, differences appeared in both expected net returns and in certainty equivalents when animals could be sorted based on the amino acid sequence of the leptin gene. The distributions of net returns shifted slightly rightwards for animals having the CC sequence instead of the CT, with even greater shifts occurring in comparing the CC and the CT animals to the TT animals. Expected net returns associated with the CC trait over CT cattle were \$3.96 greater. Expected returns for the CC animals were \$13.17 greater than those for the TT animals. Under risk aversion, the certainty equivalent differences were slightly greater than the expected return differences, reflecting the role of different distribution of animal weight and quality traits influencing net returns among the three genotypes. However, consideration of risk did not affect the relative values of CC, CT, and TT animals. In addition, differences in the certainty equivalents among the genotypes remained fairly constant (Fig. 5) regardless of the level of risk aversion assumed.

The direct answer to the question of the value of possibly changing management controls conditional upon information about the amino acid sequence in the leptin-encoding gene (i.e., the expected value of the information defined in expression (9)) is, "not much." Only slight changes in the single control variable considered resulted when animals were sorted based on genotype. Under the risk aversion assumptions underlying Table 3, the value of the genetic information is \$0.12, resulting from feeding the sorted CC, CT and TT animals one day shorter than the pooled sample.

However, the expected value of the genetic information is greater if animal selection is based on genotype. Expected net returns and expected utilities are both greater for the CC and the CT animals than for the "fat" TT animals. These gains indicate the potential for markets to value genotype in a manner currently used in breeding markets employing the use of Expected Progeny Differences (Chvosta et al., 2001; Vanek et al., 2008). Values from sorting and product differentiation are consistent with Hennessey et al.'s conclusions regarding the potential gains from using genetic information. However, a fuller understanding of the market effects must assess the longer run impacts of any significant shifts in product quality. The results of our analysis rely upon price adjustments resulting from use of the quality and yield grade grids. Significant changes in the current distributions of yield and quality grades resulting from selection of animals based on genotype will probably affect price premiums and discounts. In a manner developed in Babcock (1990), ongoing research is currently investigating these market effects should greater product differentiation develop based on sorting by genotype.

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Appendix

Direct Solution of Expected Utility Maximization Model.

Objective function: maximize the expected utility of per animal net returns:

$$\text{Maximize } EU = \sum_k \rho^k \sum_s U(W_{ks})$$

where k = animal of characteristics k , and s is a random draw from the multivariate distribution of errors for the four equation system of estimated ending carcass characteristics, and ρ^k is the probability of observing an animal having characteristics k .

Generation of discrete carcass characteristics:

$$HCW_{ks} = \exp(\gamma_1 + \gamma_2 CT_k + \gamma_3 TT_k + \gamma_4 SEX_k + \gamma_5 LnDOF_k + \gamma_6 (LnDOF_k)^2 + \gamma_7 LnW_{0k} + \varepsilon_{HCW,ks})$$

$$BF_{Tks} = \exp((\alpha_1 + \alpha_2 CT_k + \alpha_3 TT_k + \alpha_4 SEX_k) \times Ln\widehat{HCW}_{ks} + \alpha_5 LnBF_{0k} + \varepsilon_{BF,ks})$$

$$REA_{Tks} = \exp((\beta_1 + \beta_2 CT_k + \beta_3 TT_k + \beta_4 SEX_k) \times Ln\widehat{HCW}_{ks} + \alpha_5 LnREA_{0i} + \varepsilon_{REA,ks})$$

$$MS_{Tks} = \exp(\delta_1 + \delta_2 CT_k + \delta_3 TT_k + \delta_4 SEX_k + \delta_5 LnBF_{0i} + \delta_6 LnREA_{0i} + \delta_7 Ln\widehat{HCW}_{ks} + \varepsilon_{IMF,ks})$$

Determine yield grade as a function of generated carcass characteristics:

$$YG_{ks} = 2.5 + 2.5BF_{Tks} + 0.2KPH + 0.0038HCW_{ks} - 0.32REA_{Tks}$$

Determine yield and quality grade price adjustments: YG_j and MS_j are discrete break points differentiating yield grade and marbling score in the grid pricing matrix

Loop(j , where j are the discrete yield and quality grade categories

If $YG_{ks} \geq YG_j$ and $YG_{ks} \leq \overline{YG}_j$, then $YGP_{ks} = PYG_j$

Else $YGP_{ks} = 0$

If $MS_{Tks} \geq MS_j$ and $MS_{Tks} \leq \overline{MS}_j$, then $MSP_{ks} = PMS_j$

Else $MSP_{ks} = 0$

Calculate animal returns net of purchase and feeding-associated costs:

$$W_{ks} = (P_{HCW} + YGP_{ks} + MSP_{ks}) \times HCW_{ks} - (1 + r_k) \times P_0 W_0 - (1 + 0.5r_k) \times C_{DOF} \times DOF_k$$

Discount rate for animal and feed purchase and yardage costs assessed by daily capital opportunity cost rate times days on feed:

$$\text{Discount} \times DOF_k - r_k \geq 0$$

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