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January 2006

THE EXPECTED VALUE OF GENETIC INFORMATION IN LIVESTOCK FEEDING

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Acknowledgements

Funding for this research was provided by North Dakota Agricultural Experiment Station Project ND 01312. The authors acknowledge the assistance of Dr. Marc Bauer and Mr. Jared Bullinger, North Dakota State University, in acquiring and providing the data for this research. Editorial comments of Drs. Dragan Miljkovic and William Wilson are also gratefully acknowledged. Editorial assistance of Ms. Carol Jensen preparatory to final publication is appreciated.

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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 potentially increase producer and consumer benefits. This research develops a decision analysis framework to assess the expected value of genetic information. Expected returns are evaluated both in the presence of, 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.

Key Words: Value of information, genetics, livestock

THE EXPECTED VALUE OF GENETIC INFORMATION

IN LIVESTOCK FEEDING

David K. Lambert, Eric A. DeVuyst, and Charles B. Moss*

The outcomes of biological processes are seldom certain. Yields vary from field to field. Animal performance differs even among cattle raised in the same pasture. 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 farmer effort. However, even controlling for environmental variables, 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. Recent advances have led to genetic mappings for the human genome (Collins, Morgan, and Patrinos), rice (Goodman et al.), corn (Pennisi), and chicken (Hillier et al.). 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.

Important as the advances in genetics have been, little economic analysis addresses the economic contribution of genetic information. Essential to determining the value of genetic information in agricultural production is identifying the influence of genotype on production. Research has addressed the economics of genetic modification (Moschini, Lapan, and Sobolevsky), generally concluding net social welfare gains from genetic modifications in soybeans, corn, canola, and other crops. However, these studies approach the problem as discrete decisions of process adoption rather than using genetic characteristics of the plant or animal to guide production decisions.

The purpose of this paper is to evaluate decision rules affecting the acquisition of information about biological processes. Information acquisition carries a cost, but new information may generate net benefits. Two specific scenarios are analyzed: (1) genetic information can be acquired and, conditional upon the information attained, optimal management regimes are selected; and (2) the biological input is heterogeneous, such that acquired information can lead to sorting and selection of optimal management regimes conditional upon sorting. A decision analysis approach tests the value of knowledge of the amino acid sequence on the leptin-encoding gene in beef cattle feedlot performance. The modeling framework effectively measures the contribution of new information to the distributions of net returns and can therefore be applied to determine the economic value of an expanding set of information

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regarding the impacts of specific genetic information on agricultural production. The results indicate future research directions to characterize new markets arising in response to greater knowledge of the genetic bases underlying biological processes.

The Value of Information

The valuation of genetic information pursued in this research follows Stigler, who applied general neoclassical methods to derive an economics of information. Acquiring information incurs costs, yet yields information that can improve decision making. Optimizing individuals and firms acquire a set of information that equates marginal acquisition costs and marginal benefits. The framework relies upon statistical decision theory (Berger), in which prior beliefs are updated with additional information and alternative actions are reassessed. Optimal decisions are determined under the new information, and resulting improvements in the objective function define an upper limit on the value of the newly acquired information.

Analysts have applied decision theory to determine the value of information in several agricultural settings. Baquet, Halter, and Conklin determined the value of weather forecasts in farmer planting decisions. Babcock expanded the analysis to consider sectoral effects when weather information is public, resulting in supply shifts when many farmers base decisions on the forecast information. In addition to analysis of information regarding exogenous factors, such as weather, the value of additional information about the productive input itself has also been addressed. George Ladd and his graduate students developed many of the early applications. Ladd and Martin applied the input characteristics model to determine marginal implicit prices of a vector of quality traits for corn varieties. In an allusion to future developments, they proposed the use of the method to guide future product line research. To determine the value of improved animal characteristics, Ladd and Gibson used parametric programming to find the marginal value of genetic improvement in hogs based on three heritable traits (backfat, feed efficiency, and average daily gain).

The product quality model has been applied to determine optimal production regimes. Buccola and Iizuka developed a sophisticated model of dairy production in anticipation of greater market reliance upon milk component pricing. By assuming output separability, Buccola and Iizuka were able to determine a multi-output/multi-input transformation function mapping inputs to a vector of output characteristics. The authors estimated a cost function relating the vector of output characteristics to both feed costs and a set of nonfeed factors important in milk production. Differentiation of the cost function and an assumption of profit maximization permitted marginal cost functions to represent supply responses of the different product traits as functions of both feed costs and specific animal traits.

Hennessy, Miranowski, and Babcock have recently made two major contributions in determining the value of information in agricultural production. The authors clearly demonstrated the benefits of improved information about the genetic attributes of biological inputs arising from sorting and improved returns to product differentiation. The 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 these considerations are addressed in this research. Using performance data collected for 180 steers placed on feed, the influence of additional information about the genetic characteristics of the individual animals in determining management prescriptions is determined. If positive values are found to accrue to the information embedded in the genetic sequence investigated in this research, collection of the genetic information may increase returns to feeding. If net returns are found to vary for animals having different genetic characteristics, Hennessy, Miranowski, and Babcock's arguments for sorting and product differentiation may lead to new markets for animals based on linkages between genetic traits and subsequent feedlot performance and product quality. Research has found livestock markets are responsive to phenotypic and lineage information (Chvosta, Rucker, and Watts; Dhuyvetter et al.). If the current research documents performance heterogeneity due to specific genetic traits, genetic testing might augment both breeding stock and feeder cattle market transactions.

A Model of the Value of Genetic Information

We start with a profit function, where profit is a scalar-valued function of three inputs:

(1)
$$\pi = pf(x_1, z_1, z_2) - w_1 x_1$$

The price of the output is p, x_1 is a deterministic input whose level is chosen by the producer, z_1 and z_2 are random variables whose levels cannot be directly controlled, and w_1 is the price of the deterministic input. Random variable z_1 may affect production either directly or through indirect effects on the productivity of x_1 . Alternatively, z_1 may be a vector of characteristics of the final output deemed important by end-users. Random variable z_2 may affect productivity, but more importantly provides information about z_1 .

Information about z_2 can be acquired at cost C_{y_2} . The decision maker is assumed to maximize expected profits. He chooses the optimal level of x_1 and must decide whether to acquire information about z_2 :

$$E\pi(p, w_{1}, \Omega) = \max_{y \in \{0, 1\}} y \left\{ \int_{\underline{z}_{2}}^{\overline{z}_{2}} \left(\max_{x_{1}} \int_{\underline{z}_{4}}^{\overline{z}_{1}} \left[pf(x_{1}, z_{1}, z_{2}) - w_{1}x_{1} \right] g(z_{1} | z_{2}, \Omega) dz_{1} \right) g(z_{2}, \Omega) dz_{2} - C_{y} \right\} + (1 - y) \left\{ \max_{x_{1}} \int_{\underline{z}_{2}}^{\overline{z}_{1}} \left[pf(x_{1}, z_{1}, z_{2}) - w_{1}x_{1} \right] g(z_{1}, z_{2}, \Omega) dz_{1} dz_{2} \right\}$$

where $E\pi(p, w_1, \Omega)$ is the expected value of the production decision based on the information set Ω and *y* is the choice of acquiring information about random variable z_2 .

Problem (2) is a standard decision problem. If the decision maker does not acquire information about the distribution of z_2 (i.e., y = 0), he selects x_1 to maximize expected profits evaluated over the joint density function $g(z_1, z_2, \Omega)$. Alternatively, information about z_2 may be acquired (y = 1) at cost C_y , and x_1 is then chosen subject to the conditional distribution of z_1 , or $g(z_1 | z_2, \Omega)$. If expected profits are higher when z_2 is known, or at least better information about the distribution of z_2 is known, the optimal decision is to acquire the information at cost C_y .

We make two simplifying assumptions: (1) we assume that z_2 is a Bernoulli event (z_2 either equals 0 or 1); and (2) the value of z_2 does not directly affect the production function, but rather indirectly affects productivity through z_1 . These assumptions result in the following maximization problem:

$$E\pi = \max_{y \in \{0,1\}} y \Big(g \Big(z_2 = 0 | \Omega \Big) \max_{x_1} \int_{z_1}^{z_1} \Big[p f \Big(x_1, z_1 \Big) - w_1 x_1 \Big] g \Big(z_1 | z_2 = 0, \Omega \Big) dz_1 + g \Big(z_2 = 1 | \Omega \Big) \max_{x_1} \int_{z_1}^{\overline{z_1}} \Big[p f \Big(x_1, z_1 \Big) - w_1 x_1 \Big] g \Big(z_1 | z_2 = 1, \Omega \Big) dz_1 - C_y \Big) + (1 - y) \Big(\max_{x_1} g \Big(z_2 = 0 | \Omega \Big) \int_{z_1}^{\overline{z_1}} \Big[p f \Big(x_1, z_1 \Big) - w_1 x_1 \Big] g \Big(z_1 | z_2 = 0, \Omega \Big) dz_1 + g \Big(z_2 = 1 | \Omega \Big) \int_{z_1}^{\overline{z_1}} \Big[p f \Big(x_1, z_1 \Big) - w_1 x_1 \Big] g \Big(z_1 | z_2 = 1, \Omega \Big) dz_1 \Big)$$

Assuming z_2 follows a Bernoulli distribution may correspond to the presence of a specific genetic trait. If the genetic trait affects the distribution of z_1 , formulation (3) can be used to determine if information about the genetic trait should be purchased at cost C_y . Alternatively, if the information is not acquired, so that (1-y) equals 1, the decision maker selects the optimal level of x_1 without certain knowledge of the genetic trait. Although the realized outcome of z_2 is unknown, the decision maker is presumed to have priors for the probabilities of z_2 , as well as information on the conditional distribution of z_1 for both $z_2 = 0$ and $z_2 = 1$.

If y = 1, the decision maker has acquired information about z_2 . The optimal choice of x_1 is thus made with the knowledge that $z_2 = 0$ or that $z_2 = 1$. If expected profits with the information (i.e., y = 1) are greater than expected profits without the information (y = 0), then the expected value of the information is positive, and the information should be acquired at any cost less than or equal to C_y .

Data

One hundred ninety crossbred steers were placed on feed on 25-November 2003 in a commercial feedlot. During the data collection period, the identification numbers for ten animals were lost due to lost ear tags or missed tag transfers in the slaughter facility. One hundred eighty usable observations were ultimately collected. At placement, weights, ultrasonic measurements of longissmus muscle area (also call ribeye area or REA) and 12-rib fat (called backfat), and

blood samples were taken. Additional liveweights were taken on 4-February and 3-May 2004. Additional backfat and REA measurements were taken on 3-May 2004. Cattle were marketing over four marketing dates: 20-May, 26-May, 3-June, and 10-June. Cattle were marketed by the cooperating producer based on weight and visual characteristics. Hot carcass weights (HCW) were recorded at slaughter, and REA, backfat, and quality grade were measured 24 hours post slaughter. Additionally, kidney, pelvic, and heart (KPH) fat was measured 24 hours post slaughter. Summary statistics are reported in Table 1.

	2			ations in parentneses)
Cohort Data	174 Days on Feed	180 Days on Feed	187 Days on Feed	•
	n = 43	n=38	n=39	n=60
Beginning	648.14	624.74	594.18	586.83
Weight	(51.74)	(52.22)	(48.30)	(48.56)
		010 00	50610	551.00
Hot Carcass	796.64	812.29	786.13	771.30
Weight	(47.22)	(48.05)	(53.49)	(53.48)
Backfat	0.55	0.51	0.54	0.43
Duckiu	(0.22)	(0.18)	(0.18)	(0.16)
Ribeye Area	12.57	12.74	12.17	13.04
	(1.15)	(1.34)	(1.48)	(1.37)
KPH Fat	2.56	2.24	2.12	2.00
(%)	(0.47)	(0.50)	(0.47)	(0.53)
Marbling	448.81	494.74	452.82	427.67
Score	(61.97)	(98.22)	(101.07)	(97.50)
_	*** *			*• • •
Revenue	\$987.54	\$1,030.73	\$955.53	\$977.03
	(87.92)	(624.74	(81.48)	(86.85)

Table 1. Summa	ry statistics for feeder	steers (means with	standard deviations is	n parentheses)

Blood samples were used to determine genotype for a polymorphism (i.e., mutation) in the leptin gene at the 305-SNP exon 2. This polymorphism has been shown to influence fat deposition in beef cattle (Fitzsimmons et al.; Buchanan et al.). Leptin genotypes associated with this polymorphism are called "CC" for the lean homozygote, "CT" for the heterozygote, and "TT" for the fat homozygote. Of the study cattle, 11.7% were CC, 55.6% were CT, and 32.8% were TT.

Fat has offsetting impacts on carcass value, depending on where it is deposited. As KPH and external carcass fat, including backfat, increase, yield grade increases. As lower yield grades earn price premiums and higher yield grades earn price discounts, higher KPH and external backfat levels equate to lower carcass value. Intramuscular fat deposition, or marbling, results in higher quality grades. As discounts are earned for low quality grades (less than "choice") and premiums are earned for high quality grades (upper two-thirds of "choice and higher"), more

intramuscular fat equates to higher carcass value. Hence, the need to evaluate the economic impact of this polymorphism.

The value of the animal at slaughter is determined by prices, which in turn are affected by three animal quality measures: hot carcass weight (HCW), yield grade, and quality grade. Yield grade is determined by ending values of BF and REA, in addition to kidney, pelvic, and heart fat deposition (KPH) and HCW. Quality grade is determined primarily by intramuscular fat (IMF), or the marbling score. Summary statistics are in Table 1.

Table 2 presents correlation coefficients between revenue and the conditional variables employed in the study. Revenues are positively correlated with animal weights 16 days prior to first slaughter (LW₁₆), and weights in February (LW_{FEB}) and November (LW_o). Initial muscling (REA) and back fat (BF) are positively correlated to one another, yet positively and negatively correlated, respectively, with revenues. In the simple correlations, the leptin gene amino acid sequence CC and CT are positively correlated with revenue, and TT cattle tend to have lower ending carcass values. Model development will incorporate these relationships in describing conditional probability density functions for revenue and assess alternative management regimes based upon resulting distributions of expected net revenue.

	Revenue	LW_{16}	$\mathrm{LW}_{\mathrm{Feb}}$	LWo	REA _o	BF_{o}	CC	СТ	TT
Revenue	1.000								
LW_{16}	0.649	1.000							
$\mathrm{LW}_{\mathrm{Feb}}$	0.551	0.859	1.000						
LW_{o}	0.464	0.709	0.794	1.000					
REA _o	0.153	0.126	0.200	0.433	1.000				
BF_{o}	-0.193	-0.006	0.187	0.329	0.269	1.000			
CC	0.067	0.023	0.009	0.018	0.021	-0.085	1.000		
СТ	0.087	0.040	0.068	-0.019	-0.050	-0.131	-0.406	1.000	
TT	-0.139	-0.058	-0.078	0.008	0.039	0.197	-0.254	-0.781	1.000

Table 2. Correlation coefficients among revenue and observable animal characteristics

Net returns were calculated using November 2003 Oklahoma City prices for feeder steers, a combined feed and yardage cost of \$1.65 per day, and an interest rate of 6% on capital and operating costs. Revenues were based on May 2004 fed animal prices, adjusted by quality and grade discounts and premia.

The Value of Genetic Information

All animals were placed in the same feeding pen. Management during the feeding period was identical for all animals, so that the only management variable was days on feed. The feeder is interested in determining the number of days on feed for each animal that maximizes expected profit. Many conditioning variables are potentially observable, including initial weight, weight

at various times over the feeding period, and indicators of body composition such as REA and BF. In addition, genetic tests can reveal the amino acid sequence on the leptin gene. The economic value of the latter test is the focus of the empirical application.

The distribution of gross revenue *r*, or carcass value, for each animal is conditional upon observable animal characteristics z_1 and the only management variable, days on feed (*DoF*). The conditional cumulative distribution of revenue is $G(r|z_1, DoF)$ and the conditional probability density function for revenue is $g(r|z_1, DoF)$.

The maximization problem for the producer who does not acquire information about the leptin gene is:

(4)
$$\max_{DoF} E(r - wDoF) = \sum_{i=CC,CT,TT} g(L = L_i) \int_r (r - wDoF) g(r | z_1, DoF, L = L_i) dr$$

The daily yardage cost, *w*, includes feed and animal opportunity costs (including original purchase cost and interest on purchase). Given the single control variable in the unconditional problem, the producer will select days on feed to maximize expected profits for a given animal. Revenues will be determined by the days on feed, the conditioning variables z_1 , and the added cost of retaining the animal from period to period. Although the realization of L_i is unknown for a particular animal, the feeder is assumed to be familiar with average performance of animals based on his prior beliefs about the distribution of genetic traits among animals. Expression (4) assumes that a particular animal's genetic characteristic (L_i for i = CC, CT or TT) is unknown.

The problem in (4) requires information about the conditional density of revenues. We adopt Taylor's (1984, 1990) approach to represent conditional probability densities by the multivariate hyperbolic tangent. The hyperbolic form of the cdf is

(5)
$$G(r|z_1, DoF, L_i) = 0.5 + 0.5 \tanh(P(r, z_1, DoF, L_i))$$

and the associated conditional probability density function is

(6)
$$g(r|z_1, DoF, L_i) = 0.5 P_r(r, z_1, DoF, L_i) \operatorname{sech}^2(P(r, z_1, DoF, L_i))$$

where $P(r,z_I,DoF,L_i)$ is a polynomial function and P_r is the partial derivative of $P(\cdot)$ with respect to revenue.¹

Expressing (6) in logarithms for each observation results in a suitable objective function for estimating coefficients of $P(\cdot)$ using maximum likelihood procedures. Two nested

¹ Letting $u = P(r, z_1, DoF, L_i)$, the hyperbolic tangent function is $\tanh u = \frac{e^u - e^{-u}}{e^u + e^{-u}}$ and the hyperbolic secant

function is sech $u = \frac{2}{e^u + e^{-u}}$.

formulations of $P(\cdot)$ were estimated. Model 1 is based on limited information, in which only animal initial weight is known, and revenue is estimated for each of the four animal slaughter dates. Model 2 uses initial weight, but also includes both beginning REA and BF, and liveweight both in February and sixteen days prior to the initial marketing date (i.e., at 158 days on feed). Determining whether information about the sequence of the leptin gene is statistically significant is accomplished by adding two dummy variables for the CC and the CT sequence to both models (resulting in models 1_L and 2_L).

Maximum likelihood estimates for $P(\cdot)$ are reported in Table 3. Initial liveweight is significant at greater than the 99 percent level in both formulations of the model 1 (i.e., with and without knowledge of the leptin gene). Revenue is positively affected by the animal's initial weight. Marketing dates had little statistical significance in model 1, except the revenue distribution was shifted leftwards for animals sold at the first date (174 *DoF*) with greater than 95 percent significance than animals sold at the fourth marketing date (the control).

	Model 1	Model 1_L	Model 2	Model 2 _L
Constant	-4.2882	-3.9817	4.4078	4.4115
	(4.4398)	(4.4466)	(4.8346)	(4.8621)
LW_0	-1.0112	-1.0162	-0.2175	-0.2332
	(0.1538)	(0.1539)	(0.2350)	(0.2353)
Rev	0.8791	0.8552	0.5202	0.5115
	(0.8729)	(0.8738)	(0.9170)	(0.9185)
Rev ²	0.0167	0.0188	0.0493	0.0498
	(0.0443)	(0.0443)	(0.0469)	(0.0470)
Kill ₁	0.4946	0.4525	0.6600	0.6465
-	(0.2006)	(0.2036)	(0.2062)	(0.2194)
Kill ₂	-0.2353	-0.2711	0.0096	-0.0025
-	(0.1834)	(0.1850)	(0.1831)	(0.2177)
Kill ₃	0.2774	0.2278	0.3219	0.3122
-	(0.1828)	(0.1884)	(0.1864)	(0.1944)
REA_0			-0.1337	-0.1312
			(0.0788)	(0.0793)
BF_0			4.2259	3.9906
Ū			(1.4279)	(1.4553)
LW_{16}			-0.8381	-0.8417
10			(0.1759)	(0.1769)
LW_{Feb}			-0.2912	-0.2614
			(0.2233)	(0.2289)
CC		-0.3960	· · ·	-0.1897
		(0.2110)		(0.2197)
СТ		-0.2949		-0.1015
		(0.1482)		(0.1547)
LogL	-201.989	-199.350	-165.183	-164.766

Table 3. Maximum likelihood estimates of polynomial functions relating revenue and exogenous variables (standard errors in parentheses)

If the only observable difference among animals is initial weight, then the effects of the amino acid sequence are statistically significant at about the 95 percent level. Both the CC and the CT sequences positively affect the revenue distribution. For example, expected revenues were higher for both the CC and CT animals than for animals having the TT sequence. The likelihood ratio test comparing the two versions of model 1 indicated the addition of the genetic information did result in a moderately better specification (i.e., the probability of the genetic information having no impact on revenues was fairly low at 0.0714).

Statistical significance need not imply economic significance or increased profitability from knowledge of the genetic information imbedded in the leptin gene. In order to estimate economic value, the decision analysis framework is used to determine optimal levels of the management input (here, *DoF*), with and without knowledge of the leptin gene.

Estimation of the conditional probability function allows calculation of the moments of the distribution of animal revenue conditional upon both animal characteristics and days on feed. Conditional expected net revenues can be estimated:

(7)
$$E((r-wDoF)|z_1, DoF, L_i) = \int_{-\infty}^{\infty} (r-wDoF)(0.5 P_r(r, z_1, DoF, L_i) \operatorname{sech}^2(P(r, z_1, DoF, L_i)))dr$$

Mean net revenues for models 1 and 1_L are in Table 4. Expression (7) was evaluated using the *Intsimp* routine (Simpson's method) in Gauss v7.0 (Aptech Systems, Inc.). Net returns are reported for mean initial liveweight (611 pounds), and for 90% (550 pounds) and 110% (672 pounds) of the mean liveweight.

Mean net return is the decision criterion in this model. To test the significance of differences in the mean net returns reported in Table 4, distributions of the estimated mean net returns by kill date, initial weight, and information content were obtained via Monte Carlo simulation. Two hundred subsamples of 120 observations were randomly drawn without replacement from the full set of 180 observations. Coefficients of the conditional polynomial function $P(r,z_1,DoF,L)$ were estimated, and expected net returns were estimated for each of the 200 draws. Simulated values of expected net returns then allowed formal testing of H_o: ER^{*} = ER_k versus H_a: ER^{*} > ER_k, where ER_k are expected returns for alternative kill dates for cattle having beginning weights of 550, 611, or 672 pounds.

The second marketing date (180 days on feed) was optimal both when genetic information was not known and when information about the amino acid sequence on the leptin gene is known. T-statistics comparing expected net returns from this second marketing date to each of the other three dates indicated the null hypothesis of no difference in means of the expected returns was rejected with greater than a 99 percent confidence.

Days on Feed:	174 days	180 days	187 days	193 days
	-		-	
No genetic inform	ation			
$LW_o = 550 lbs$	\$28.00	\$82.77	\$25.57	\$39.82
	(16.832)	(11.347)	(12.183)	(7.978)
$LW_o = 611 lbs$	\$18.51	\$68.76	\$14.22	\$26.80
	(8.733)	(8.272)	(11.276)	(7.838)
$LW_o = 672 lbs$	\$5.09	\$51.49	-\$0.34	\$10.83
	(9.140)	(8.558)	(11.666)	(12.438)
CC genotype				
$LW_o = 550 lbs$	\$47.09	\$98.69	\$44.29	\$53.38
	(17.085)	(13.562)	(13.312)	(12.405)
$LW_o = 611 lbs$	\$35.52	\$83.47	\$31.26	\$39.19
	(11.772)	(9.571)	(14.366)	(9.838)
$LW_o = 672 lbs$	\$20.80	\$64.62	\$15.40	\$22.09
	(11.439)	(10.476)	(15.035)	(13.150)
CT genotype				
$LW_o = 550 lbs$	\$37.89	\$90.30	\$35.43	\$44.76
	(18.931)	(9.417)	(13.538)	(7.945)
$LW_o = 611 lbs$	\$27.05	\$75.52	\$22.96	\$31.04
	(9.520)	(8.466)	(12.045)	(8.387)
$LW_o = 672 lbs$	\$12.77	\$57.45	\$7.56	\$14.50
	(9.898)	(10.099)	(14.807)	(12.052)
TT genotype				
$LW_o = 550 lbs$	\$9.79	\$65.38	\$8.72	\$19.03
	(21.189)	(12.239)	(13.565)	(12.175)
$LW_o = 611 lbs$	\$1.85	\$51.92	-\$1.67	\$6.90
	(14.103)	(11.196)	(10.968)	(11.574)
$LW_o = 672 lbs$	-\$11.04	\$35.62	-\$15.78	-\$8.27
	(10.499)	(11.843)	(15.098)	(14.722)

Table 4. Expected net carcass values for animal weights 90%, 100%, and 110% of mean initial liveweight, with and without genetic information (Model 1) (standard deviations in parentheses)

When marketing date is the only management input, it follows from formulation (3) that knowledge of the leptin gene has no economic value. Results of t-tests confirm these results. Comparing the vectors of simulated expected net returns when no genetic information is available to expected net returns weighted by the proportion of CC, CT, and TT cattle in the samples confirmed that the null of equal expected returns could not be rejected. T-values for the different initial weights were -0.285 for the light cattle (550 pounds), 0.143 for the average weights (611 pounds), and 0.155 for the heavy cattle (672 pounds).

However, expected net revenues did differ when animals were separated based upon the amino acid sequence. Expected gains associated with the CC trait over CT cattle ranged from \$7.17 to \$8.39 in model 1_L, depending upon initial weight. Gains of CC cattle over TT ranged between \$29.00 and \$33.31. T-tests strongly supported rejection of the null of equal expected returns for cattle having different amino acid sequences. The greater expected returns from CC cattle may indicate a potential economic benefit if feeders can sort animals prior to purchase, or

if feeder steer sellers can use guarantees of genetic traits to both guide breeding programs or to demand price premiums for CC and CT cattle.

Model 2

Additional animal characteristic data were included in maximum likelihood estimation of the conditional probability density function in model 2. Initial measures of backfat and ribeye were obtained by ultrasounding animals as they entered the feedlot in November. Liveweight in February and again 16 days prior to the first marketing date were also included. Parameter estimates for the polynomial $P(r, z_1, DoF, L_i)$ are reported in Table 3.

Initial liveweight was no longer statistically significant. Instead, weight of the animal 16 days before the first slaughter was positively related to carcass value at greater than a 99 percent level of confidence. Similar to model 1, revenues were significantly lower for animals slaughtered at the first marketing date. Initial backfat measurement had a negative effect on ending value at a greater than 99 percent confidence level. The raw data indicated a high positive correlation between backfat and animal yield grade (correlation = 0.86), supporting the negative relationship between backfat present at placement and the distribution of eventual carcass value. Ending backfat was negatively correlated to carcass value (correlation = -0.21). Conversely, initial ribeye area had a positive impact on revenue at around a 90 percent level. Ending ribeye area was negatively correlated with yield grade (correlation = -0.73) and positively correlated with animal carcass value (correlation = 0.35).

With the additional information about initial body composition, the leptin gene dummy variables were not statistically significant in explaining revenue distribution. The likelihood ratio between the restricted and unrestricted formulations of model 2 indicated addition of the CC and CT variables did not improve model specification ($\chi^2 = 0.833$).

Since knowledge of the leptin gene sequence was not statistically significant in the revenue distribution, it is not expected that the management input, *DoF*, would vary with knowledge of the amino acid sequence. Comparison of expected net returns supports this conclusion. Table 5 reports carcass values net of yardage and opportunity costs both without knowledge of the genetic trait and with the revenue distribution generated assuming the animals had the CC, CT, or the TT amino acid sequence. Given the large number of conditioning variables in the polynomial function $P(\cdot)$, expected net returns are generated using just the mean values of animal weights, backfat, and ribeye area.

Days on Feed:	174 days	180 days	187 days	193 days
No Info	\$24.64 (8.249)	\$58.09 (7.176)	\$24.93 (9.761)	\$35.92 (6.689)
	(0.2+)	(7.170)	().701)	(0.007)
CC	\$32.48	\$65.51	\$32.33	\$42.55
	(11.446)	(10.095)	(12.398)	(10.472)
СТ	\$26.42	\$59.69	\$26.40	\$36.73
	(9.384)	(7.557)	(10.808)	(6.608)
TT	\$19.39	\$52.96	\$19.54	\$30.00
	(10.191)	(9.739)	(11.541)	(10.529)

Table 5. Expected net carcass values for mean animal characteristics with and without genetic information (Model 2) (standard deviations in parentheses)

Similar to model 1 results, the optimal time on feed was 180 days regardless of genetic sequence. The expected net returns after 180 days on feed were statistically significant when no genetic information was known, or for each of the genotypes assessed in the project. Consistent again with the discussion of expression (3), no change in the management variable regardless of knowledge of the amino acid sequence on the leptin gene implies no economic value derived from the knowledge. Use of the vectors of simulated net expected values confirm the knowledge confers no economic value, with a t-statistic of -0.084 associated with the hypothesis that there is no difference in expected net returns with or without the genetic information.

Expected net returns of \$65.51 per animal from homozygous CC cattle were, however, statistically greater than expected returns of \$59.69 from CT (t=6.53) or \$52.96 from TT (t=12.65) steers. Expected returns from heterozygous CT cattle were, in turn, significantly higher than returns from the TT animals (t=7.72). Although knowledge of an animal's amino acid sequence does not alter optimal days on feed for our sample, the results do indicate significant improvements in animal carcass values and, consequently, net returns for animals having either the CC or the CT sequence.

Concluding Comments

One measure of the value of information is the change in expected returns net of information acquisition costs resulting from changes in decisions conditional upon any new information. A sample of 180 feeder steers was fed to four alternative marketing dates. A probability density function of carcass values was derived conditional upon both a management decision, days on feed, and a vector of animal characteristics. Choice of the optimal number of days on feed did not change when knowledge of the amino acid sequence was included as a conditioning variable. By the criterion of expected net return maximization, and based on the experimental protocol of adjusting days on feed, knowledge of the amino acid sequence on the

leptin gene in beef cattle had no value. In this case, knowledge of the genetic trait *ex ante* did not lead to heterogeneous production decisions, one of the potential benefits identified in Hennessy, Miranowski, and Babcock arising from increasing knowledge of an animal's genotype.

However, statistically significant gains were observed in expected net returns depending upon whether animals carried the CC, CT, or TT gene sequence. The distributions of expected net returns shifted rightwards for animals having the CC sequence instead of either CT or TT. These gains indicate the potential for market adjustment with increased knowledge of the genetic traits of feeder animals, consistent with Hennessy, Miranowski, and Babcock's contribution in the area of potential gains resulting from sorting and product differentiation. Differences in expected returns to cattle due to the amino acid sequence and, consequently, expression of the leptin gene may indicate opportunities for market gains when animals are placed on feed. Quasirents associated with knowledge of the animal's amino acid sequence should exist based on the results of this research. Capture of these rents by buyers and sellers will depend upon the relative power of market participants, as well as the degree of information asymmetry between the participants.

As Sherwin Rosen wrote, markets value diversity. If an agricultural input's genotype clearly affects performance or quality, and knowledge of this genotype is available, markets will react. The number of margins at which transactions occur will increase. Following Ladd and Martin's observation of nearly 30 years ago, crop and animal development programs may further diversify to target particular markets. There is a long tradition of analyzing alternative margins for agricultural input and output traits. Increasing knowledge of plant and animal genetics, and unraveling the linkages between genetics and quality, demonstrate the need for further development of analytical procedures to quantify the private and public benefits of this new information.

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