ESSAYS ON THE ECONOMIC VALUE OF GENETIC

TESTING IN BEEF CATTLE PRODUCTION

By

NATHANAEL MARK THOMPSON

Bachelor of Science in Economics
University of South Florida
Tampa, Florida
2010

Master of Science in Agricultural Economics
University of Tennessee
Knoxville, Tennessee
2012

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Dissertation Approved:

Dr. Francis M. Epplin

Dissertation Adviser

Dr. B. Wade Brorsen

Dr. Eric A. DeVuyst

Dr. Jayson L. Lusk

Dr. Megan M. Rolf

Name: NATHANAEL MARK THOMPSON

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Abstract: Recent advancements in genomic technology have made genetic marker panels for a variety of economically-relevant beef cattle traits commercially available. Although independent validations have found that many of these markers are correlated with the traits they are designed to predict, economists have considered few of these markers and their value to producers. The objective of this dissertation is to contribute to the understanding of the economic value of these markers.

The first essay estimates the value of using information from genetic marker panels characterizing seven economically-relevant traits for management and selection of feedlot cattle. The values of using genetic information to sort cattle by optimal days-on-feed are less than $1/head for each of the traits evaluated, and the values associated with using genetic information to select cattle for placement are as much as $38/head. Therefore, it would not be profitable at the current cost of testing (about $40/head) to sort cattle by optimal days-on-feed, but it could be profitable to use the genetic tests for breeding cattle selection.

The second essay examines the potential to increase the value of genetic information by improving fed cattle marketing decisions. The value of using genetic information to selectively market cattle ranges from $1-$13/head depending on how a producer currently markets their cattle and the grid structure. Although these values are generally higher than those reported in previous research, they are still not enough to offset the current cost of genetic testing.

The third essay evaluates the potential for reducing the overall cost of genetic testing by assuming that, instead of testing each individual animal, a random sample of animals could be tested to measure the genetic potential of the group. Using a fully Bayesian approach, we determine that an optimal sample size of 10 out of 100 animals generated returns from sampling of nearly $10/head. Although sensitivity analysis suggests that these values will vary depending on the particular pen of cattle, results indicate that random sampling has the potential to provide a context in which the benefits of genetic testing outweigh the costs.

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CHAPTER I

INTRODUCTION

The U.S. beef industry is made up of several disaggregated sectors: seed-stock, cow-calf, stocker/backgrounder, feedlot, and processor. As a result, misaligned incentives between producers at different points in the supply chain inhibit information flow from beef consumers back upstream to cattle producers, resulting in market inefficiency. For example, the revenue of cow-calf producers is a function of calf weight rather than feed efficiency or rate of gain potential of their calves, traits that are important for stocker and feedlot operators. Similarly, desirable traits for feedlots and processors do not always align with consumer preferences.

The beef industry recognized these issues in the 1990s with the realization that they were losing market share to pork and poultry (Fausti, Feuz, and Wagner, 1998). To counter this trend, the beef industry introduced a number of programs, the most notable of which was grid pricing that was designed to reflect consumer preferences and transmit these signals back up stream to producers using a system of premiums and discounts for yield grade and quality grade outcomes. However, the benefits of grid pricing, in reality, only extend back to the feedlot, as there is still little to no incentive for cow-calf producers to invest in quality traits desired by consumers. In addition, returns to grid pricing are consistently more variable than the returns to live weight or dressed weight pricing and grid pricing has not become the dominant fed cattle marketing strategy as many had projected (Feuz, Fausti, and Wagner, 1993; Schroeder and Graff, 2000; Anderson and Zeuli, 2001; Fausti and Qasmi, 2002; Lusk et al., 2003). Therefore, the cattle

industry suffers from an asymmetric information problem. One way to alleviate the inefficiency created by these information gaps between sectors is to introduce credible information regarding the potential of the live animal to efficiently convert feed into products valued by consumers. In this dissertation genetic testing is evaluated as a potential source of information for aligning the incentives of the beef industry.

Recent advancements in genomic technology have made genetic marker panels for a variety of economically-relevant beef cattle traits commercially available. Although independent validations have found that many of these markers are correlated with the traits they are designed to predict (Van Eenennaam et al., 2007; DeVuyst et al., 2011; Hall et al., 2011), to date, economists have considered few of these markers and their value to producers. Therefore, the objective of this dissertation is to contribute to the understanding of the economic value of commercially-available genetic marker panels using data from 10,209 animals.

Previous research on the economic value of genetic testing has been limited to tests for leptin genotype (DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008). However, in recent years leptin tests have been replaced with more precise genetic data, in the form of genetic marker panels, for a variety of economically-relevant traits. These marker panels include several, potentially hundreds or even thousands, of single nucleotide polymorphisms (SNP) to better predict phenotypic expressions (DeVuyst et al., 2011). Moreover, the availability of marker panels for several traits allows decision makers to better consider the chance that selecting for desirable attributes would have adverse effects on other economically-relevant traits. Therefore, the first essay, found in Chapter II, estimates the expected value of genetic information for seven economically-relevant traits at the feedlot stage, which results in two scenarios of value: marker-assisted management (sorting cattle by optimal days-on-feed) or marker-assisted selection (differentially selecting cattle for placement in the feedlot).

Results indicate that the values of using genetic information to sort cattle by optimal days-on-feed are less than $1/head for each of the traits evaluated. However, the values associated with using

genetic information to select cattle for placement are as much as $38/head. The most economically relevant genetic traits are average daily gain and marbling. However, even with improved accuracy of genetic marker panels, the qualitative implications of these results are similar to those reported in previous literature evaluating the value of genetic testing for leptin genotype (DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008). Therefore, it would not be profitable at the current cost of testing (about $40/head) to sort cattle by optimal days-on-feed, but it could be profitable to use genetic tests for selecting bulls and cows and determining breeding strategies.

The results from the first essay indicate that it would not be cost-effective to use genetic testing for marker-assisted management. However, marker-assisted management in that case was limited to sorting cattle by days-on-feed. Therefore, there still remains potential to increase the value of marker-assisted management by using the information derived from genetic testing to improve other management decisions within the feedlot that have yet to be evaluated, including how cattle are fed and marketed. Therefore, the second essay, found in Chapter III, evaluates for the first time a marker-assisted management scenario in which genetic information is used to improve fed cattle marketing decisions, including decisions for both marketing method (live weight, dressed weight, or grid pricing) and timing to market (days-on-feed) for each marketing group.

Results indicate that the value of using genetic information to selectively market cattle ranged from $1-$13/head depending on how a producer currently markets cattle and the grid structure. Although these values of marker-assisted management were generally greater than those reported in previous research, they were still not enough to offset the current cost of genetic testing. Nonetheless, sorting cattle into marketing groups also led to efficiency gains, including more accurate optimal days-on-feed and reduced variability of returns to cattle feeding. Therefore, the use of genetic testing to selectively market cattle may encourage producers, who might not otherwise do so, to market cattle on a grid (Fausti et al., 2010; Fausti, Wang, and Lange, 2013). This will result in improved quality

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and consistency of beef products and improved transmission of market signals throughout the beef cattle supply chain, and may help address consumer demand problems.

Despite improved accuracy of genetic marker panels, findings as reported in the first two essays consistently indicated that the value of genetic information is still not sufficient to offset the cost of testing. Therefore, either the value of genetic information must increase or the cost of testing must decrease. While animal scientists are continually progressing towards providing more accurate genetic markers that have the potential to increase the value of genetic information (for example, see Akanno et al. 2014), producers seeking to use this technology have no control over the pace at which these new variations are released. Therefore, the third essay of this dissertation, found in Chapter IV, presents a strategy for reducing the overall cost of genetic testing that has yet to be evaluated: random sampling. That is, instead of testing each individual animal in a group of cattle, a random sample of animals from a given ranch or farm could be tested to measure the genetic potential of the group. While appealing in theory, there is a thorny practical question: "What size sample should I take?" To answer this question a Bayesian decision theoretic approach to economically-optimal sample size determination is introduced (Grundy, Healy, and Rees, 1956; Riffa and Schlaifer, 1961; Lindley, 1997). Although this method appears to be rarely used in economic research, it is theoretically sound and could be useful for a wide range of applied economics problems.

Results indicate that the marginal benefit to testing is high for small sample sizes indicating that a large portion of the additional value for higher-quality cattle can be estimated by testing a relatively small portion of a lot of feeder cattle. For example, at the baseline parameter values the optimal sample size was 10 animals from a group of 100, and the returns from sampling were nearly $10/head, resulting in a 250% return-on-investment. Therefore, random sampling provides a context in which the benefits of genetic testing outweigh the costs, making this the first research to demonstrate cost-effective genetic testing for the beef industry. This research represents an important

contribution to the literature evaluating the economic value of genetic testing for beef cattle and potentially more importantly to the beef cattle industry.

This dissertation provides several important building blocks for evaluating the economic value of genetic information in beef cattle production. Most importantly, by providing a context for cost-effective genetic testing this research has the potential to have some very big picture implications for the beef industry. Genetic testing can provide information that could be useful to incentivize cow-calf producers to select bulls and cows to produce calves that will efficiently yield products valued by consumers. Economically-optimal random sampling and genetic testing has the potential to improve the flow of information from beef consumers back upstream to cattle producers and improve aggregate welfare.

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CHAPTER II

VALUE OF GENETIC INFORMATION FOR MANAGEMENT AND SELECTION OF

FEEDLOT CATTLE[*]

Abstract

We estimate the value of using information from genetic marker panels for seven economically

relevant feedlot cattle traits. The values of using genetic information to sort cattle by optimal

days-on-feed are less than $1/head for each of the traits evaluated. However, the values associated

with using genetic information to select cattle for placement are as much as $38/head. The most

economically relevant genetic traits are average daily gain and marbling. It would not be

profitable at the current testing cost of $38/head to sort cattle by optimal days-on-feed, but it

could be profitable to use the genetic tests for breeding cattle selection.

Keywords: Beef cattle, genetics, molecular breeding value, value of information

Introduction

Genomic technology has the potential to generate value in each sector of the beef industry – seed

stock, cow-calf, feedlot, and processing – by aiding in both management and selection decisions

(Van Eenennaam and Drake, 2012). Commercial testing services can provide livestock producers with a range of genetic information, including parentage assignment, detection of genetic defects, and genetic markers, or single nucleotide polymorphisms (SNP) for qualitative traits, such as hide color, and quantitative traits, such as marbling score. Many quantitative traits, such as growth and carcass characteristics, are economically important but can be difficult to measure preharvest. Therefore, genetic markers associated with these traits may provide valuable information to decision makers prior to investing considerable time and expense. Although independent validations have found that many of these markers are correlated with the traits they are designed to predict (Van Eenennaam et al., 2007; DeVuyst et al., 2011; Hall et al., 2011; National Beef Cattle Evaluation Consortium, 2013), economists have considered few of these markers and their value to producers to date.

Early interest in genetic testing for beef cattle involved the leptin gene, which is associated with fat deposition (Fitzsimmons et al., 1998; Buchanan et al., 2002). Mitchell et al. (2009) found leptin genotype to be correlated with calf weaning weight and cow productive life. As a result, differences in annualized returns for dams with different genotypes range from $15 to $64 per head. Feedlot studies have had differing results with respect to the most profitable leptin genotypes (DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008) but report differences in expected profit between the best and worst performing genotypes of as much as $60 per head. These same studies found that the leptin genotype has little effect on optimal days-on-feed.

Today, leptin tests have been replaced with more accurate marker panels for a variety of economically relevant traits. These panels include several (potentially hundreds) of SNP to better predict phenotypic expressions (DeVuyst et al., 2011). Moreover, the availability of marker panels for several traits allows decision makers to better consider the chance that selecting for desirable attributes would have adverse effects on other economically relevant traits. Previous research has found economically meaningful relationships between genetic marker panel scores for average daily gain, tenderness, marbling, yield grade, and rib eye area and growth and carcass characteristics such

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as average daily gain, feed efficiency, days-on-feed, hot-carcass weight, rib-eye area, yield grade, and quality grade (see DeVuyst et al., 2011, for an example). However, much remains to be learned about the economic value of utilizing such genetic information to improve feedlot profitability.

Prior research has provided useful, preliminary analysis of the biological and economic impacts of genetic marker panels. However, the limited data and simplified approach have failed to capture the full value of information obtained from genetic marker panels. To realize the full value of genetic information, it is important to determine whether cattle with different genetic makeups progress differently throughout the feeding process (Ladd and Gibson, 1978; Lusk, 2007). In other words, genetic markers do not directly influence profit, but they influence growth and carcass traits that, in turn, determine profitability. Accordingly, this study seeks to provide such an analysis using a large sample of cattle with considerable genetic diversity. Genetic information is conveyed as molecular breeding values (MBVs), which, like panel scores, represent an animal's propensity to express a given trait. Unlike discrete panel scores, MBVs are continuous, allowing for more precise depictions of the traits they characterize. In addition, genetic information is only useful if it conveys meaningful information beyond visual appraisal. Therefore, hide color is used to partially control for breed effects not considered in previous literature.

The increasing accuracy of genetic marker panels and the rapidly declining costs of genotyping present livestock producers with the opportunity to increase profitability by taking advantage of the information derived from genetic testing. However, the usefulness and value of this information will vary among the seed stock, cow-calf, feedlot, and processing sectors. The objective of this research is to estimate the expected value of genetic information for seven economically relevant traits at the feedlot stage, which results in two scenarios of value. First, genetic information could be used for marker-assisted management, sorting cattle that are already owned by a feedlot into management groups that are likely to perform similarly. Here we specifically focus on the value of using this information for choosing optimal days-on-feed. That is, what is the economic benefit of being able to feed cattle with differing genetics for different numbers of days-on-feed? Second,

genetic information could be used for marker-assisted selection to differentially select cattle for placement in the feedlot.[2] In other words, how much more or less are animals with superior or inferior genetics worth compared to their contemporaries? Expected values of genetic information derived in this study have important implications, not just for decision makers in the feedlot sector, but for those throughout the beef cattle supply chain.

This study uses data from feedlot cattle to estimate the expected value of genetic information at the feedlot stage. Prediction equations for average daily gain, dressing percentage, yield grade, and quality grade are estimated using live-animal performance characteristics and MBVs for seven economically relevant traits. Prediction equations and a multivariate normal distribution of error terms are used as part of a stochastic simulation to estimate expected profits per head. The expected value of genetic information is calculated as the difference in expected profit, with and without genetic information, for both marker-assisted management and marker-assisted selection.

Expected Profit Maximization and the Value of Information

Due to the capacity of large scale feeding operations, management of individual cattle with different feed rations or different expected sale dates is cost prohibitive. Therefore, feedlot cattle are managed in a group environment, such as pens or lots (Kolath, 2009). We assume that producers maximize expected per head profit for each group:

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[2] In the animal science literature, marker-assisted selection specifically refers to using the results of genetic testing to assist in the selection of breeding stock (Van Eenennaam, Werf, and Goddard, 2011). However in this analysis, marker-assisted selection at the feedlot stage is defined as using genetic information to select feeder cattle for placement in the feedlot based on their genetic makeup.

(1)

$$\max_{DOF_k \geq 0} E[\pi_k] = \frac{1}{n_k} \sum_{i=1}^{n_k} P_{ik}(YG_{ik}, QG_{ik}, HCW_{ik}) \times HCW_{ik}(PW_{ik}, ADG_{ik}, DP_{ik}, DOF_k)$$

$$\times (1 - MR) - PC_{ik}(PW_{ik}, SEX_{ik}) - FC_{ik}(W_{ik}, DOF_{ik}) - YC_k(DOF_k)$$

$$- IC_{ik}(PC_{ik}, DOF_k),$$

where DOF_k is days-on-feed for the kth management group; n_k is the total number of animals in the kth group; and P_{ik} is dressed fed-cattle price, which is determined in part by yield grade, YG_{ik}, quality grade, QG_{ik}, and hot-carcass weight, HCW_{ik}, for the ith animal in the kth group. Hot-carcass weight is a function of placement weight, PW_{ik}, average daily gain, ADG_{ik}, and dressing percentage, DP_{ik}, $HCW_{ik} = (PW_{ik} + ADG_{ik} \times DOF_{ik}) \times DP_{ik}$. MR is mortality rate, which is bounded by 0 and 1, PC_{ik} is the purchase cost of feeder cattle, FC_{ik} is feed cost, W_{ik} is weight, YC_k is yardage costs, and IC_{ik} is interest cost on the purchase of feeder cattle. At placement, purchase cost and placement weight are the only variables known with certainty. Other profit determinants are a function of random growth and carcass characteristics ADG, DP, YG, and QG and the choice variable, DOF. Although the producer is assumed to have contracted a guaranteed future price grid, it is unknown how animals will develop and therefore what weight and carcass premiums or discounts they will receive. Information derived from genetic testing can be used to predict unknown growth and carcass characteristics. This information gives the feedlot the opportunity to differentially manage and select cattle based on genetic potential. Although acquiring this information incurs costs, it yields information that may increase profitability (Stigler, 1961).

Stigler (1961) first developed the economics of information, which has since been extended to many agricultural settings, including the value of genetic information in livestock production (Ladd and Gibson, 1978; Hennessy, Miranowski, and Babcock, 2004; DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008). Typically, the value of information is calculated as "the difference between expected returns (or utility) using the information and expected returns without the information, with both expectations taken with respect to the more informed distribution" (Babcock, 1990, p.63). Note that

expected profit in equation (1) does not include genetic testing costs. As a result, the improvement in the objective function from acquiring genetic information sets an upper limit on the cost of genetic testing.

Data

Data for 10,209 cattle from six commercial feedlots were provided by Neogen, the parent company of Igenity. Animals were weighed at placement, and a hair sample or tissue punch from ear tag application was collected for genetic testing. Molecular breeding values characterizing average daily gain, hot-carcass weight, yield grade, rib-eye area, marbling, tenderness, and days-on-feed were provided. Although many breed associations are working toward developing breed-specific MBVs (MacNeil et al., 2010), much as they have done for expected progeny differences (EPDs), the MBVs used in this study were developed using a sample of commercial cattle.[3] Unlike EPDs, which represent the genetic potential of an animal as a parent, MBVs represent the genetic potential of an animal to express a given trait. Increases in MBVs increase the likelihood of expressing more favorable outcomes.[4] While MBVs (like EPDs) are reported in units of the trait, they "reflect the relative differences expected in animals across breeds compared to their contemporaries" (Igenity, 2013a, p.2). That is, if two animals have marbling MBVs of -100 and 20, we would expect, on average, that these two animals' marbling scores would differ by 120 units. Additional live-animal characteristics for gender, hide color, average daily gain, and days-on-feed were also provided. At

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[3] For more information on the development and validation of MBVs, see the National Beef Cattle Evaluation Consortium, Commercial Genetic Test Validation (National Beef Cattle Evaluation Consortium, 2013).

[4] Intuitively, more favorable outcomes are increases in a given trait (e.g., higher marbling score), except for yield grade, for which lower outcomes are more favorable.

slaughter, data were collected for final live weight and carcass measurements for hot-carcass weight, back fat, rib-eye area, calculated yield grade, and marbling score.

Missing data were common for a few critical variables. Final live weight was unavailable for 4,436 observations. Although not used directly, final live weight is essential to the estimation of dressing percentage (dressing percentage=hot-carcass weight/final live weight). Additionally, 422 observations were missing for marbling score. After deleting these and other observations with missing data, 5,353 complete records were available for analysis. These data consist of six sets, each of which represents a different commercial feedlot or time period.[5] In addition, each set is divided into contemporary groups, which are defined as groups "of animals that have had an equal opportunity to perform: same sex, managed alike, and exposed to the same environmental conditions and feed resources" (Northcutt, 2005, p.144). The 197 contemporary groups averaged 27 head per group with a range from 1 to 202 head. The sample is made up of 74% steers and 68% black-hided cattle (table II-1). On average, cattle were fed for 165 days and finished with a yield grade of almost 3 and a marbling score of 412 (low Choice on the quality grade scale).[6]

Investigation of the empirical, joint yield- and quality-grade distribution suggests that cattle in the sample are of average quality (table II-2). The majority of cattle grade either Select (44%) or low Choice (42%) on the quality-grade scale and yield grade two (46%) or three (40%) on the yield-grade scale, although the sample includes cattle in each yield-grade and quality-grade category.

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[5] The majority of the cattle used in this study represent year-round placements in commercial feedlots in Iowa and Kansas in the year 2007 with a small number of placements (127 head) in January 2008.

[6] Marbling scores between 200--299 are said to have traces of intramuscular fat and are graded Standard, 300--399 or slight marbling are Select, 400--499 or small marbling are low Choice, 500--599 or modest marbling are average Choice, 600--699 or moderate marbling are high Choice, and scores over 700 are Prime (USDA AMS, 1997, 2006).

To remove time-varying effects in our simulation, all animals are assumed to face the same market prices for March 2013. Purchase costs for feeder cattle are estimated using feeder cattle prices for steers and heifers based on placement weight (U.S. Department of Agriculture, Agricultural Marketing Service (USDA AMS), 2013a). Finished cattle are assumed to be priced on a fixed grid with a base price of $201.71/cwt. dressed, with appropriate premiums and discounts for yield grade, quality grade, and weight (table II-3) (USDA AMS, 2013b).

Procedures

Average daily gain (*ADG*), dressing percentage (*DP*), yield grade (*YG*), and quality grade (*QG*) in equation (1) are assumed to be random variables. A mixed model regression equation for each of these growth and carcass characteristics is estimated such that the data generating process is specified as

(2) $$Y_{ijkl} = \beta_{0l} + PW_{ijk}\beta_{1l} + DOF_{ijk}\beta_{2l} + DOF_{ijk}^2\beta_{3l} + PW_{ijk}DOF_{ijk}\beta_{4l} + STR_{ijk}\beta_{5l}$$

$$+ BLK_{ijk}\beta_{6l} + \sum_{m=1}^{7} MBV_{ijkm}\beta_{7lm} + v_{jl} + u_{jkl} + \varepsilon_{ijkl},$$

where Y_{ijkl} is the dependent variable for the *i*th animal in the *j*th set and the *k*th contemporary group for the *l*th equation, where *l*=1,2,3,4 for ADG_{ijk}, DP_{ijk}, YG_{ijk}, and QG_{ijk}, respectively; PW_{ijk} is placement weight; DOF_{ijk} is days-on-feed; STR_{ijk} is a dummy variable equal to 1 if the animal was a steer and 0 otherwise; BLK_{ijk} is a dummy variable equal to 1 if the animal had black hide and 0 otherwise; MBV_{ijkm} is the molecular breeding value of the *m*th economically relevant trait; $v_{jl}\sim N(0, \sigma_{v_l}^2)$ is a set random effect; $u_{jkl}\sim N(0, \sigma_{u_l}^2)$ is a contemporary group random effect nested within sets (Greene, 2012); and $\varepsilon_{ijkl}\sim N(0, \sigma_{\varepsilon_l}^2)$ is an error term, where v_{jl}, u_{jkl}, and ε_{ijkl} are independent. A full set of MBV, days-on-feed interactions are also investigated as slope shifters in the *YG* and *QG* equations. Only the marbling MBV, days-on-feed interaction is statistically significant in both equations; all other MBV, days-on-feed interactions are therefore dropped from the models.

Dependent variables *YG* and *QG* are both represented as continuous variables. Yield grade is a continuous variable as a function of backfat; kidney, pelvic, and heart fat; hot-carcass weight; and rib-eye area (USDA AMS, 1997), and the marbling score is used as a continuous representation of *QG*.

Models are estimated independently using Proc Mixed in SAS (SAS, 2012). The D'Agostino-Pearson K^2 omnibus test for skewness and kurtosis rejects the null hypothesis of normality in each of the four prediction equations, and conditional variance tests identify static heteroskedasticity. Cluster robust standard errors are estimated to obtain estimates of standard errors that are consistent in the presence of nonnormality and heteroskedasticity (Liang and Zeger, 1986). Given the large sample size, asymptotic properties are relevant, and the small sample biases common with generalized method of moments estimators should be of little concern.

Expected Profit

Feed costs are also needed to calculate expected profits. Given that observations of feed intake were unavailable, a dry matter intake (DMI) model is used following the National Research Council's (NRC) *Nutrient Requirements of Beef Cattle* (NRC, 2000).[7] The DMI model generates an estimate of "standardized" feed intake. That is, we ignore additional factors that may have influenced feed intake across different feedlots or time periods, such as weather. Much like holding prices constant, this approach places all animals on a level playing field in order to estimate an expected value of genetic information. Prior to calculating DMI, a projected live weight for each animal for each day on feed is estimated as

(3) $$W_{it} = PW_i + \left(\frac{LW_i - PW_i}{DOF_i}\right) \times t_i \forall\, t \in \{1, \dots, DOF_i\},$$

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[7] A constant cost-of-gain approach could also be used to estimate feed costs. However, such an approach is just a parallel shift of the revenue curve. The DMI model reflects that the cost of gain goes up as the cattle weight increases and thus provides concavity to the profit function.

where W_{it} is the weight of the ith animal at the tth day on feed, LW_i is final live weight, PW_i is placement weight, and DOF_i is days-on-feed. The NRC's DMI equation also allows for adjustment factors for breed, percentage of empty body fat, growth hormones, air temperature, and muddy soils that may influence growth in the feedlot. Based on available information, a body fat adjustment factor (BFAF) is included in the analysis. The BFAF is determined by empty body fat percentage (*EBF*) (Perry and Fox, 1997):

$$(4) \qquad EBF_{it} = \left(\frac{0.351 \left(0.389 \left(\frac{W_{it}}{2.2} \right) \right) + 21.6 YG_i - 80.8}{0.389 \left(\frac{W_{it}}{2.2} \right)} \right) \times 100.$$

Essentially, the BFAF corrects for over prediction of DMI as animals become larger (table II-4) (NRC, 2000).

Using this information, we then estimate *DMI* (lbs/day) for the ith animal for the tth day on feed as

$$(5) \qquad DMI_{it} = \left(0.96 \left(\frac{W_{it}}{2.2} \right) \right)^{0.75} \times \frac{(0.2435 NE_m - 0.0466 NE_m^2 - 0.1128)}{NE_m} \times BFAF_{it} \times 2.2,$$

where NE_m is the net energy required for maintenance, which is set to a constant of two megacalories per kilogram (NRC, 2000). Finally, cumulative dry matter intake (*CDMI*) of the ith animal is

$$(6) \qquad CDMI_i = \sum_{t=1}^{DOF_i} DMI_{it}.$$

Additional information needed to estimate expected profit includes dry matter cost of $230/ton ($0.115/lb.), yardage costs of $0.40/day, a 7% interest rate on the purchase of feeder cattle, and a

mortality rate of 1% (Lardy, 2013).[8] This information can be used in conjunction with equations (2)--(6) to estimate profit per head.

However, expected profit in equation (1) is nonlinear. Therefore, because of Jensen's inequality, profit calculated at the expected value of prediction equations will not equal expected profit (Greene, 2012). For this reason, stochastic simulation is used to estimate expected profit per head. The Cholesky decomposition of the four-by-four variance-covariance matrix of the error terms from equation (2) is calculated and used to generate a multivariate normal distribution of 1,000 error terms for each of the four prediction equations for each animal in the sample. Profit per head is evaluated at each draw using actual live-animal characteristics and MBVs. The average across draws is expected profit per head. This process is repeated for days-on-feed from 150 to 200.

Marker-Assisted Management

The advantage of genetic testing is the ability to differentially manage or select cattle based on unobservable growth and carcass characteristics. As a result of producer interest in which MBVs are most economically relevant, the primary objective here is to determine the value associated with each individual genetic marker panel. To do so, cattle are divided into quartiles for each of the seven MBVs, and the expected profit per head is calculated for each quartile.[9] A grid search is then employed to determine the days-on-feed that maximizes expected profit per head for each group. This

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[8] Costs for sick treatments, which are generally assessed on an animal-by-animal basis (for example, $1 per head for each pull plus material costs), are not included. Information on animals being pulled for sick treatment was not available.

[9] The choice of four groups used in this analysis is subjective. However, Cargill Cattle Feeders utilize a four group management system to "allow for efficient management within a group production environment by preventing groups with too few animals, while still allowing us to come close to maximizing the genetic potential of each animal" (Kolath, 2009, p.105).

approach makes it possible to identify which MBVs capture the most economic value. Marker-assisted management is the process of using genetic information to sort cattle already in the feedlot into management groups that are most likely to achieve similar endpoints (Van Eenennaam and Drake, 2012). Although it can include several objectives, such as implant strategies and value-added marketing, marker-assisted management for this analysis is limited to optimal marketing dates, or days-on-feed. The value of genetic information associated with marker-assisted management (VOI_{MAM}) for a given trait is calculated by comparing expected profit when a feedlot can differentially choose optimal marketing dates for each quartile of a given trait relative to the case where all cattle are fed for the same number of days-on-feed:

(7)
$$E[VOI_{MAM}] = \sum_{i=1}^{4} \frac{E[\pi_{Qi}]}{4} - E[\pi_{ALL}],$$

where π_{Qi} is maximum profit for the ith quartile and π_{ALL} is maximum profit when all cattle in the sample are fed for the same number of days-on-feed.

Marker-Assisted Selection

At the feedlot stage, marker-assisted selection involves differentially selecting cattle for placement based on genetic information. Feedlots are still expected to feed both high- and low-quality cattle. However, access to genetic information allows feedlot operators the opportunity to place premiums on cattle with superior genetic potential and discounts on cattle with poor genetics. The maximum value of genetic information associated with marker-assisted selection (VOI_{MAS}) for a given trait is calculated by comparing expected profits for the best performing quartile relative to the case where genetic information is unavailable and all cattle are fed for the same number of days-on-feed:[10]

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[10] The expected value of marker-assisted selection in some previous studies has been calculated as the difference in expected profit per head for the best and worst performing quartiles (or genotypes).

(8) $$E[VOI_{MAS}] = \max\{E[\pi_{Q1}], E[\pi_{Q2}], E[\pi_{Q3}], E[\pi_{Q4}]\} - E[\pi_{ALL}].$$

Although currently genetic information is not typically available to feedlots prior to purchasing feeder cattle (Kolath, 2009), knowledge of the value associated with marker-assisted selection at the feedlot stage is important. These values provide estimates of the premiums or discounts that feedlots could place on cattle with varying levels of genetic potential, or a bid-price differential. In addition, knowledge of the traits that generate the most value to the feedlot sector may also guide selection decisions in the breeding sectors. The values reported here reflect short-run partial equilibrium effects. If the majority of feedlots begin selecting for MBVs – or if breeders begin to selecting for certain MBVs – then the returns to a genetic trait will change as a result of changes in supply and demand for the trait.

Equations (7) and (8) treat the "base" scenario as the maximum expected profit when all cattle are fed for the same number of days-on-feed (π_{ALL}), rather than using actual observed returns.[11] This approach allows us to confidently make comparisons across all animals in the sample. Alternatively, these same comparisons may not be appropriate when using actual observed returns, given that the cattle were fed under different conditions. For example, the dataset consists of animals from several commercial feedlots over multiple time periods. Therefore, differences in marketing decision rules among feedlots as well as differences in input and output prices over time influence the observed days-on-feed decisions and returns to cattle feeding. In addition to these obvious differences, unobservable constraints (such as capacity constraints and weather conditions) are also

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However, this assumes that the original state of nature involves the feedlot owning all cattle from the worst performing quartile, which is likely not the case.

[11] Observed returns based on pen-level cost data were unavailable. However, access to this information would not have changed our approach to estimating the expected value of genetic information. This additional data may have been used to calibrate the intake equations, but even this may have been inappropriate given the potential for differences in feed rations across time and space.

likely to influence the observed outcomes. However, feedlots do not have a constant days-on-feed expectation with or without genetic information. Therefore, the values reported here are likely upper bounds on the value of genetic information.

Multiple-Trait Marker-Assisted Management and Selection

Genetic information characterizing economically relevant traits may also be supra- or subadditive. That is, managing for multiple traits simultaneously may increase the value associated with marker-assisted management or marker-assisted selection. If cattle are divided into quartiles for each MBV, simultaneously managing for two traits yields sixteen potential management groups. Again, a grid search is employed to determine days-on-feed that maximizes the expected profit per head for each group. The expected value of marker-assisted management and marker-assisted selection is estimated similarly to equations (7) and (8), except that each group no longer makes up an equal proportion of the sample.

Further, there is also interest in the value of utilizing the entire profile of genetic information simultaneously. That is, instead of utilizing genetic information for one or two traits, what is the value of managing cattle based on their overall performance? This inquiry requires a slightly different approach than the procedures described above. First, we must find the days-on-feed that maximizes the expected profit per head for each animal in the sample. However, when looking at each animal individually, live-animal characteristics other than MBVs will influence optimal days-on-feed. For example, animals with lower placement weights will obviously command higher optimal days-on-feed. For this reason, placement weight, gender, and hide color are held constant at their mean values in order to separate these effects from those of genetic information. Following a stochastic simulation procedure similar to that described above, we can then determine the expected profit-maximizing number of days-on-feed for each animal in the sample. As has been previously discussed, individual management is cost prohibitive in a feedlot setting. Therefore, animals are sorted into quartiles based on their individual performance (optimal days-on-feed), and a single expected profit-maximizing

number of days-on-feed is determined for each quartile. Dividing cattle into quartiles also provides us with an estimated value of the entire genetic profile that is comparable to the other values of genetic information reported here.

Results

Regression estimates for growth and carcass characteristics *ADG*, *DP*, *YG*, and *QG* are reported in table II-5. Missing observations for dependent variables in the sample are deleted so that all four equations have the same number of observations (n=5,353).[12] Coefficients for live-animal characteristics generally exhibit expected relationships. Heavier placement weights increase predicted values for *ADG*, *DP*, *YG*, and *QG*. Growth and carcass characteristics *ADG*, *DP*, and *QG* display a concave relationship with days-on-feed, increasing at a decreasing rate, but only in the *DP* equation are linear and squared terms both statistically significant. Consistent with expectations, the effect of days-on-feed on each of the performance characteristics is diminished as placement weight increases, which is suggested by the negative coefficient of the placement weight, days-on-feed interaction terms. Steers have higher *ADG* and lower *YG* and *QG* compared to heifers. Additionally, black-hided cattle have higher *ADG* and *QG*.

Molecular breeding values influence corresponding fed cattle traits in the expected direction. Average daily gain MBV positively influences actual *ADG*, hot-carcass weight MBV positively influences actual *DP*, yield grade and rib-eye area MBVs negatively influence *YG*, and marbling MBV positively influences actual *QG*. Each of these effects except for the marbling MBV is statistically significant at the 1% level. However, a joint test of the marbling MBV and marbling MBV, days-on-feed interaction terms in the *QG* equation is statistically significant at the 1% level (df=2, 5128; *F*=306.91). Additional effects of MBVs on growth and carcass characteristics offer

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[12] Each of the four equations is also estimated with its own maximum number of observations to investigate fragility. Differences are minimal, and results are presented as is for conciseness.

many interesting relationships. Most notably is the significant, inverse relationship between yield and quality grade. Higher yield grade and rib-eye area MBVs decrease *QG*, and higher marbling MBV increases *YG*.[13] These cross-trait MBV effects suggest the need to consider multiple MBVs when making management or selection decisions.

Prediction equations are used as part of a stochastic simulation to estimate expected profit according to equation (1) for days-on-feed from 150 to 200. Results indicate that if a feedlot was restricted to pick the same marketing date for all cattle, maximum expected profit of $146.14 per head would be realized at 185 days-on-feed. This result is higher than mean actual days-on-feed observed in the sample of 165 days,[14] but is well within the range of observed values, which has a maximum of 308 days. A variety of circumstances contribute to the discrepancy between predicted and observed days-on-feed. One potential explanation is the unobservable constraints faced by feedlot operators (Boys et al., 2007), such as differences in input and output prices actually faced when the cattle were on feed and the prices we use in this simulation.[15] In addition, feedlot operators may be risk averse.

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[13] Marbling MBV has a negative coefficient in the *YG* equation. However, the marbling MBV, days-on-feed interaction is positive. Therefore, the sum of the two effects is positive and jointly significant at the 1% level (df=2, 5128; *F*=41.44) over the range of days-on-feed analyzed (150-200).

[14] At the mean actual days-on-feed observed in the sample of 165 days expected profit would be $135.44 per head. Therefore, an additional twenty days-on-feed increased expected profit by about $10.70 per head.

[15] The corn-to-dressed fed cattle price ratio in 2007 ($4.20/146.37 = 0.029$) is similar to the price ratio used in this analysis ($6.44/201.71 = 0.032$). However, the current price grid rewards higher quality grades, incentivizing feedlot operators to feed cattle longer. The use of a price grid from the period when cattle were actually fed may lead to more similar results between predicted and actual days-on-feed. However, because we are ultimately interested in the current value of genetic information to producers, the use of a current price grid is appropriate.

Therefore, cattle may be harvested prior to reaching maximum profits in order to avoid the potentially large discounts associated with higher yield grades if cattle are overfed.

Optimal days-on-feed and expected profits per head are determined at the quartiles of MBVs for each economically relevant trait (table II-6). Results indicate differences in expected profit among quartiles ranging from $8 per head for days-on-feed MBV to $46 per head for marbling MBV. Higher MBVs increase expected profit for all traits except yield grade, rib-eye area, and days-on-feed. The inverse relationship between expected profit and MBVs characterizing yield grade and rib-eye area is likely the result of the inverse relationship between yield grade and quality grade. More favorable yield grade and rib-eye area outcomes result in less favorable quality grade. Therefore, for the budgeted price grid, yield-grade premiums are insufficient to offset lower quality-grade premiums (or higher quality-grade discounts). Despite differences in expected profit, optimal endpoints for the quartiles of each trait are similar to the uniform endpoint for all cattle in the sample of 185 days-on-feed.

Marker-assisted management increases expected profit for each of the economically relevant traits evaluated. The ability to choose optimal marketing dates for each quartile of the rib-eye area MBV increases expected profit to $146.63 per head, resulting in the highest value of genetic information for marker-assisted management, $0.49 ($146.63-$146.14) per head (table II-7). Rib-eye area partially determines yield grade, which is directly reflected in the price grid. However, the value of marker-assisted management associated with the yield grade MBV is only $0.03 per head. Therefore, the rib-eye area MBV appears to capture markers that are more economically sensitive to days-on-feed than the yield grade MBV. The expected value of marker-assisted management for other key profit determinants of marbling, average daily gain, and hot-carcass weight are $0.35, $0.20, and $0.10 per head. In general, low values associated with marker-assisted management are partially influenced by limited differences among optimal days-on-feed for the quartiles of each trait and the uniform endpoint for all cattle in the sample. This result is consistent with the findings of previous

research (DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008) and supports the finding that agricultural profit functions are often flat near the optimum (Pannell, 2006).

Results also indicate that expected profits could be increased considerably if a feedlot could differentially select cattle based on genetic information for each trait. Marker-assisted selection for the MBV characterizing average daily gain increases expected profits to $168.35 per head, resulting in the highest value of genetic information for selection, $22.21 ($168.35 - $146.14) per head (table II-7). The ability to select for animals with higher average daily gain will result in heavier finished weights or fewer days-on-feed, both of which increase profitability. Similarly, MBVs characterizing marbling and hot-carcass weight generate value for selection of $21.27 and $18.42 per head. These results are similar to the findings reported by Lusk (2007), who found values for marker-assisted selection at the feedlot stage for leptin genotype of approximately $23 and $28 per head for steers and heifers.[16]

The above results estimate the value of marker-assisted management and marker-assisted selection when focusing on a single economically relevant trait. However, the ability to manage or select for multiple traits may further increase expected profits and the value of genetic information. For example, a feedlot operator could simultaneously manage or select for MBVs characterizing average daily gain and marbling (table II-8). When each management group is fed for its own optimal number of days-on-feed, expected profits across all sixteen groups increase to $146.62 per head.[17] Therefore, the value of multiple-trait marker-assisted management for average daily gain and marbling MBVs is $0.47 ($146.62 - $146.14) per head. The group comprising the fourth quartiles for

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[16] Other studies either did not report values of marker-assisted selection or reported values that were not comparable given differences in the estimation of the value of marker-assisted selection at the feedlot stage.

[17] The sum across groups of each group's expected profit multiplied by its effective proportion of the sample.

both traits generates the highest expected profit of $176.57 per head, resulting in a value of multiple-trait selection for average daily gain and marbling MBVs of $30.43 ($176.57 - $146.14) per head.

Similar analyses are conducted for each pairwise combination of the seven MBVs to determine the value of genetic information when simultaneously managing or selecting for multiple economically relevant traits (table II-9). Results indicate that the highest value of multiple-trait marker-assisted management is realized when simultaneously managing yield grade and rib-eye area MBVs, $0.79 ($146.93 - $146.14) per head. Similar to single-trait management, the economic impacts of the rib-eye area MBV appear to be more sensitive to days-on-feed than other economically relevant traits. The highest value of multiple-trait marker-assisted selection is realized when selecting for MBVs characterizing hot-carcass weight and marbling, $37.56 ($183.70 - $146.14) per head. Although selecting cattle based on multiple economically relevant traits increases the expected value of genetic information, this information is generally subadditive.[18] This result is intuitive given the positive correlation among many of the marker panels. The values reported in table II-9 may underestimate the value of genetic information that would be available if the entire profile of genetic information were used.

We estimate the value of the entire profile of genetic information by "indexing" animals based on performance (optimal days-on-feed). Because this approach is slightly different from the previous analyses, it requires that we estimate a new "base" scenario. That is, the stochastic simulation is reassessed, holding placement weight, gender, and hide color constant at their mean values. Results indicate that if a feedlot were restricted to pick a uniform marketing date for all cattle, maximum expected profits of $142.68 per head would be realized at 189 days-on-feed. Cattle are then indexed based on their individual genetic performance. That is, the expected profit maximizing days-on-feed is determined for each individual animal in the sample. However, because individual

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[18] The value of simultaneously selecting for two traits is less than the sum of the values when selecting for each trait individually.

management is cost prohibitive, cattle are divided into quartiles based on each animal's optimal days-on-feed. The ability to sort cattle into quartiles based on the performance of their entire genetic profile increases expected profit to $144.97 per head, resulting in a value of marker-assisted management of $2.29 per head ($144.97 - $142.68).[19]

Conclusions

This study estimates the expected value of genetic information at the feedlot stage. Using data from 5,353 feedlot cattle, prediction equations for growth and carcass traits average daily gain, dressing percentage, yield grade, and quality grade are estimated using live-animal characteristics and molecular breeding values for seven economically relevant traits. Prediction equations and a multivariate normal distribution of error terms are used as part of a stochastic simulation to estimate expected profit per head for each day-on-feed. A grid search is employed to determine the optimal number of days-on-feed and maximum expected profits both with and without genetic information.

The expected value of genetic information for marker-assisted management is low when sorting cattle into management groups for one or two economically relevant traits (less than $1 per head) and when cattle are sorted based on their entire profile of genetic information (less than $3 per head). However, the value associated with selecting and feeding cattle based on genetic potential is rather high (as much as $22 per head for single-trait selection and $38 per head for multiple-trait selection). Should feedlots have the opportunity to obtain genetic information prior to purchasing feeder cattle, the values of marker-assisted selection reported here may be of value in determining

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[19] Dividing cattle into quartiles based on each animal's individual profit-maximizing number of days-on-feed allows us to generate a value of the entire profile of genetic information that is comparable to the other values of genetic information reported here. However, the expected profit when each animal is fed for its own optimal number of days-on-feed is $153.56 per head. This figure results in a much higher value of marker-assisted management of $10.88 per head ($153.56 - $142.68).

bid-price differentials. Even with improved accuracy of genetic marker panels for economically relevant traits, the qualitative implications of these results are similar to those reported in previous literature evaluating the value of genetic testing for leptin genotype (DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008). This study identifies average daily gain and marbling as the most economically relevant feedlot cattle traits. The estimated values of marker-assisted management and marker-assisted selection reported in this study may be overestimates of their true values if the same information could be obtained by visual appraisal. Although a hide-color dummy variable is used to partially control for breed effects, additional characteristics, such as frame size and muscling, may be observable independent of breed. Therefore, estimated values of genetic information are likely an upper bound for traits that may have the potential to be partially determined without genetic testing.

To put the results of this study into context, consider that the net returns to finishing steers and heifers in Kansas have averaged -$31.45 and -$19.32 per head over the past ten years (Tonsor and Dhuyvetter, 2013). The values of marker-assisted selection reported here represent meaningful economic value to the cattle feeding industry. Comparing the value of information with the cost of genetic testing services is also instructive. Currently, Igenity offers a profile of marker panels that includes each of the traits evaluated in this study (except hot-carcass weight and days-on-feed) for $38.00 per head (Igenity, 2013b).[20] Despite the low value of using genetic information to sort and optimally choose days-on-feed, the potential for using such strategies remains. As genomic testing technology continues to advance, the potential for declining costs of genetic testing and the development of markers for other important feedlot profit drivers, such as disease resistance and feed efficiency, may lead to cost-effective marker-assisted management in the feedlot sector (Van Eenennaam and Drake, 2012). In addition, random sampling could be used to measure the genetic potential of a group of cattle without having to test each animal. Still, the functional value of genetic

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[20] This profile also includes additional traits not included in this study, such as maternal calving ease, docility, and stayability.

information at the feedlot stage continues to be the ability to improve the genetic distribution of cattle entering the feedlot. These improvements will need to take place in the industry's breeding sectors. In particular, selection for desirable traits in the seed-stock sector will accelerate the rate of genetic gain (Weaber and Lusk, 2010; Van Eenennaam, Werf, and Goddard, 2011). However, selecting breeding stock for traits that are valuable in the feedlot sector may or may not be advantageous in other sectors. Although beyond the scope of this research, the impacts of these traits on other sectors must be considered.

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Table II-1. Summary Statistics for Live-Animal, Carcass Performance, and Molecular Breeding Value Characteristics (n=5,353)

Variable	Mean	Standard Deviation	Minimum	Maximum
Live-Animal and Carcass Performance				
Placement weight (cwt)	6.83	1.22	2.94	11.16
Steer[a]	0.74			
Black[b]	0.68			
Average daily gain (lbs/day)	3.33	0.77	0.42	6.52
Days-on-feed	165.45	34.09	81.00	308.00
Final live weight (cwt)	12.09	1.42	7.06	17.27
Hot-carcass weight (cwt)	7.58	0.95	4.58	11.06
Dressing percentage	0.63	0.03	0.49	0.83
Rib-eye area (in^2)	12.90	1.66	8.30	20.90
Calculated yield grade	2.86	0.69	0.06	5.71
Marbling score	412.32	76.86	190.00	830.00
Molecular Breeding Values (MBV)				
Average daily gain MBV	0.18	0.10	–0.19	0.48
Hot-carcass weight MBV	27.63	9.24	–17.73	55.91
Yield grade MBV	–0.06	0.07	–0.34	0.21
Rib-eye area MBV	–0.63	0.51	–2.16	1.59
Marbling MBV	–22.53	28.24	–119.37	68.26
Tenderness MBV	–1.18	1.43	–5.90	2.92
Days-on-feed MBV	–2.58	2.99	–14.35	8.49

Notes: Molecular breeding values (MBVs) are reported in units of the trait, and reflect the differences expected in animals across breeds compared to their contemporaries (Igenity, 2013a). Therefore, mean MBVs offer little insight. Instead, the range of MBVs is more informative. For example, the range of average daily gain MBVs suggests that the animal with the highest genetic potential for average daily gain in the sample would be expected, on average, to gain approximately 0.67 lbs per day more than the animal with the lowest genetic potential for average daily gain [0.48 - (-0.19)].
[a] Steer is a dummy variable equal to 1 if the animal was a steer and 0 otherwise.
[b] Black is a dummy variable equal to 1 if the animal was black hided and 0 otherwise.

Table II-2. Empirical Distribution of Yield Grade and Quality Grade (n=5,353)

Quality Grade	Yield Grade					Total
	1	2	3	4	5	
Standard	0.0118	0.0155	0.0047	0.0006	0.0000	0.0325
Select	0.0620	0.2285	0.1364	0.0082	0.0002	0.4353
Low Choice	0.0211	0.1775	0.2057	0.0196	0.0009	0.4248
Average Choice	0.0024	0.0271	0.0404	0.0058	0.0002	0.0758
High Choice	0.0013	0.0080	0.0116	0.0041	0.0002	0.0252
Prime	0.0000	0.0024	0.0032	0.0007	0.0000	0.0064
Total	0.0986	0.4590	0.4018	0.0390	0.0015	1.0000

Table II-3. Yield Grade, Quality Grade, and Carcass Weight Premiums and Discounts for Price Grid

Grid Component	Premium/ (Discount)
	$/cwt.
Base Price[a]	$201.71
Yield Grade (YG) Adjustment	
YG < 2	$4.58
$2 \leq$ YG < 3	$2.18
$3 \leq$ YG < 4	$0.00
$4 \leq$ YG < 5	($9.25)
YG ≥ 5	($15.02)
Quality Grade Adjustment	
Prime	$19.40
Choice	$0.00
Select	($2.69)
Standard	($17.87)
Hot-Carcass Weight (HCW) Adjustment	
HCW < 500	($25.48)
$500 \leq$ HCW < 550	($19.62)
$550 \leq$ HCW < 600	($3.89)
$600 \leq$ HCW < 900	$0.00
$900 \leq$ HCW < 950	($0.24)
$950 \leq$ HCW < 1000	($0.24)
HCW ≥ 1000	($21.99)

Notes: Discounts are designated by parentheses.

Source: U.S. Department of Agriculture, Agricultural Marketing Service, 2013b.

[a] The base price is the five-area weighted average for 65%--80% USDA Choice dressed weight for mixed lots of steers and heifers.

Table II-4. Dry Matter Intake Empty Body Fat Adjustment Factor for Beef Cattle

Empty Body Fat Percentage (EBF)	Body Fat Adjustment Factor (BFAF)
EBF < 23.8	1.00
23.8 ≤ EBF < 26.5	0.97
26.5 ≤ EBF < 29.0	0.90
29.0 ≤ EBF < 31.5	0.82
EBF ≥ 31.5	0.73

Source: National Research Council (2000).

Table II-5. Mixed Model Regression Results for Average Daily Gain, Dressing Percentage, Yield Grade, and Quality Grade Prediction Equations (n=5,353)

	Equation			
Variable	*ADG*	*DP*	*YG*	*QG*
Constant	2.2582*	0.3830**	1.0798	218.1700**
Placement weight	0.1805	0.0094**	0.2079***	22.8606***
Days-on-feed	0.0097	0.0019*	0.0039	1.2387**
Days-on-feed^2	−2.00E−05	−3.55E−06*	2.69E−06	−0.0006
Placement weight × days-on-feed	−0.0014*	−4.00E−05	−0.0006	−0.1145***
Steer	0.3923***	0.0001	−0.1452***	−34.2965***
Black	0.0225*	−0.0003	0.0217	4.0083**
Average daily gain MBV	0.3877***	−0.0055*	0.0081	−11.6896
Hot-carcass weight MBV	0.0026**	0.0001***	0.0024	0.3596***
Yield grade MBV	0.2221**	−0.0089	−0.7557***	−10.1476**
Rib-eye area MBV	−0.0341	0.0023	−0.3241***	−9.3658***
Marbling MBV	0.0004	−7.89E−06	−0.0022	0.1504
Marbling MBV × days-on-feed	—	—	2.40E−05**	0.0033***
Tenderness MBV	0.0126**	0.0002	0.0018	−0.8510
Days-on-feed MBV	1.00E−05	−3.00E−05	−0.0040*	−0.4305
Random effects[a]				
Set	0.2185*	0.0005*	0.1219	60.8511
Contemporary group	0.1104***	0.0002***	0.0370***	491.6800***

Notes: Joint tests for marbling molecular breeding value (MBV) and marbling MBV, days-on-feed interactions are statistically significant at the 1% level in both the *YG* (df=2, 5128; *F*=41.44) and *QG* (df=2, 5128, *F*=306.91) equations. Single, double, and triple asterisks (*, **, ***) denote significance at the 10%, 5%, and 1% levels. Dependent variables in the four equations are average daily gain (*ADG*), dressing percentage (*DP*), calculated yield grade (*YG*), and marbling score (*QG*).
[a] Random effects for set and contemporary groups nested within sets are included in the estimation of each equation, (i.e., mixed model regression, Greene, 2012). Sets represent a different commercial feedlot and/or time period, and contemporary groups are groups of animals that have had an equal opportunity to perform.

Table II-6. Maximum Expected Profit ($/head) and Optimal Days-on-Feed for Quartiles of Economically Relevant Molecular Breeding Values

Molecular Breeding Value	Quartile			
	Q1	Q2	Q3	Q4
Average daily gain				
Expected profit	$125.19	$140.23	$151.61	$168.35
Days-on-feed where expected profit is maximized	181	184	185	187
Hot-carcass weight				
Expected profit	$129.21	$141.46	$149.73	$164.56
Days-on-feed where expected profit is maximized	185	184	187	186
Yield grade				
Expected profit	$158.42	$147.69	$143.53	$135.06
Days-on-feed where expected profit is maximized	187	184	185	185
Rib-eye area				
Expected profit	$161.83	$154.00	$145.37	$125.34
Days-on-feed where expected profit is maximized	192	188	185	181
Marbling				
Expected profit	$121.05	$140.93	$156.57	$167.41
Days-on-feed where expected profit is maximized	181	185	185	188
Tenderness				
Expected profit	$143.05	$142.21	$146.47	$152.98
Days-on-feed where expected profit is maximized	187	185	185	184
Days-on-feed				
Expected profit	$149.46	$146.65	$146.62	$141.93
Days-on-feed where expected profit is maximized	187	185	185	183

Notes: If all cattle are fed for the same number of days-on-feed, maximum expected profit of $146.14 per head would be realized at 185 days-on-feed.

Table II-7. Expected Value of Marker-Assisted Management and Marker-Assisted Selection at the Feedlot Stage for Molecular Breeding Values Characterizing Economically Relevant Traits

	Value of Information	
Molecular Breeding Value	Marker-Assisted Management	Marker-Assisted Selection
	———— $/head ————	
Average daily gain	$0.20	$22.21
Hot-carcass weight	$0.10	$18.42
Yield grade	$0.03	$12.28
Rib-eye area	$0.49	$15.69
Marbling	$0.35	$21.27
Tenderness	$0.04	$6.84
Days-on-feed	$0.02	$3.31

Notes: The value of marker-assisted management is calculated by comparing expected profit when a feedlot can differentially choose optimal marketing dates for each quartile of a given trait relative to the case where all cattle are fed for the same number of days-on-feed. The value of marker-assisted selection at the feedlot stage is calculated by comparing expected profits for the best performing quartile relative the case where all cattle are fed for the same number of days-on-feed.

Table II-8. Maximum Expected Profit ($/head), Optimal Days-on-Feed, and Effective Proportion of Management Groups for Simultaneous Management of Average Daily Gain and Marbling Molecular Breeding Values

Quartile for Marbling Molecular Breeding Value	Quartile for Average Daily Gain Molecular Breeding Value			
	Q1	Q2	Q3	Q4
Q1	$111.13	$120.79	$132.02	$146.40
	(181)	(180)	(181)	(184)
	[0.11]	[0.07]	[0.05]	[0.02]
Q2	$127.58	$139.82	$144.21	$159.82
	(183)	(187)	(185)	(185)
	[0.07]	[0.07]	[0.06]	[0.05]
Q3	$141.66	$148.72	$159.73	$169.56
	(180)	(189)	(188)	(190)
	[0.04]	[0.07]	[0.07]	[0.07]
Q4	$149.80	$161.49	$164.69	$176.57
	(188)	(188)	(188)	(192)
	[0.03]	[0.04]	[0.07]	[0.11]

Notes: Numbers in parentheses are days-on-feed for each group where expected profit ($/head) is maximized. Numbers in brackets are the proportion of cattle in the sample for each group.

Table II-9. Expected Value of Marker-Assisted Management and Marker-Assisted Selection at the Feedlot Stage for Pairwise Combinations of Molecular Breeding Values Characterizing Economically Relevant Traits

Pairwise Combinations of Molecular Breeding Values	Value of Information	
	Marker-Assisted Management	Marker-Assisted Selection
	———— $/head ————	
Average daily gain-Hot-carcass weight	$0.37	$33.58
Average daily gain-Yield grade	$0.39	$31.92
Average daily gain-Rib-eye area	$0.66	$26.44
Average daily gain-Marbling	$0.47	$30.43
Average daily gain-Tenderness	$0.42	$30.07
Average daily gain-Days-on-feed	$0.38	$23.87
Hot-carcass weight-Yield grade	$0.22	$31.83
Hot-carcass weight-Rib-eye area	$0.70	$32.61
Hot-carcass weight-Marbling	$0.50	$37.56
Hot-carcass weight-Tenderness	$0.30	$28.80
Hot-carcass weight-Days-on-feed	$0.23	$23.76
Yield grade-Rib-eye area	$0.79	$24.38
Yield grade-Marbling	$0.49	$27.15
Yield grade-Tenderness	$0.26	$16.86
Yield grade-Days-on-feed	$0.15	$16.75
Rib-eye area-Marbling	$0.67	$23.08
Rib-eye area-Tenderness	$0.70	$20.25
Rib-eye area-Days-on-feed	$0.62	$22.08
Marbling-Tenderness	$0.59	$23.94
Marbling-Days-on-feed	$0.47	$24.00
Tenderness-Days-on-feed	$0.23	$10.52

Notes: The value of marker-assisted management is calculated by comparing expected profit when a feedlot can differentially choose optimal marketing dates for each quartile of a given trait relative to the case where all cattle are fed for the same number of days-on-feed. The value of marker-assisted selection at the feedlot stage is calculated by comparing expected profits for the best performing quartile relative the case where all cattle are fed for the same number of days-on-feed.

CHAPTER III

USING GENETIC TESTING TO IMPROVE FED CATTLE MARKETING DECISIONS[*]

Abstract

We estimate the value of using genetic information to make fed cattle marketing decisions. Efficiency gains result from sorting cattle into marketing groups, including more accurate optimal days-on-feed and reduced variability of returns to cattle feeding. The value of using genetic information to selectively market cattle ranged from $1-$13/head depending on how a producer currently markets cattle and the grid structure. Although these values of genetic information were generally higher than those reported in previous research, they were still not enough to offset the current cost of genetic testing (about $40/head).

Keywords: Fed cattle marketing, genetics, molecular breeding value, risk aversion, value of information

Introduction

The beef industry has promoted value-based marketing strategies since the early 1990s in an effort to improve the quality and consistency of beef products (National Cattlemen's Beef

Association [NCBA], 1990). Most notably, grid pricing, introduced in the mid-1990s, provides transparent price signals. Traditional cash pricing mechanisms, such as live weight and dressed weight pricing, are not based on the actual quality and yield grade of carcasses. As a result, above-average cattle are paid less than their cutout value and below-average cattle are paid more than their cutout value. Therefore, traditional pricing mechanisms inhibit information flow from beef consumers to cattle producers (Feuz, Fausti, and Wagner, 1993; Fausti, Feuz, and Wagner, 1998). Grid pricing, on the other hand, determines value based on the carcass merit of each individual animal. Premiums and discounts that make up the grid reflect consumer preferences and transmit these signals upstream to cattle producers. Feedback on individual carcass performance and value provides an incentive for producers to make necessary changes to "their breeding, feeding, and sorting programs" (Johnson and Ward, 2005, p. 562).

The National Beef Quality Audit (NBQA) reported that the share of fed cattle marketed on a grid increased from 15% in 1995 to 34% in 2005 (NCBA, 2006). However, grid pricing has yet to become the dominant fed cattle marketing strategy as many projected (Schroeder et al., 2002), accounting for only 40%-45% of fed cattle marketings (Fausti et al., 2010). While there is ample literature investigating producer incentives and disincentives to adopt grid pricing, the fundamental marketing risk created by the system has been identified as the primary barrier to adoption (Fausti, Feuz, and Wagner, 1998; Anderson and Zeuli, 2001; Fausti and Qasmi, 2002). Depending on the sample period, live weight, dressed weight, or grid pricing can have the highest returns, but variability is consistently highest for grid pricing (Feuz, Fausti, and Wagner, 1993; Schroeder and Graff, 2000; Anderson and Zeuli, 2001; Fausti and Qasmi, 2002; Lusk et al., 2003). This problem is further exacerbated by varying levels of risk aversion among cattle producers (Fausti and Feuz, 1995; Feuz, Fausti, and Wagner, 1995; Fausti et al., 2013; Fausti et al., 2014).

The risk associated with buying and selling fed cattle has two main components: general price risk and informational (or carcass) risk (Fausti and Feuz, 1995). In this paper we focus on the carcass risk associated with marketing fed cattle. That is, because marketing decisions are made prior

to slaughter, carcass merit (yield grade, quality grade, and hot-carcass weight) is unknown. Therefore, better predictions of carcass quality may allow decision makers to improve their marketing decisions. Recent technological advancements in beef production, such as ultrasound technology and genetic testing, have made such information available. However, a producer would only be expected to use this technology if its benefits outweigh the costs. As a result, a branch of the agricultural economics literature evaluating the economic benefits of these technologies has emerged (Fausti et al., 2010).

For example, Lusk et al. (2003) and Walburger and Crews (2004) reported that using ultrasound technology to selectively market cattle, as opposed to simply marketing all cattle on a live weight, dressed weight, or grid basis, increased revenue by $4 to $32/head. However, both of these studies held days-on-feed constant when making these comparisons. Koontz et al. (2008) contend that such an approach uses additional information to exploit pricing inefficiencies and is unlikely to change returns to producers in the long run. Therefore, they argue that improving meat quality and beef industry profitability requires changing the product form. They found that using ultrasound measurements to sort cattle into groups that were marketed to optimize returns by choosing days-on-feed was between $15 and $25/head (Koontz et al., 2008).

Advancements in the field of cattle genomics have made genetic marker panels for a variety of traits commercially available. Independent validations have found many of these markers to be correlated with the traits they are designed to predict (DeVuyst et al., 2011; National Beef Cattle Evaluation Consortium, 2015). While previous literature has found considerable economic value (up to $60/head) to using genetic information for selecting feeder cattle for placement in the feedlot (DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008; Thompson et al., 2014), this information is not typically available prior to purchasing feeder cattle. Therefore, feedlots are limited to using this information to sort cattle into management groups that are most likely to achieve similar outcomes, or marker-assisted management (Van Eenennaam and Drake, 2012). In previous research, marker-assisted management has been limited to sorting cattle by optimal days-on-feed. As a result, reported values of genetic information for marker-assisted management have consistently been less than

$3/head (DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008; Thompson et al., 2014). Still, there remains potential for using the information derived from genetic testing to improve other management decisions within the feedlot that have yet to be evaluated, including how cattle are fed, how technologies such as implants and beta agonists are utilized, and how cattle are marketed.

Therefore, using the same dataset of genetic information and phenotypic outcomes for 10,209 commercially-fed cattle as Thompson et al. (2014), we evaluate for the first time a marker-assisted management scenario in which genetic information is used to selectively target cattle to different marketing methods. The objective of this research is to estimate the expected value of genetic information for improving fed cattle marketing decisions, including decisions for both marketing method (live weight, dressed weight, or grid pricing) and timing to market (days-on-feed). Although several previous studies have attempted to estimate the value of genetic information, none have considered the potential of this information to improve fed cattle marketing decisions, other than days-on-feed. Therefore, the results of this analysis represent an important and unique contribution to the literature evaluating the economic value of genetic testing for beef cattle. In addition, previous research evaluating fed cattle marketing decisions examined either marketing method or optimal days-on-feed, but did not evaluate both of these decisions simultaneously. This is important because accurately targeting cattle to the appropriate marketing method is only economically beneficial if cattle are appropriately managed once they are at market.

Data collected from commercially-fed cattle are used to estimate regression equations characterizing phenotypic outcomes for average daily gain, dressing percentage, yield grade, and quality grade as a function of live-animal characteristics and genetic information. These equations and Monte Carlo integration are used to estimate expected net returns and expected utility for several marketing scenarios. Three baseline scenarios are created in which all cattle are marketed in a single group on a live weight, dressed weight, or grid basis without using of any genetic information. These baseline scenarios are then compared with alternative marketing scenarios in which genetic information is known and used to sort cattle into groups to be targeted to specific marketing methods.

Conceptual Framework

Cattle feeders are assumed to maximize expected profit by choosing both how and when to market cattle. At placement in the feedlot, placement weight and purchase cost are the only variables known with certainty. Other profit determinants are a function of random growth and carcass characteristics, including average daily gain (ADG), dressing percentage (DP), yield grade (YG), and quality grade (QG). Although we assume that at the time marketing decisions are made output prices are known by the decision maker, it is unknown how animals will perform and, as a result, what weight and carcass quality they will achieve. Therefore, the feedlot operator's expected profit maximization problem can be written as

$$(1) \qquad \max_{\substack{j \in \{1,2,3\} \\ DOF_j \geq 0}} \iiiint E\pi_{ij}\left(DOF_j, ADG_i, DP_i, YG_i, QG_i\right) \times$$

$$f(ADG, DP, YG, QG)dADGdDPdYGdQG \quad \forall \ i = 1, \dots, n.$$

where the feeder chooses the jth marketing method that maximizes expected profit for each ith animal and the optimal days-on-feed for each marketing group (DOF_j).

However, depending on their risk preferences, decision makers may not always prefer the alternative that generates the highest expected profit. Instead, preferences may also be influenced by the variability, covariance, and higher moments of the joint distribution of returns for each marketing alternative and the correlation of these returns among animals. Therefore, the single-animal objective function in equation (1) can be converted into an aggregate expected utility maximizing portfolio of marketing strategies for a group of n animals

$$(2) \qquad \max_{\substack{p_{ij} \in \{0,1\} \\ DOF_j \geq 0 \\ i=1,\dots,n \\ j=1,2,3}} \iiiint EU\left[\sum_{i=1}^{n}\sum_{j=1}^{3} p_{ij}\pi_{ij}\left(DOF_j, ADG_i, DP_i, YG_i, QG_i\right)\right]$$

$$\times f(ADG, DP, YG, QG)dADGdDPdYGdQG$$

$$s.t. \sum_{j=1}^{3} p_{ij} = 1 \ \forall \ i,$$

where $U[\pi(\cdot)]$ is a constant absolute risk aversion (CARA) utility function and the feeder chooses

whether or not the ith animal is targeted to the jth marketing method (p_{ij}) and the days-on-feed

(DOF_j) for each jth marketing group. Under the assumption of risk neutrality ($U'' = 0$), equation (2)

reduces to an expected profit maximization problem similar to equation (1) given that the risk-neutral

solution for the aggregate and individual-animal objective functions are equivalent.

Fed cattle are primarily marketed by live weight pricing ($LIVE$), dressed weight pricing

($DRES$), and grid pricing ($GRID$). These three marketing methods differ primarily by whether the

buyer or the seller bears the risk of carcass outcomes. When using live weight pricing, the packer and

the feeder generally negotiate a carcass price based on the expected quality traits of a pen of cattle

assessed through visual appraisal. This carcass price is then converted to a live-animal price by

multiplying it by the expected dressing percentage. Net return for this scenario can be written

(3) $\pi_{LIVE} = P_{LIVE} \times FWT(PWT, ADG, DOF) \times (1 - PS) \times (1 - MR) - PC(PWT, SEX)$

$$- FC(DOF) - YC(DOF) - IC(PC, DOF),$$

where P_{LIVE} is the live weight price, FWT is final live weight which is a function of placement

weight (PWT), ADG, and DOF, as $FWT = PWT + ADG \times DOF$, $PS \in [0, 1]$ is pencil shrink,

$MR \in [0, 1]$ is mortality rate, PC is purchase cost of feeder cattle, FC is feed cost, YC is yardage cost,

and IC is interest cost on the purchase of feeder cattle. Under this alternative the buyer takes on all of

the carcass risk. Because these characteristics can be difficult to predict preharvest, live prices tend to

undervalue high-quality cattle and overvalue low-quality cattle. Notice that the cost of genetic testing

is not included in equation (3). Therefore, π_{LIVE} is defined as net return and not profit and the

improvement in the objective function from acquiring genetic information sets an upper limit on the

cost of genetic testing.

Marketing cattle on a dressed basis is similar to live weight pricing, except that the producer is paid based on the actual dressed weight, or hot-carcass weight, and the seller assumes the dressing percentage risk. In principle, the dressed price will be comparable to the live price adjusted for dressing percentage for the same pen of cattle. However, over time the average dressed price is expected to be greater than the average live price adjusted for dressing percentage given packers' incentive to offset errors in estimating dressing percentage (Feuz, Fausti, and Wagner, 1993). Net return for dressed weight pricing is

$$(4) \qquad \pi_{DRES} = P_{DRES} \times HCW(PWT, ADG, DOF, DP) \times (1 - MR) - PC(PWT, SEX)$$
$$- FC(DOF) - YC(DOF) - IC(PC, DOF) - TC,$$

where P_{DRES} is dressed weight price and HCW is hot-carcass weight which is a function of PWT, ADG, DOF, and DP, $HCW = [PWT + (ADG \times DOF)] \times DP$, and TC is transportation cost. When cattle are sold on a dressed weight basis (or grid basis) the seller pays the transportation cost, whereas the buyer generally pays for trucking when cattle are sold based on live weight (Ward, Schroeder, and Fuez, 2001). So, transportation cost was not included in equation (3) above.

Lastly, when marketing cattle on a grid, the seller assumes the yield grade, quality grade, and dressing percentage risk for each individual animal. Net return is

$$(5) \qquad \pi_{GRID} = P_{GRID}(YG, QG, HCW) \times HCW(PWT, ADG, DOF, DP) \times (1 - MR)$$
$$- PC(PWT, SEX) - FC(DOF) - YC(DOF) - IC(PC, DOF) - TC,$$

where P_{GRID} is the grid price which is a function of YG, QG, and HCW outcomes. Although grids vary across the packing industry, they generally list a base price (P_{BASE}) for yield grade 3, Choice carcasses weighing between 600-900 pounds. Depending on how each carcass grades this base price is then subject to an additive set of premiums and discounts for yield grade, quality grade, and weight outcomes, $P_{GRID} = P_{BASE} + premiums/discounts(YG, QG, HCW)$. In practice, packers use a variety of methods for determining the base price. Here we use Ward, Feuz, and Schroeder's (1999) formula to determine the base price,

$P_{BASE} = P_{DRES} + [(Choice/Select\ spread) \times (plant\ average\ percent\ Select)]$, where we assume the plant average percent Select is equal to the percentage of animals that graded Select or lower in our data set (45%).

Stigler (1961) first developed the economics of information, which has since been extended to many agricultural settings, including the value of genetic information in livestock production (e.g., Ladd and Gibson, 1978). The value of information is calculated as "the difference between expected returns (or utility) using the information and expected returns without the information, with both expectations taken with respect to the more informed distribution" (Babcock, 1990, p.63).

Data

Data for 10,209 commercially-fed cattle from six different Midwestern feed yards were provided by Neogen, the parent company of commercial testing service Igenity.[21] Cattle represented year-round placements in the years 2007 and 2008. At placement, animals were weighed and a hair sample or tissue punch from ear tag application was collected for genetic testing. Genetic information was provided in the form of molecular breeding values (MBVs) for the following seven traits: yield grade, marbling, average daily gain (lbs./day), hot-carcass weight (lbs.), rib-eye area (in^2), tenderness (lbs. of Warner-Bratzler shear force [WBSF]), and days-on-feed (days) (Igenity, 2013).[22] The correlations among these seven MBVs are reported in table III-1. Molecular breeding values are a continuous representation of an animal's genetic potential to express a given trait. Similar to expected progeny differences (EPDs), MBVs are reported in the units of the trait they represent. However, they are interpreted as the "relative differences expected in animals across breeds compared to their

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[21] At least half of the cattle were fed in Iowa and Kansas.

[22] Each of these markers, except hot-carcass weight and days-on-feed, have been found to be significantly correlated with the traits they are designed to predict in independent validations (DeVuyst et al., 2011; National Beef Cattle Evaluation Consortium, 2015).

contemporaries" (Igenity, 2013, p. 2). For example, if two animals exposed to the same environmental and management conditions have marbling MBVs of -100 and 100, respectively, we would expect, on average, that these two animals' marbling scores would differ by 200 units (100 - [-100] = 200). Additional live-animal characteristics for days-on-feed, sex, and hide color were also provided, and carcass measurements for calculated yield grade, marbling score, and hot-carcass weight were collected at slaughter.

After deleting observations with missing data for live-animal characteristics and MBVs there were 9,465 observations. The data consisted of seven "sets" each of which represented a different commercial feedlot, time period, or both. Nested within each set were contemporary groups which were groups of animals that had an equal opportunity to perform: same sex, managed alike, and exposed to the same feed resources. A total of 242 contemporary groups had an average size of 39 animals per group.

Additional missing data were common for growth and carcass performance variables. Average daily gain, calculated yield grade, and marbling score had 1,795, 25, and 421 missing observations, respectively, and there were 3,692 missing observations for final live weight. Although final live weight was not used directly, it was essential to the estimation of dressing percentage (dressing percentage = hot-carcass weight/final live weight). Observations with missing data for these growth and carcass performance variables were not deleted from the sample. Instead, regression equations characterizing these outcomes were estimated with their own maximum number of observations. Subsequent simulation analyses used the sample of 9,465 complete observations for live-animal characteristics and MBVs. Summary statistics for growth and carcass performance, live-animal characteristics, and MBVs are reported in table III-2.

A joint distribution of observed yield and quality grade outcomes for the cattle in our sample is reported in table III-3. The majority of cattle graded either yield grade 2 (44%) or 3 (37%) and quality grade Choice (54%) or Select (42%), and the single most likely outcome is yield grade 3, Choice (24%). This distribution is similar to the distribution of yield grade and quality grade

outcomes reported in the 2011 NBQA, which represented 7,941 animals from 28 federally-inspected beef processing facilities throughout the United States (Moore et al., 2012, p. 5146). Therefore, our sample is representative of the current distribution of carcass quality in the U.S. beef industry.

The relationship between live weight and dressed weight prices fluctuates throughout the year. Therefore, a simple average of weekly prices for the 2014 marketing year was used to avoid seasonal fluctuations in live weight and dressed weight prices. Weekly prices were obtained from Livestock Marketing Information Center (LMIC) spreadsheets that are based on USDA Agricultural Marketing Service (AMS) reports (LMIC, 2015). Live weight and dressed weight prices for steers and heifers were obtained from the *5 Area Weekly Weighted Average Direct Slaughter Cattle Report*, LM_CT150 (USDA AMS, 2015a), and grid premiums and discounts were from the *5 Area Weekly Weighted Average Direct Slaughter Cattle Report – Premiums and Discounts*, LM_CT169 (USDA AMS, 2015b) (table III-4). Two additional grids representing the weeks with the maximum (September 22, 2014) and minimum (February 2, 2014) Choice-Select spread for 2014 were also evaluated to determine the sensitivity of our results to seasonal changes in the grid (table III-4).

It is unknown how or when animals were weighed. Therefore, net returns to the baseline live weight and dressed weight marketing scenarios were "calibrated" using pencil shrink to impose market efficiency between these two marketing methods. That is, any inconsistencies in the relationship between actual (not simulated) final live weight and hot-carcass weight were standardized by increasing pencil shrink until the net returns for the live weight and dressed weight baseline marketing scenarios were equal. Pencil shrink was assumed to be 2%.

Feed costs were needed to calculate expected net returns. Given that observations of feed intake were unavailable, a dry matter intake (DMI) model was used following the National Research Council's (NRC) *Nutrient Requirements of Beef Cattle* (NRC, 2000).[23] The DMI model estimates "standardized" feed intake. Additional information needed to estimate expected net returns include a

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[23] For examples of the dry matter intake model see Lusk (2007) or Thompson et al. (2014).

dry matter feed cost of $230/ton ($0.12/lb.), yardage cost of $0.40/day, a 7% interest rate on the

purchase of feeder cattle, a mortality rate of 1%, and transportation cost of $16/head (Lardy, 2013;

Ellis and Schulz, 2015).

Procedures

Predicting Growth and Carcass Performance Using Genetics

Mixed model regression equations characterizing phenotypic outcomes for average daily gain (AGD),

dressing percentage (DP), yield grade (YG), and quality grade (QG) were estimated independently

using restricted maximum likelihood (REML). Dependent variables in each of the four equations

were continuous. In particular, YG and QG are often thought of in terms of discrete outcomes.

However, calculated yield grade, as defined by the USDA AMS, is a continuous function of backfat,

kidney, pelvic, and heart fat, hot-carcass weight, and rib-eye area (USDA AMS, 1997), and marbling

score was used as a continuous representation of quality grade. Marbling scores between 200-299 are

said to have traces of intramuscular fat and are graded Standard, 300-399 are Select, 400-699 are

Choice, and scores over 700 are Prime (USDA AMS, 1997, 2006). The models were

(6) $\quad Y_{ijkl} = \beta_{0l} + PWT_{ijk}\beta_{1l} + DOF_{ijk}\beta_{2l} + DOF_{ijk}^2\beta_{3l} + PWT_{ijk}DOF_{ijk}\beta_{4l} + STR_{ijk}\beta_{5l}$

$$+ BLK_{ijk}\beta_{6l} + \sum_{m=1}^{7} MBV_{ijkm}\beta_{7lm} + v_{jl} + u_{k(j)l} + \varepsilon_{ijkl},$$

were Y_{ijkl} is the dependent variable for the ith animal in the jth set and kth contemporary group for

the lth equation, where $l = 1, 2, 3,$ or 4 for ADG_{ijk}, DP_{ijk}, YG_{ijk}, and QG_{ijk}, respectively. The model

included fixed effects for live-animal characteristics and genetic information, where PWT_{ijk} is

placement weight, DOF_{ijk} is days-on-feed, STR_{ijk} is a dummy variable equal to 1 if the animal was a

steer and 0 otherwise, BLK_{ijk} is a dummy variable equal to 1 if the animal had black hide and 0

otherwise, and MBV_{ijkm} are the seven MBVs characterizing yield grade, marbling, average daily

gain, hot-carcass weight, rib-eye area, tenderness, and days-on-feed. Set random effects,

$v_{jl} \sim N(0, \sigma_v^2)$, contemporary group random effects nested within sets (Greene, 2012),

$u_{k(j)l} \sim N(0, \sigma_u^2)$, and a random error term $\varepsilon_{ijkl} \sim N(0, \sigma_\varepsilon^2)$ are also included in each equation. Yield

grade MBV by days-on-feed and marbling MBV by days-on-feed interaction terms are also included

as slope shifters in the YG and QG equations. In addition, a yield grade MBV by marbling MBV

interaction is also included in the YG and QG equations to account for the positive phenotypic and

genetic correlation between these two carcass traits (DeVuyst et al., 2011; Thompson et al., 2015).

Models were estimated using Proc Mixed in SAS (SAS Institute Inc., 2013). D'Agostino-

Pearson K^2 omnibus test for skewness and kurtosis and a conditional variance test identified evidence

of nonnormality and static heteroskedasticity. Sandwich estimators of the standard errors were

estimated to obtain estimates of standard errors that were consistent in the presence of nonnormality

and static heteroskedasticity (White, 1982). Given the large sample size, asymptotic properties are

relevant, and the small sample biases common with generalized method of moments estimators

should be of little concern.

Expected Net Return Maximization for Alternative Marketing Scenarios

Baseline Marketing Scenarios

To determine the value of genetic information for improving fed cattle marketing decisions, three

baseline marketing scenarios were created in which all cattle were marketed in a single group on a

live weight, dressed weight, or grid basis. Expected net returns are a nonlinear function of the random

terms. Therefore, because of Jensen's inequality, net returns calculated at the expected value of

prediction equations will not equal expected net returns (Greene, 2012). For this reason, the integrals

in equation (1) were evaluated using Monte Carlo integration. The Cholesky decomposition of the

four-by-four variance-covariance matrix of the error terms in equation (6) was calculated and used to

generate a multivariate normal distribution of 200 error terms for each of the four prediction

equations for each animal in the sample ($n = 9,465$) using "intelligent," quasi-random Halton draws

(Morokoff and Caflisch, 1995; Greene, 2012). Net returns were evaluated at each draw using observed MBVs for each animal in the sample, and the average across animals was expected net return. This process was repeated for days-on-feed from 100-200 days, and a grid search was used to determine the day at which expected net return was maximized for each of the three marketing scenarios.

Live-animal characteristics other than MBVs may also influence fed cattle marketing decisions. In particular, placement weight has a substantial impact on how long cattle are fed, how they are marketed, and, as a result, profitability. For this reason, placement weight was held constant at its mean value (700 lbs.) to separate this effect from the effect of genetic information.

Decision makers in the feedlot have access to information that can be used to sort cattle into different marketing groups without using genetic testing. However, access to the information necessary to imitate a "true" baseline marketing scenario is unavailable. Therefore, similar to previous research we assume naïve baseline scenarios in which all animals are marketed in a single group using the same marketing method (Schroeder and Graff, 2000; Lusk et al., 2003; Walburger and Crews, 2004). As a result, expected net returns for the baseline scenarios may be underestimated and the values of information reported here are likely an upper bound on the value of genetic information for selectively marketing fed cattle.

Genetic Information Marketing Scenario

Baseline scenarios were compared with alternative marketing scenarios in which additional information was used to enhance fed cattle marketing decisions. The genetic information marketing scenario used the results of genetic testing to sort cattle into marketing groups based on their expected performance. To do this, a "decision rule" characterizing the relationship between expected net returns for each of the three marketing methods and MBVs for yield grade and marbling was developed using a random sample of 1,000 animals. Twenty discrete values for the yield grade and marbling MBVs were chosen to represent the range of MBVs observed in our sample, and a Monte

Carlo integration procedure similar to the one described above was then used to estimate expected net returns for each unique combination of these values (400 times). Plotting the results on a three dimensional surface allows us to visualize the decision rule by identifying which of the three marketing methods generated the highest expected net returns at various levels of genetic potential for yield grade and marbling.

Applying this decision rule to the data, the full sample of animals ($n = 9,465$) was sorted into three marketing groups (live weight, dressed weight, or grid pricing) based on their actual yield grade and marbling MBVs. Monte Carlo integration was used to estimate expected net returns for each group for days-on-feed from 100-200 days, and a grid search was used to determine the optimal days-on-feed. The overall expected net return was calculated as the weighted average expected net return across the three groups, where the proportion of cattle that fell into each group was used as the weight.

Perfect Information Marketing Scenario

While genetic information can be used to improve predictions of animal performance in the feedlot, it is not 100% accurate.[24] Therefore, we evaluated the potential of genetic testing by estimating a "perfect information" marketing scenario. This was identical to the genetic information marketing scenario described above, except that instead of sorting animals based on genetic information, each animal was sorted into the marketing group that maximized its own expected net return.

Expected Utility Maximization for Alternative Marketing Scenarios

The risk-return tradeoff associated with fed cattle marketing suggests that it is also important to consider how decision makers' risk preferences affect their marketing decisions. Given nonlinearities, the expected utility maximizing solution for a single animal may differ from the solution if that

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[24] For further discussion of the accuracy of genetic marker panels see Weber et al. (2012) and Akanno et al. (2014).

animal was marketed as part of a group. Therefore, the objective function in equation (2) for a group

of n animals is used to determine the optimal portfolio of marketing strategies for the full sample of

animals ($n = 9,465$) for several levels of risk aversion.

Again, three baseline marketing scenarios were created in which all animals were marketed in

a single group using live weight, dressed weight, or grid pricing. Distributions of net returns were

used to calculate expected utility assuming a negative exponential utility function (Chavas, 2004),

$U(\pi) = -e^{-r\pi}$, where $U(\pi)$ is the utility of the aggregate net returns for the full sample of $n = 9,465$

animals and r is the Arrow-Pratt absolute risk aversion coefficient. A range of risk aversion

coefficients were evaluated, and following Raskin and Cochran (1986) and Anderson and Dillon

(1992) risk aversion coefficients of $r = 0.0000003$, $r = 0.0000006$, and $r = 0.0000010$ were

determined to approximately represent slight, moderate, and severe risk aversion, respectively.

The expected utility maximizing portfolio of marketing methods was then determined using a

nonlinear mathematical programming model in GAMS (GAMS, 2013). The expected utility

maximization optimization poses significant computational challenges. The decision problem

involves at least $3^{9465 \times 101}$ possible combinations of marketing strategies and days-on-feed. As an

integer programming problem, this is computationally infeasible to solve. Even after assuming away

the days-on-feed joint decision,[25] there are still 3^{9465} possible combinations of marketing methods. We

explored reducing the number of head of cattle (i.e., genetic profiles) using Gaussian cubature

(DeVuyst and Preckel, 2007) to a representative sample of 22 head that maintained the mean and

variance/covariance structure of the data. The result was a discrete choice problem of 3^{22} or about

31.381 billion combinations of marketing methods. While it may be possible to solve the problem

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[25] Previous research has shown that fed cattle profit functions are often flat near the optimal days-on-

feed (Pannell, 2006; Lusk, 2007). Therefore, days-on-feed for each marketing method is held constant

at their profit maximizing baseline levels (live weight = 151 days, dressed weight = 179 days, and

grid = 181 days).

with several months of computational time, we chose a less computationally intensive approach. We approximated the discrete decision problem with a continuous, nonlinear optimization or the equivalent of a relaxed nonlinear integer optimization. So, the optimization problem simultaneously chose percentages of all animals to market with the three pricing methods. The relaxed nonlinear integer problem took considerably less time to solve (20 minutes to two hours), varying with starting point and risk aversion level.

The marketing scenario with the highest expected utility is the preferred marketing strategy for a given level of risk aversion. However, these values offer little insight into the value of information. For this reason, expected utilities were converted to certainty equivalents, which represent the amount of money a producer would have to receive to be indifferent between that payoff and a given gamble (Chavas, 2004). Given that the expected utility model is based on aggregate net returns, these certainty equivalents were then converted to $/head by dividing by the number of animals in the sample ($n = 9,465$). Differences in certainty equivalents for the expected utility maximizing portfolio of marketing scenarios and the three baseline marketing scenarios for a given level of risk aversion can then be interpreted as the value of information inclusive of risk preferences.

Results and Discussion

Regression Equations

The mixed model regression estimates are reported in table III-5. Each equation was estimated with its own maximum number of observations. Coefficients for live-animal characteristics, including placement weight, days-on-feed, sex, and hide color, generally exhibited the expected relationships.

Molecular breeding values influenced corresponding growth and carcass performance variables in expected directions. For example, the average daily gain MBV had a significant, positive effect in the average daily gain equation. The relative interpretation of MBVs implies a linear relationship with a coefficient of one between MBVs and the traits they characterize (Weber et al.,

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2012). Therefore, we tested the null hypothesis that the marginal effect of the average daily gain MBV was equal to one, $H_0: \partial ADG / \partial MBV_{ADG} = 1$. Results indicated that the observed marginal effect, 0.757, was not statistically different from one (t = -0.79; df = 7,437; P = 0.43).

The hot-carcass weight MBV had a significant, positive effect on dressing percentage outcomes as expected. However, because this MBV does not directly reflect genetic potential for dressing percentage, we were unable to test the hypothesis that this effect was equal to one.

Due to interaction terms, the marginal effect of the yield grade MBV on yield grade outcomes was a function of days-on-feed and marbling MBV: $\partial YG / \partial MBV_{YG} = -0.382 - 0.002 \times DOF + 0.009 \times MBV_{MARB}$. Therefore, the test of the null hypothesis that this marginal effect was equal to negative one, $H_0: \partial YG / \partial MBV_{YG} = -1$,[26] was conducted at the mean value of days-on-feed (176 days) and marbling MBV (-21.661). At these values, the marginal effect was approximately -0.929, and we failed to reject the null hypothesis that this value was negative one (t = 0.46; df = 9,169; P = 0.65).

Similarly, the marginal effect of the marbling MBV on quality grade outcomes was a function of days-on-feed and yield grade MBV: $\partial QG / \partial MBV_{MARB} = -0.148 + 0.005 \times DOF - 0.170 \times MBV_{YG}$. Therefore, the test of the null hypothesis that this marginal effect equals one, $H_0: \partial QG / \partial MBV_{MARB} = 1$, was conducted at the mean value of days-on-feed (176 days) and yield grade MBV (-0.054). At these values, the marginal effect was approximately 0.741, and we rejected the null hypothesis that this value was one (t = -4.45; df = 8,779; P < 0.01). This was consistent with the finding that MBVs underestimate the expected change in phenotypic outcomes relative to a change in MBVs (Weber et al., 2012). Despite advancements in the procedures for estimating MBVs, their accuracy still depends on the persistency of linkage disequilibrium between single nucleotide polymorphisms (SNP) and quantitative trait loci (QTL) and the relationship between training and

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[26] The marginal effect of the yield grade MBV on yield grade outcomes had an expected value of negative one because lower yield grade outcomes are more favorable.

target populations (Akanno et al., 2014). Therefore, it was not surprising that this effect shrunk towards zero when the MBV procedure was applied to new data. Nevertheless, the marginal effect of the marbling MBV was still statistically different from zero ($t = 11.05$; df = 8,779; $P < 0.01$), indicating that higher genetic potential for marbling resulted in more favorable quality grade outcomes.

Expected Net Returns for Alternative Marketing Scenarios

Baseline Marketing Scenarios

For the set of animals used in this analysis and average 2014 prices, maximum expected net returns for the three baseline scenarios in which all animals were marketed in a single group on a live weight, dressed weight, or grid basis was -$35.84, -$34.25,[27] and -$28.03/head, respectively (table III-6). The finding that grid pricing generated the highest returns was consistent with Anderson and Zeuli (2001) and Walburger and Crews (2004). However, live weight and dressed weight pricing have also been found to generate the highest returns in other studies (Feuz, Fausti, and Wagner, 1993; Fausti, Feuz, and Wagner, 1998; Schroeder and Graff, 2000; Lusk et al., 2003). As previously discussed, the marketing method that generated the highest returns depends on prices and quality characteristics of the cattle used in each study. Given the large, representative sample of cattle used in this study, the finding that grid pricing generated the highest returns suggests that the market has already started to adjust to higher quality animals being targeted towards grid pricing. This is consistent with Fausti et al. (2014) who found that the grid premium and discount structure is adjusting market signals to encourage producers to market on a grid and discourage live weight and dressed weight pricing.

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[27] Calibration of live weight and dressed weight baseline marketing scenarios to market efficiency was conducted using actual final live weights and hot-carcass weights. Therefore, when applied to simulation analyses values of expected net returns for live weight and dressed weight marketing scenarios differed slightly due to differences in optimal days-on-feed.

Although grid pricing generated the highest expected net returns, it also had the highest standard deviation ($33.49). This result was consistent with the findings of previous research (Feuz, Fausti, and Wagner, 1993; Schroeder and Graff, 2000; Anderson and Zeuli, 2001; Fausti and Qasmi, 2002; Lusk et al., 2003), and has been identified as the primary barrier to the adoption of grid pricing (Fausti, Feuz, and Wagner, 1998; Anderson and Zeuli, 2001; Fausti and Qasmi, 2002).

Genetic Information Marketing Scenario

The decision rule indicated that net return maximizing decision makers would target animals with higher genetic potential for marbling to the grid and animals with lower genetic potential for marbling to either live weight or dressed weight pricing (figure III-1). At lower levels of genetic potential for marbling, dressed weight pricing generated the highest expected net return for animals with lower yield grade MBVs and live weight pricing generated the highest expected net return for animals with higher yield grade MBVs.

Applying this decision rule to the data, 10% of cattle were targeted to live weight pricing, 17% to dressed weight pricing, and 73% to grid pricing (table III-6). Investigation of the outcomes for individual marketing groups indicated that expected net return for live weight (-$57.74/head) and dressed weight (-$51.24/head) pricing decreased relative to their respective baseline scenarios, but expected net return for grid pricing increased to -$16.71/head. Therefore, the ability to identify animals that will perform poorly at slaughter and pull them off of the grid increased expected net return for grid pricing by more than $11/head. As a result, overall expected net return for the genetic information marketing scenario increased to -$26.68/head. Comparing this value with expected net return for the grid baseline marketing scenario, the expected value of genetic information for a producer currently marketing cattle in a single group using grid pricing was $1.35/head (-$26.68 - [-$28.03] = $1.35) (table III-7). While this value is relatively low, it is important to remember that few producers currently market all of their cattle on the grid as a result of higher variability. The value of

genetic information for producers currently using live weight or dressed weight pricing was $9.16 and $7.57/head, respectively.

In addition to improvements in expected net returns, using genetic information to sort cattle into marketing groups also resulted in efficiency gains to cattle feeding. For example, relative to their respective baseline scenarios, optimal days-on-feed decreased for live weight (146 days) and dressed weight (177 days) pricing and increased for grid pricing (182 days) (table III-6). This indicated that when sorted and targeted to their optimal marketing method, animals with lower genetic potential for marbling could be fed for fewer days, and animals with higher genetic potential for marbling could be fed slightly longer to achieve more favorable quality grade outcomes.

Furthermore, the standard deviation of expected net return for all three marketing groups decreased relative to the standard deviations in their respective baseline scenarios. This is particularly important given that one of the primary motivations for sorting cattle into marketing groups was to reduce the variability among animals treated alike (Fausti, Wang, and Lange, 2013). More importantly, the standard deviation of overall expected net return for the genetic information marketing scenario ($31.47) was less than the grid baseline marketing scenario ($33.49). Therefore, in addition to improving the returns to cattle feeding, genetic sorting can also reduce the variability, or risk, associated with value-based marketing.

Sensitivity analysis was conducted using the grids associated with the maximum and minimum weekly Choice-Select spread for 2014. As expected, the decision rule for the maximum grid was similar to figure III-1, with a lower marbling MBV threshold, indicating that a slightly larger portion of cattle were targeted to the grid (74%). The decision rule for the minimum grid was also similar to figure III-1, with a slightly higher (lower) marbling MBV threshold at lower (higher) levels of genetic potential for yield grade. Contrary to expectations, when this decision rule was applied to the data the portion of cattle targeted to the grid actually increased (77%). The lower Choice-Select spread made yield grade outcomes more economically important relative to quality grade outcomes,

and, as a result, animals with higher yield grade MBVs were more likely to be targeted to the grid regardless of their genetic potential for marbling.

Other notable results for the maximum and minimum grid scenarios were qualitatively similar to the average pricing scenario described above. However, the values of genetic information for the maximum grid increased for each of the three baseline marketing scenarios and ranged from $2.47 to $13.00/head depending on how a producer currently markets cattle (table III-7). Conversely, the values of genetic information for the minimum grid decreased and ranged from just $0.59 to $5.28/head.

Perfect Information Marketing Scenario

For the set of animals and prices used, perfect information dictated that 19% of cattle be targeted to live weight pricing, 19% to dressed weight pricing, and 62% to grid pricing (table III-6). Expected net returns for the perfect information marketing scenario increased to -$24.19/head and the standard deviation decreased ($30.88), indicating that more accurate sorting could further increase returns and further decrease the variability associated with cattle feeding. As a result, values of perfect information were consistently higher than the values of genetic information and ranged from $4.12 to $14.75/head depending on how a producer currently markets cattle and which grid was used (table III-7).

Expected Utility for Alterative Marketing Scenarios

Incorporating risk preferences into the model indicated that as risk aversion increased, decision maker's preferences shifted away from grid pricing towards less risky live weight pricing (table III-8). For example, certainty equivalents identified live weight pricing as the preferred baseline marketing method for moderate (-$75.00/head) and severe (-$104.42/head) levels of risk aversion, and the expected utility maximizing portfolio targeted fewer animals to the grid and more animals to live weight pricing as risk aversion increased.

Despite differences in optimal marketing strategies, the range of values of information for selectively marketing cattle was largely unchanged when risk was considered, ranging from $1 to $19/head[28] (table III-9). Instead, as risk aversion increased, values of information for producers currently using live weight pricing to market cattle decreased and values of information for producers using dressed weight and grid pricing increased. This result is consistent with Lambert (2008) who found that certainty equivalents fell as risk aversion increased, but the differences in certainty equivalents among cattle with different leptin genotypes did not change significantly. Therefore, our results indicate that while risk aversion is important for understanding how producers market cattle, it did not have a substantial impact on the value of genetic information.

Conclusions

This study examined the value of genetic information for improving fed cattle marketing decisions. Results indicated that using genetic information characterizing yield grade and marbling to sort cattle into marketing groups (live weight, dressed weight, or gird pricing) and to determine optimal days-on-feed increased expected net returns by $1 to $13/head depending on how a producer currently markets cattle and the grid structure. Despite differences in optimal marketing strategies, the range of the values of information was largely unchanged when risk was considered. In addition, the perfect

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[28] Thaler's (1999) discussion of mental accounting indicates that decision makers may fail to appropriately quantify risk. That is, instead of maximizing the aggregate expected utility for a group of animals, decision makers may maximize expected utility on an animal-by-animal basis (i.e., "pockets of money"). Therefore, we also evaluated an expected utility objective function where animals were targeted to the marketing method that maximized expected utility for each individual animal. Although the values of information for this analysis were slightly lower, as would be expected, they were very similar to the results reported here for the aggregate expected utility maximizing portfolio.

information marketing scenario offered slight improvements over genetic information, but it shows that even improved genetic tests would not be economical unless the cost of testing plunged. Given the use of naïve baseline marketing scenarios, the values reported here are likely an upper bound on the value of genetic information for selectively marketing fed cattle.

Previous research examining the value of genetic information for marker-assisted management has been limited to sorting cattle by optimal days-on-feed (DeVuyst et al., 2007; Lusk, 2007; Thompson et al., 2014). In this study, we extend the definition of marker-assisted management to include a more holistic view of fed cattle marketing, including decisions for marketing method as well as timing to market. As a result, the values of genetic information for marker-assisted management reported in this study were generally higher than those reported in previous research. However, these values were still not enough to offset the cost of genetic testing.

Currently, Igenity offers a comprehensive profile of 12 genetic markers for $40/head (Igenity, 2015). In addition to markers characterizing carcass traits, such as yield grade and marbling, this profile also includes markers for maternal traits, docility, growth, feed efficiency, and tenderness. While this comprehensive profile is beneficial for producers using this information to make selection and breeding decisions (Thompson et al., 2014), most of this information is superfluous in the context of managing feedlot cattle. For this reason, commercial testing companies might consider marketing a reduced profile of markers relevant to a particular decision. For example, Igenity currently offers a reduced profile of six traits relevant to the selection of replacement heifers for a cost of $22/head (Igenity, 2015). A similar reduced profile of growth and carcass characteristics may provide the opportunity for cost-effective marker-assisted management of feedlot cattle. Additional sorting and management costs may be associated with implementing a selective marketing management scheme that are not considered here. It may also be possible to use random sampling to reduce the cost of genetic testing by measuring the genetic potential of a group of cattle without having to test each animal.

To put the results of this study into context, consider that because cattle feeding is a competitive industry average profitability is close to zero. Therefore, the values of genetic information reported here represent meaningful economic value. However, it is important to caution that the results presented here are conditional on the set of animals and prices used in this analysis. In addition, the values of genetic information reported here will not persist in the long run. First adopters and owners of the genetic identification technologies may realize profitability gains (Lusk, 2007; Koontz et al., 2008), but eventually selective marketing will signal to buyers that animals marketed on a live weight or dressed weight basis are likely lower quality than animals targeted to the grid. As a result, the market will adjust by decreasing live weight and dressed weight prices relative to grid prices (Schroeder and Graff, 2000; Koontz et al., 2008; Fausti et al., 2014), and the value of information to the feedlot will dissipate. In fact, there is already some evidence of these general equilibrium effects in the fed cattle market (Fausti et al., 2014).

Nevertheless, value to consumers will remain. That is, although improved marketing decisions will increase returns to the feedlot in the short run, results also indicated the potential for long-run efficiency gains that will persist because of changes in the product form. Sorting cattle into marketing groups allowed producers to more accurately determine optimal days-on-feed. In addition, sorting cattle into marketing groups generally decreased the variability of expected net returns. Therefore, the use of genetic testing to selectively market cattle may encourage producers, who might not otherwise do so, to market cattle on a grid (Fausti et al., 2010; Fausti, Wang, and Lange, 2013). This will result in improved quality and consistency of beef products and improved transmission of market signals throughout the beef cattle supply chain, and may help address consumer demand problems.

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Table III-1. Correlation Matrix of the Seven Molecular Breeding Values (n = 9,465)

Molecular Breeding Value	Molecular Breeding Value						
	YG	MARB	ADG	HCW	REA	TDR	DOF
YG	1.00						
MARB	-0.50	1.00					
ADG	-0.23	0.34	1.00				
HCW	0.06	0.09	0.35	1.00			
REA	0.73	-0.64	-0.39	0.08	1.00		
TDR	-0.33	0.28	0.04	-0.01	-0.19	1.00	
DOF	0.26	-0.15	-0.18	0.10	0.36	-0.17	1.00

Notes: Molecular breeding value abbreviations are yield grade (YG), marbling (MARB), average daily gain (ADG), hot-carcass weight (HCW), rib-eye area (REA), tenderness (TDR), and days-on-feed (DOF).

Table III-2. Summary Statistics for Growth and Carcass Performance, Live-Animal Characteristics, and Molecular Breeding Values

Variable	n	Mean	Standard Deviation	Minimum	Maximum
Growth and carcass performance					
Average daily gain, lbs/day	7,670	3.390	0.803	0.370	7.383
Dressing percentage	5,773	0.627	0.028	0.490	0.827
Yield grade	9,440	2.704	0.853	0.056	5.905
Marbling score[a]	9,044	416.3	79.5	190.0	830.0
Live-animal characteristics					
Placement weight, cwt[a]	9,465	7.0	1.2	2.9	11.2
Days-on-feed, days[a]	9,465	176.0	35.4	81.0	308.0
Steer	9,465	0.826			
Black	9,465	0.623			
Molecular breeding values (MBV)					
Yield grade MBV	9,465	-0.054	0.073	-0.338	0.210
Marbling MBV	9,465	-21.661	28.017	-124.020	76.353
Average daily gain MBV, lbs./day	9,465	0.168	0.100	-0.229	0.482
Hot-carcass weight MBV, lbs.	9,465	27.231	8.969	-17.728	55.913
Rib-eye area MBV, in^2	9,465	-0.572	0.523	-2.172	1.588
Tenderness MBV, lbs. of WBSF[b]	9,465	-0.991	1.348	-5.900	2.920
Days-on-feed MBV, days	9,465	-2.628	2.811	-14.351	9.160

Notes: Molecular breeding values (MBVs) are reported in the units of the trait and reflect the differences expected in animals across breeds compared to their contemporaries (Igenity, 2013). Therefore, mean MBVs offer little insight. Instead, the range of MBVs is more informative. For example, the range of average daily gain MBVs suggests that the animal with the highest genetic potential for average daily gain in the sample would be expected, on average, to gain approximately 0.71 lbs. per day more than the animal with the lowest genetic potential for average daily gain (0.482 - [-0.229] = 0.711).

[a] Summary statistics for marbling score, placement weight, and days-on-feed are only reported to one decimal place as a result of significant digits.

[b] Warner-Bratzler shear force.

Table III-3. Joint Distribution of Observed Yield and Quality Grade Outcomes (n = 9,029)

USDA Yield Grade	USDA Quality Grade				
	Prime	Choice	Select	Standard	Total
1	<1%	5%	8%	1%	14%
2	<1%	20%	21%	1%	44%
3	<1%	24%	12%	<1%	37%
4	<1%	4%	1%	<1%	5%
5	0%	<1%	<1%	<1%	<1%
Total	<1%	54%	42%	3%	100%

Table III-4. Live Weight Prices, Dressed Weight Prices, and Grid Premiums and Discounts for 2014

Marketing Method		Average Prices	Maximum Grid[a]	Minimum Grid[b]
		——————— $/cwt ———————		
Live weight				
Steers		$154.31		
Heifers		$154.44		
Dressed weight				
Steers		$244.22		
Heifers		$244.21		
Grid	Base price[c]			
	Steers	$248.10	$250.78	$245.16
	Heifers	$248.09	$250.77	$245.15
	Quality grade adjustment			
	Prime	$19.26	$21.33	$18.35
	Choice	$0.00	$0.00	$0.00
	Select	($8.63)	($14.57)	($2.09)
	Standard	($20.84)	($23.92)	($17.72)
	Yield grade adjustment			
	1.0-2.0	$4.58	$4.58	$4.58
	2.0-2.5	$2.25	$2.25	$2.24
	2.5-3.0	$2.13	$2.13	$2.11
	3.0-4.0	$0.00	$0.00	$0.00
	4.0-5.0	($8.63)	($8.23)	($9.21)
	>5.0	($13.64)	($13.06)	($14.99)
	Carcass weight adjustment			
	400-500	($25.42)	($25.40)	($25.49)
	500-550	($22.19)	($22.80)	($19.62)
	550-600	($2.93)	($2.70)	($3.89)
	600-900	$0.00	$0.00	$0.00
	900-1000	($0.24)	($0.19)	($0.24)
	1000-1050	($2.27)	($2.22)	($2.35)
	>1050	($23.24)	($23.33)	($23.05)

Source: Livestock Marketing Information Center (LMIC) spreadsheets based on USDA AMS reports LM_CT150 and LM_CT169 (USDA AMS, 2014a; USDA AMS, 2014b; LMIC, 2015).

[a] The "maximum grid" is the grid from the week with the highest Choice-Select spread for 2014 (September 22, 2014).

[b] The "minimum grid" is the grid from the week with the smallest Choice-Select spread for 2014 (February 2, 2014).

[c] The base price for the grid was calculated as the dressed weight price plus the Choice-Select spread times the percent of cattle that graded Select or lower in our data set (Ward, Feuz, and Schroeder, 1999). For example, the base price for the average price grid for steers was: $244.22 + 8.63 \times 45\% = 248.10$.

Table III-5. Mixed Model Regression Equations for Average Daily Gain, Dressing Percentage, Yield Grade, and Quality Grade

Variable	Equation ADG ($n = 7{,}670$)	DP ($n = 5{,}773$)	YG ($n = 9{,}440$)	QG ($n = 9{,}044$)
Intercept	1.961	0.340**	1.124	262.200**
Placement weight	0.205	0.010***	0.259***	17.990***
Days-on-feed	0.014*	0.002**	0.002	0.646
Days-on-feed squared	-4.00E-5***	-4.16E-6*	1.40E-5	0.001
Placement weight × days-on-feed	-0.002**	-5.00E-5*	-0.001*	-0.078***
Steer[a]	0.399***	0.004	-0.144***	-34.366***
Black[b]	0.023***	-9.70E-5	0.008	0.583
Yield grade MBV[c]	0.152	-0.007	-0.382	-154.670***
Yield grade MBV × days-on-feed	—	—	-0.002	0.819***
Marbling MBV	0.001	-6.96E-6	0.001	-0.148
Marbling MBV × days-on-feed	—	—	6.77E-6	0.005***
Yield grade MBV × marbling MBV	—	—	0.009***	-0.170
Average daily gain MBV	0.757**	-0.006**	0.028	-0.339
Hot-carcass weight MBV	0.001	1.21E-4***	0.003*	0.176*
Rib-eye area MBV	0.017	0.002	-0.345***	-11.406***
Tenderness MBV	0.002	1.92E-4	0.007	-1.027*
Days-on-feed MBV	-0.001	-2.00E-5	-9.00E-5	-0.266
Random effects[d]				
Set	0.236*	4.99E-4	0.136*	52.483
Contemporary group(Set)	0.101***	2.93E-4***	0.040***	388.960***
quasi-R^2 excluding MBVs[e]	0.463	0.562	0.404	0.130
quasi-R^2 including all variables[e]	0.470	0.565	0.470	0.193

Notes: Single, double, and triple asterisks (*, **, ***) indicate significance at the 10%, 5%, and 1% levels. Dependent variables in the four equations are average daily gain (ADG), dressing percentage (DP), calculated yield grade (YG), and marbling score (QG).

[a] Steer is a dummy variable equal to one if the animal was a steer and zero otherwise.

[b] Black is a dummy variable equal to one if the animal was black hided and zero otherwise.

[c] Molecular breeding value.

[d] Random effects for set and contemporary groups nested within sets are included in the estimation of each equation (i.e., mixed model regression equations) (Greene, 2012). Sets represent different commercial feedlots, time periods, or both, and contemporary groups are groups of animals that have had an equal opportunity to perform.

[e] Quasi-R^2 values are calculated as the squared correlations of the actual and predicted values including random effects.

Table III-6. Expected Net Returns and Corresponding Optimal Days-on-Feed for Alternative Marketing Scenarios for 2014 Average Prices

Marketing Scenario	Proportion	Optimal Days-on-Feed	Expected Net Return	Standard Deviation
			——— $/head ———	
Baseline marketing scenarios				
Market all live weight		151	-$35.84	$27.07
Market all dressed weight		179	-$34.25	$27.09
Market all grid		181	-$28.03	$33.49
Genetic information marketing scenario				
Live weight	10%	146	-$57.74	$23.87
Dressed weight	17%	177	-$51.24	$21.86
Grid	73%	182	-$16.71	$28.28
Weighted average			-$26.68	$31.47
Perfect information marketing scenario				
Live weight	19%	143	-$26.76	$32.10
Dressed weight	19%	179	-$50.35	$21.15
Grid	62%	183	-$15.38	$28.21
Weighted average			-$24.19	$30.88

Table III-7. Expected Value of Information for Alternative Marketing Scenarios Compared with Baseline Marketing Scenarios for Three Different Grids

Alternative Marketing Scenarios	Baseline Marketing Scenarios		
	Live Weight	Dressed Weight	Grid
	———————— $/head ————————		
Average grid			
Genetic information	$9.16	$7.57	$1.35
Perfect information	$11.65	$10.06	$3.84
Maximum grid			
Genetic information	$13.00	$11.41	$2.47
Perfect information	$14.75	$13.16	$4.22
Minimum grid			
Genetic information	$5.28	$3.69	$0.59
Perfect information	$8.81	$7.22	$4.12

Table III-8. Optimal Marketing Portfolios and Certainty Equivalents for Alternative Marketing Scenarios for Three Levels of Risk Aversion and 2014 Average Prices

Marketing Scenario	Slight Risk Aversion ($r = 0.0000003$)		Moderate Risk Aversion ($r = 0.0000006$)		Severe Risk Aversion ($r = 0.0000010$)	
	Proportion	Certainty Equivalent	Proportion	Certainty Equivalent	Proportion	Certainty Equivalent
		$/head		$/head		$/head
Baseline marketing scenarios						
Market all live weight		-$58.01		-$75.00		-$104.42
Market all dressed weight		-$63.38		-$85.49		-$122.81
Market all grid		-$57.58		-$80.08		-$118.09
Expected utility maximizing portfolio						
Live weight	31%		54%		81%	
Dressed weight	10%		3%		0%	
Grid	59%		43%		19%	
Overall		-$52.02		-$71.54		-$103.34

Note: Days-on-feed for each marketing method is held constant at their profit maximizing baseline levels (live weight = 151 days, dressed weight = 179 days, and grid = 181 days).

Table III-9. Expected Value of Information for Alternative Marketing Scenarios Compared with Baseline Marketing Scenarios for Three Levels of Risk Aversion and 2014 Average Prices

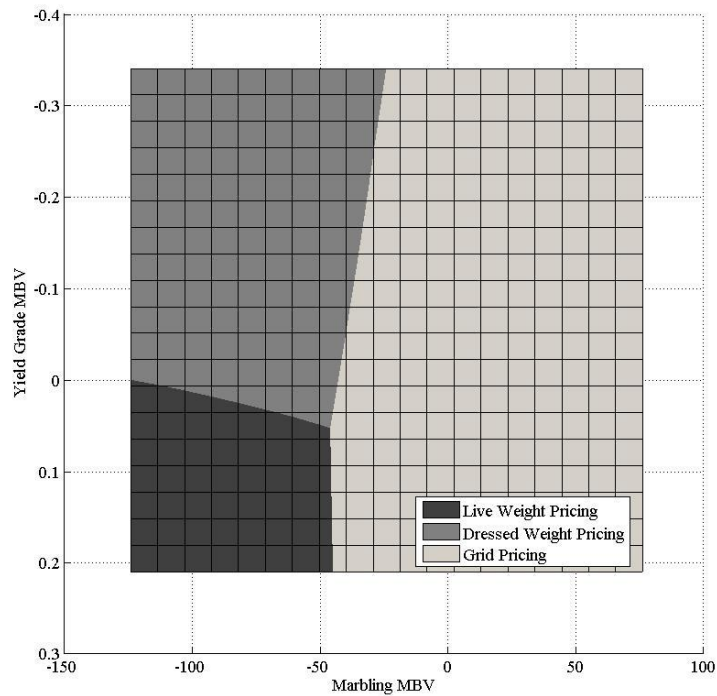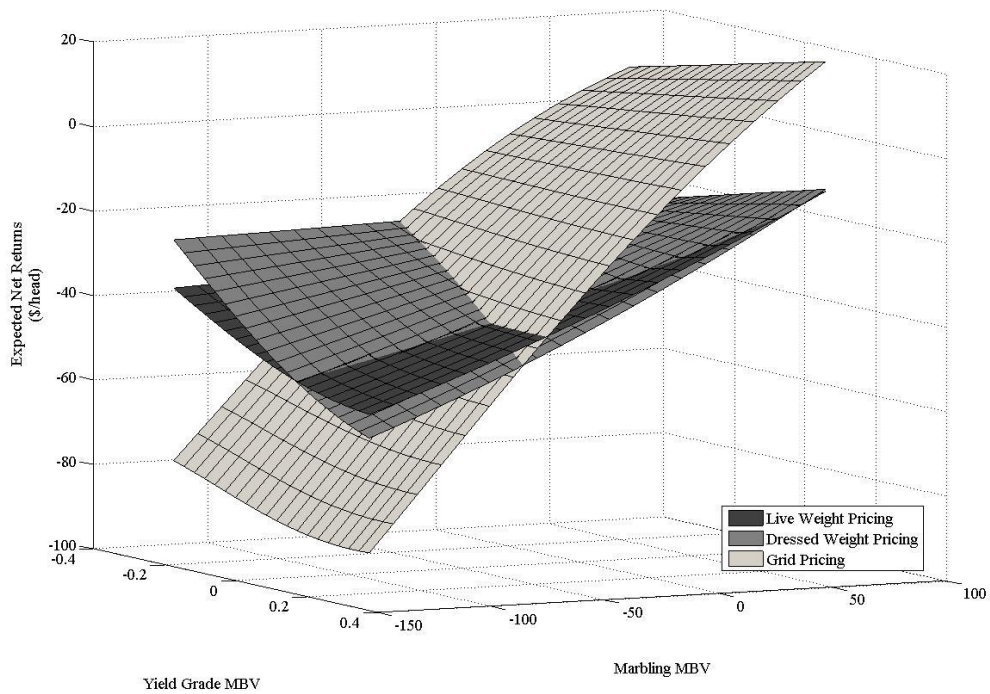|	Baseline Marketing Scenarios		
Risk Aversion	Live Weight	Dressed Weight	Grid
	———————— \$/head ————————		
Slight risk aversion	\$5.99	\$11.36	\$5.56
Moderate risk aversion	\$3.46	\$13.95	\$8.54
Severe risk aversion	\$1.08	\$19.47	\$14.75

Figure III-1. Three-dimensional surface and corresponding contour plot of the fed cattle marketing decision rule using molecular breeding values (MBV) characterizing yield grade and marbling for 2014 average prices

CHAPTER IV

A BAYESIAN DECISION THEORETIC APPROACH TO ECONOMICALLY-OPTIMAL

SAMPLE SIZE DETERMINATION: RANDOMLY SAMPLING BEEF CATTLE FOR

GENETIC TESTING

Abstract

Sample size is often dictated by budget and acceptable error bounds. However, there are many

economic problems where sample size directly affects a benefit or loss function, and in these

cases, sample size is an endogenous variable. We introduce an economic approach to sample size

determination utilizing a Bayesian decision theoretic framework that balances the expected costs

and benefits of sampling using a Bayesian prior distribution for the unknown parameters. To

demonstrate the method for a relevant applied economics problem, we turn to randomly sampling

beef cattle for genetic testing. A theoretical model is developed, and several simplifying

assumptions are made to solve the problem analytically. Data from 101 pens (2,976 animals) of

commercially-fed cattle are then used to evaluate this solution empirically. Results indicate that at

the baseline parameter values an optimal sample size of $n^* = 10$ out of 100 animals generate

returns from sampling of nearly \$10/head, or a return-on-investment of 250%. Therefore, a large

portion of the additional value for higher-quality cattle can be captured by testing a relatively

small percentage of the lot. These results vary depending on the actual quality (or profitability) of

a particular pen of cattle, the homogeneity within the pen, the variance of the buyer's subjective

prior distribution of expected profit, and the per-head cost of genetic testing. Nonetheless, results

suggest that random sampling has the potential to provide a context in which the benefits of genetic testing outweigh the costs, which has not generally been the case in previous research.

Keywords: Bayesian decision theory, beef cattle genetics, random sampling, sample size determination

Introduction

The methods for determining sample size can be generally classified into two broad categories: frequentist and Bayesian (Adcock, 1997). The debate between proponents of these two approaches has occupied entire issues of statistical journals (for example, *Journal of the Royal Statistical Society: Series D (The Statistician)* 46(2), 1997) and is ongoing. In practice, sample size has often been a function of budget and acceptable error bounds. Therefore, the commonly used frequentist approach determines sample size by specifying a null and alternative hypothesis for the parameter of interest and using predetermined specifications of size, power, variance, and a minimum detectible difference (Adcock, 1997; Wilan, 2008). However, there are many economic problems where sample size directly affects a benefit or loss function. In these cases, sample size is an endogenous variable that should be considered jointly with other choice variables in an optimization problem. In this article we introduce an economic approach to sample size determination utilizing a Bayesian decision theoretic framework. The Bayesian framework for sample size determination appears to be rarely used in economic research, but is arguably the theoretically sound approach to determining sampling for many applied economic problems. In addition to introducing the method, we develop a practical, currently relevant application of the model for randomly sampling beef cattle for genetic testing.

The issue of endogenous sample size was first identified by Grundy, Healy, and Rees (1956). In this seminal piece, the authors acknowledge that in order to determine the economically justifiable amount of experimentation, the costs of the experiment must be set against the potential benefits of the new process being evaluated. However, they point out that the main difficulty is that the expected benefits of the new process depend on the outcome of the experiment. Their model has since been

generalized and further developed by Riffa and Schlaifer (1961) and, more recently, by Lindley (1997), and has come to be known as the Bayesian decision theoretic approach to sample size determination. In this fully Bayesian framework, the economically-optimal sample size is determined using an objective function to balance the expected costs and benefits of sampling using a Bayesian prior distribution for the unknown parameters.

Despite its potential for application to a variety of research problems, to date, the use of this method has been largely limited to clinical trials in medical research (Gittins and Pezeshk, 2000, 2002; O'Hagan and Stevens, 2001; Kikuchi, Pezeshk, and Gittins, 2008; Wilan, 2008; Willan and Pinto, 2005, 2006) and substantive tests in financial auditing (Smith 1976, 1979; Patterson, 1993; Laws and O'Hagan, 2002). Still, there remain many research problems to which this method could, and likely should, be applied for determining the economically-optimal sample size. For example, in a variety of audit/inspection contexts (for example, internal bank audit, environmental regulation compliance audit, Food and Drug Administration [FDA] inspections, health inspections, etc.), it is much too costly to examine each individual unit of interest. However, there is significant value associated with obtaining a sufficient sample to identify potential losses or costly, undesirable outcomes. Therefore, the fully Bayesian approach allows the decision maker to determine the sample size that will balance the expected costs and benefits of sampling. In addition, a sampling error of ±3% in many survey based research methods is dictated by convention. However, researchers rarely discuss, or even consider, the tradeoff between the cost and accuracy of a given survey question. Likewise, issues of quality control/statistical tolerancing or sampling related problems (for example, grain sampling, livestock sampling, soil sampling, etc.) could also benefit from this approach.

To demonstrate the method for a relevant applied economics problem, we turn to genetic testing for market livestock. Recent advancements in genomic technology have the potential to generate value throughout the beef industry (Van Eenennaam and Drake, 2012). Previous research has shown significant differences in the profitability of animals with different genetic profiles suggesting some merit in using the tests for selection (Lusk, 2007; Thompson et al., 2014). However,

economic evaluations of commercially available genetic marker panels have indicated that the value of this information for feedlot management is generally not enough to offset the current cost of genetic testing (about $40/head; Igenity, 2015). For example, the value of using genetic information for sorting feedlot cattle by optimal days-on-feed is less than $3/head (DeVuyst et al., 2007; Lusk, 2007; Lambert, 2008; Thompson et al., 2014), and the value of using this information to selectively market (live weight, dressed weight, or grid pricing) fed cattle is less than $13/head (Thompson et al., 2016).

Therefore, in order to achieve a scenario in which genetic testing is cost-effective, the value of genetic information must increase or the cost of testing must decrease. While animal scientists are continually progressing towards providing more accurate genetic markers that have the potential to increase the value of genetic information (for example, see Akanno et al., 2014), producers seeking to use this technology have no control over the pace at which these new variations are released. So, we introduce a strategy for reducing the overall cost of genetic testing that has been previously discussed, but has yet to be evaluated: random sampling (Thompson et al., 2014, 2016). That is, instead of testing each individual animal in a group of cattle, a random sample of animals could be tested to measure the genetic potential of the group. While appealing in theory, there is a thorny practical question: "What size sample should I take?" To answer this question we use a Bayesian decision theoretic approach to determine the economically-optimal sample size.

Unlike previous research evaluating the value of genetic information, which has generally focused on marker-assisted management at the feedlot stage, in this research we approach the problem from the feeder cattle producer's perspective. That is, producers who know that their feeder cattle have high-value genetics may want to try to convince buyers (for example, wheat stocker producers or feedlot owners) that their cattle are higher quality in order to receive a premium. However, in order to establish the actual genetic makeup of a lot of feeder cattle the seller must incur the cost of genetic testing. Therefore, the objective of this research is to determine if randomly sampling a group of feeder cattle for genetic potential is cost-effective and, if so, to determine the

economically-optimal sample size. A general framework is introduced, and a theoretical model

specific to randomly sampling feeder cattle for genetic testing is developed. Several simplifying

assumptions are made to solve the problem analytically, and the solution is then evaluated empirically

using data from 101 pens (2,976 animals) of commercially-fed cattle. After estimating the optimal

sample size and the returns from sampling, sensitivity analysis is conducted to evaluate the robustness

of these results to varying levels of quality and homogeneity of a particular lot of cattle. Our results

suggest sampling could be a viable strategy to reduce the costs of genetic testing for beef cattle.

Conceptual Framework

The objective of the Bayesian decision theoretic approach to economically-optimal sample size

determination is to determine how large of a sample (n) to take from a population to make an

inference/decision about some feature of the population considering that both the costs and benefits of

sampling are a function of n (Grundy, Healy, and Rees, 1956; Riffa and Schlaifer, 1961; Lindley,

1997). The framework for the fully Bayesian treatment of this problem is set was set out in detail by

Riffa and Schlaifer (1961) and was later updated by Lindley (1997). Both descriptions approach the

problem in temporal order: first the sample size n is chosen, n realizations of random quantity X are

then collected $(x_1, x_2, \dots, x_n)$ where the density of X is of a known form dependent on the unknown

parameter θ, the information from this sample is used to make decision d concerning some feature of

the population, and finally the unknown parameter θ is considered. The merit of this decision

sequence is captured by specifying a utility function, $u(n, x, d, \theta)$.

       Before performing the optimization the decision maker has a prior distribution of the

unknown parameter θ, $p_{prior}(\theta)$. An application of Bayes rule to θ and x gives the posterior

distribution of θ conditional on x and n, $p_{post}(\theta|x, n) = p(x|\theta, n)p_{prior}(\theta)/p(x|n)$, where

$p(x|\theta, n) = \prod p(x_i|\theta)$ is the usual likelihood function and $p(x|n) = \int p(x|\theta, n)p_{prior}(\theta)d\theta$ is a

normalizing constant.

With the posterior distribution of θ available, Riffa and Schlaifer's (1961) resolution of this problem is to proceed in reverse time order, taking expectations of utility over random variables θ and x, and maximixing over choice variables d and n. Assuming that utility does not depend on x and is additive and linear in n, the utility function can be written as $u(n, x, d, \theta) = u(d, \theta) - cn$, where c is the cost in utiles of each additional observation (Riffa and Schlaifer, 1961; Lindley, 1997). Therefore, the objective function is (Lindley, 1997):

(1)
$$\max_{n \geq 0} \left\{ \int_x \max_{d \geq 0} \left[\int_\theta u(d, \theta) p_{post}(\theta | x, n) d\theta \right] p(x|n) dx - cn \right\}.$$

The problem can be solved by taking the expectation over θ of the utility of d, given x and n, and then maximizing over the decision variable d. Subsequently, the expectation over x of this maximized value can be found using $p(x|n)$, and finally, this expectation can be maximized over n to answer the original question, "What size sample should I take?"

Application to Genetic Testing for Beef Cattle

Although equation (1) offers a well-defined algorithm for solving the general form of the Bayesian decision theoretic approach to sample size determination, applications of this method are still limited. Most notably, several studies have used the fully Bayesian approach to determine the optimal sample size for clinical trials in medical research. Although these studies have been conducted from a variety of different perspectives, including societal/public health (Gittins and Pezeshk, 2002; Wilan and Pinto, 2005, 2006) and industry/pharmaceutical companies (Gittins and Pezeshk, 2000, 2002; O'Hagan and Stevens, 2001; Kikuchi, Pezeshk, and Gittins, 2008; Wilan, 2008), they focus on a single market participant. Conversely, there are two participants in the market for feeder cattle: buyers and sellers. Therefore, we extend the model to take into account both buyer and seller information.

Suppose $\boldsymbol{X_i}$ $(i = 1, 2, \ldots, m)$ is a column vector of molecular breeding values (MBVs) characterizing p economically relevant traits for the ith animal in a lot of m feeder cattle. Within a

pen of cattle, this vector of genetic markers is assumed to be independent and identically distributed

across animals with a multivariate normal density (Mrode, 2014):[29]

(2)
$$X_i \sim iid \; MVN_p(\boldsymbol{\theta}, \boldsymbol{\Sigma}),$$

where the true value of $\boldsymbol{\theta}$ is unknown and the $p \times p$ variance-covariance matrix $\boldsymbol{\Sigma}$ is known from

previous experience. Both the buyer (feedlot) and the seller (producer) of a lot of feeder cattle have

their own subjective prior distributions of the unknown parameter $\boldsymbol{\theta}$. For example, the seller's prior

distribution of $\boldsymbol{\theta}$ can be expressed as:

(3)
$$\boldsymbol{\theta} \sim MVN_p(\boldsymbol{\mu}_s, \boldsymbol{V}_s),$$

and the buyer's prior distribution can be written similarly as:

(4)
$$\boldsymbol{\theta} \sim MVN_p(\boldsymbol{\mu}_b, \boldsymbol{V}_b).$$

Given previous experience with their own cattle, the seller is expected to have a narrower distribution

of $\boldsymbol{\theta}$ than the buyer (i.e., $\boldsymbol{V}_s \leq \boldsymbol{V}_b$). Although buyers often have access to some information about

how animals will perform, in the extreme case that the buyer is completely uninformed $\boldsymbol{V}_b$ is

characterized by the variance-covariance matrix of the MBVs between lots of cattle.

A model examining the consequences of asymmetric information between buyers and sellers

was first introduced by Akerlof (1970) using the example of the market for used cars. This model has

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[29] The independence assumption is a common simplifying assumption (Hoff, 2009). However, in

practice genetic markers are likely to be positively correlated across animals. For example, a lot of

feeder cattle from the same ranch often have a high degree of relatedness with dams frequently being

cousins and bulls being able to service 20-25 head. Holding all else constant, relaxing the

independence assumption would likely result in a lower optimal sample size and higher returns from

sampling as the information collected from each animal is more informative about the pen as a whole.

Therefore, our model, which assumes independence, represents the extreme case in which animals are

completely unrelated, and as a result, the optimal sample sizes presented here are likely an upper

bound on the true profit maximizing sample size.

since been extended to a variety of topics, including asymmetric information in cattle auctions (Allen, 1993; Chymis, 2007). Results indicate that one way to alleviate the inefficiency created by this information gap is to introduce credible information to the decision problem. However, as indicated by Stigler (1961) a rational decision maker will only obtain additional information if the benefits outweigh the costs. Therefore, given the discrepancy between buyer and seller expectations of the genetic makeup of a lot of feeder cattle, sellers who know that their cattle have valued genetics may want to differentiate their cattle by convincing buyers that they are higher quality. One way to do this would be to use genetic testing to establish the actual genetic makeup of the lot. However, previous research has consistently found that testing each individual animal is not cost-effective. Therefore, the seller may choose to randomly sample a subset of the cattle. The question is how many cattle should the seller test to maximize returns?

An objective function characterizing the costs and benefits of randomly sampling n animals out of a lot of m feeder cattle is specified using a Bayesian prior distribution for the unknown vector of parameters $\boldsymbol{\theta}$. The cost of testing is known to be $\frac{c}{m}n$, where c is the cost of commercial testing services ($/head). The benefit of persuading the buyer that a pen of cattle has higher quality genetics than expected is characterized by the increase in the buyer's expected profit which is specified as a function of genetics, $\pi(\boldsymbol{\theta})$. For simplicity, the buyer is assumed to be risk neutral so that the seller receives the entire surplus profit created from testing. Moreover, in application the presence of a large number of buyers would result in the additional value to buyers being bid away given the reasonable assumption that the market for feeder cattle is perfectly competitive (Zhao, Du, and Hennessy, 2011).

As a result, the seller's objective function $r(n)$, which is the total expected benefit from the resulting improvement in the buyer's profit function minus the cost of testing, can be written as:

(5)
$$\max_{n \geq 0} r(n) = \int_X \left[\int_\theta \pi(\theta) p_{post}(\theta | X, n) d\theta \right] p(X|n) dX$$

$$- \int_\theta \pi(\theta) p_{prior}(\theta) d\theta - \frac{c}{m} n,$$

where $p_{post}(\theta | X, n)$ is the buyer's posterior distribution of θ conditional on the genetic information X collected from a random sample of n animals and $p_{prior}(\theta)$ is the buyer's prior distribution of θ given in equation (4). An application of Bayes rule indicates that the posterior distribution is proportional to the product of the likelihood function and the buyer's prior distribution of θ, $p_{post}(\theta | X, n) \propto p(X|\theta) p_{prior}(\theta)$. Therefore, in order to maximize the returns from sampling in equation (5), the seller is assumed to know the buyer's prior distribution of θ, which could be implied from the initial bid received.

If, for simplicity of exposition, we assume that the buyer's profit function in equation (5) is linear in the MBVs, $\pi = \alpha + \beta X$, the multivariate distribution of genetics in equation (2) can be transformed into a univariate normal distribution of profit per head within a pen of cattle:

(6)
$$\pi_i \sim iid\ N(\alpha + \beta\theta, \beta\Sigma\beta'),$$

where the mean is still unknown. Similarly, buyer and seller subjective prior distributions of genetics can also be transformed into prior distributions of profit. For example, the seller's prior distribution of expected profit is a linear transformation of the prior distribution of genetics in equation (3):

(7)
$$\alpha + \beta\theta \sim N(\alpha + \beta\mu_s, \beta V_s \beta'),$$

and the linear transformation of the prior distribution of genetics in equation (4) returns the buyer's prior distribution of expected profit:

(8)
$$\alpha + \beta\theta \sim N(\alpha + \beta\mu_b, \beta V_b \beta').$$

Replacing distributions of genetics with distributions of profit, the objective function in equation (5) can be rewritten as:

(9)
$$\max_{n \geq 0} r(n) = \int_{\bar{\pi}} \left[\int_{\alpha+\boldsymbol{\beta}\boldsymbol{\theta}} (\alpha + \boldsymbol{\beta}\boldsymbol{\theta}) p_{post}(\alpha + \boldsymbol{\beta}\boldsymbol{\theta}|\bar{\pi}, n) d(\alpha + \boldsymbol{\beta}\boldsymbol{\theta}) \right] p(\bar{\pi}|n) d\bar{\pi}$$

$$- \int_{\alpha+\boldsymbol{\beta}\boldsymbol{\theta}} (\alpha + \boldsymbol{\beta}\boldsymbol{\theta}) p_{prior}(\alpha + \boldsymbol{\beta}\boldsymbol{\theta}) d(\alpha + \boldsymbol{\beta}\boldsymbol{\theta}) - \frac{c}{m} n,$$

where $p_{post}(\alpha + \boldsymbol{\beta}\boldsymbol{\theta}|\bar{\pi}, n)$ is the buyer's posterior distribution of profit conditional on the sufficient

statistic $\bar{\pi} = \frac{1}{n} \sum_{i=1}^{n} \pi_i$ and sample size n and $p_{prior}(\alpha + \boldsymbol{\beta}\boldsymbol{\theta})$ is the buyer's prior distribution of

expected profit in equation (8). Given that both the likelihood function and the buyer's prior

distribution of expected profit are normally distributed, the posterior distribution is also well known

to be normally distributed as (Hoff, 2009):

(10)
$$\alpha + \boldsymbol{\beta}\boldsymbol{\theta}|\bar{\pi}, n \sim N \left(\frac{(\boldsymbol{\beta}\boldsymbol{\Sigma}\boldsymbol{\beta}')(\alpha + \boldsymbol{\beta}\boldsymbol{\mu}_b) + n(\boldsymbol{\beta}\boldsymbol{V}_b\boldsymbol{\beta}')\bar{\pi}}{(\boldsymbol{\beta}\boldsymbol{\Sigma}\boldsymbol{\beta}') + n(\boldsymbol{\beta}\boldsymbol{V}_b\boldsymbol{\beta}')}, \frac{(\boldsymbol{\beta}\boldsymbol{\Sigma}\boldsymbol{\beta}')(\boldsymbol{\beta}\boldsymbol{V}_b\boldsymbol{\beta}')}{(\boldsymbol{\beta}\boldsymbol{\Sigma}\boldsymbol{\beta}') + n(\boldsymbol{\beta}\boldsymbol{V}_b\boldsymbol{\beta}')} \right).$$

From this familiar solution we can see that when $n = 0$ the mean and variance of the posterior

distribution reduce to the buyer's prior distribution of profit in equation (8). However, at values of

$n > 0$ the mean and variance of the posterior distribution converge towards the sample mean and

sample variance.

Because of the linearity assumption of the profit function, the integrals in equation (9) can be

evaluated by replacing the random parameters with their expected values. For example, the integrals

with respect to $\alpha + \boldsymbol{\beta}\boldsymbol{\theta}$ can be evaluated by replacing the unknown values of profit with the expected

values of the buyer's posterior and prior distributions of profit, respectively:

(11)
$$\max_{n \geq 0} r(n) = \int_{\bar{\pi}} \left[\frac{(\boldsymbol{\beta}\boldsymbol{\Sigma}\boldsymbol{\beta}')(\alpha + \boldsymbol{\beta}\boldsymbol{\mu}_b) + n(\boldsymbol{\beta}\boldsymbol{V}_b\boldsymbol{\beta}')\bar{\pi}}{(\boldsymbol{\beta}\boldsymbol{\Sigma}\boldsymbol{\beta}') + n(\boldsymbol{\beta}\boldsymbol{V}_b\boldsymbol{\beta}')} \right] p(\bar{\pi}|n) d\bar{\pi}$$

$$- (\alpha + \boldsymbol{\beta}\boldsymbol{\mu}_b) - \frac{c}{m} n.$$

Given that the objective function is from the seller's perspective, the density of the sample mean is

known to be $\bar{\pi}|n \sim N \left(\alpha + \boldsymbol{\beta}\boldsymbol{\mu}_s, \frac{1}{n}(\boldsymbol{\beta}\boldsymbol{V}_s\boldsymbol{\beta}') \right)$. Therefore, the integral with respect to $\bar{\pi}$ can also be

evaluated by replacing $\bar{\pi}$ with its expected value, $\alpha + \boldsymbol{\beta\mu_s}$. As a result, equation (11) can be rewritten as:

(12)
$$\max_{n \geq 0} r(n) = \frac{(\boldsymbol{\beta\Sigma\beta'})(\alpha + \boldsymbol{\beta\mu_b}) + n(\boldsymbol{\beta V_b\beta'})(\alpha + \boldsymbol{\beta\mu_s})}{(\boldsymbol{\beta\Sigma\beta'}) + n(\boldsymbol{\beta V_b\beta'})} - (\alpha + \boldsymbol{\beta\mu_b}) - \frac{c}{m}n.$$

In practice, sample size n is an integer. However, if we treat n as continuous for ease of exposition, we can maximize $r(n)$ by letting $\frac{dr(n)}{dn} = 0$. Taking the derivative of equation (12) and solving for n, the optimal sample size, n^*, is:

(13)
$$n^* = \frac{\sqrt{(\boldsymbol{\beta\Sigma\beta'})(\boldsymbol{\beta V_b\beta'})(\boldsymbol{\beta\mu_s} - \boldsymbol{\beta\mu_b})} - (\boldsymbol{\beta\Sigma\beta'})\sqrt{\frac{c}{m}}}{(\boldsymbol{\beta V_b\beta'})\sqrt{\frac{c}{m}}}.$$

The second order condition indicates that the solution in equation (13) maximizes the seller's returns from sampling for values of $\boldsymbol{\beta\mu_s} > \boldsymbol{\beta\mu_b}$:

(14)
$$\frac{d^2 r(n)}{dn^2} = \frac{-2(\boldsymbol{\beta\Sigma\beta'})(\boldsymbol{\beta V_b\beta'})^2(\boldsymbol{\beta\mu_s} - \boldsymbol{\beta\mu_b})}{[(\boldsymbol{\beta\Sigma\beta'}) + n(\boldsymbol{\beta V_b\beta'})]^3} < 0 \ \forall \ \boldsymbol{\beta\mu_s} > \boldsymbol{\beta\mu_b}.$$

That is, as long as the seller's prior expectation of profit is higher than the buyer's prior expectation of profit, $n^* = \text{agrmax}\{r(n)\}$. This makes sense given that a seller who knows that the quality of their cattle is lower than the buyer's prior expectation has no incentive to test.

Alternative Applications for Genetic Testing of Beef Cattle

The framework described above is just one of many applications of this method to genetic testing for beef cattle. For example, similar to the scenario described above, a producer could use a sample of genetic information to determine whether or not to retain ownership of a lot of feeder cattle. Another potential alternative is that a feedlot may want to differentially manage cattle based on genetics, or marker-assisted management, but cannot collect genetic information until after they have purchased a lot of feeder cattle. In this case, the benefit portion of the objective function will be the improvement in feedlot profit from improved management decisions, including how cattle are fed, how

technologies such as implants and beta agonists are used, and how cattle are marketed (Van

Eenennaam and Drake, 2012), and the cost portion will remain the same. Therefore, the feeder now

chooses some feedlot management decision variable (d; e.g., marketing method and/or days-on-feed)

and the number of animals to be sampled (n), and the objective function in equation (5) can be re-

specified as:

(15)
$$\max_{n \geq 0} \left\{ \int_X \max_{d \geq 0} \left[\int_\theta \pi(d, \boldsymbol{\theta}) p_{post}(\boldsymbol{\theta}|\boldsymbol{X}, n) d\boldsymbol{\theta} \right] p(\boldsymbol{X}|n) d\boldsymbol{X} \right.$$

$$\left. - \int_\theta \pi(d, \boldsymbol{\theta}) p_{prior}(\boldsymbol{\theta}) d\boldsymbol{\theta} - \frac{c}{m} n \right\},$$

where profit is now a function of the feedlot management decision variable d and genetics $\boldsymbol{\theta}$,

$p_{post}(\boldsymbol{\theta}|\boldsymbol{X}, n)$ is the feeder's posterior distribution of $\boldsymbol{\theta}$ conditional on the genetic information $\boldsymbol{X}$

collected from a random sample of n animals, and $p_{prior}(\boldsymbol{\theta})$ is the feeder's prior distribution of $\boldsymbol{\theta}$.

While it is important to acknowledge alternative applications of this model, for simplicity in this

paper we focus on the original context discussed above of a seller trying to convince a buyer that their

cattle are higher quality in order to receive a premium.

Data

Data were provided by Neogen, the parent company of commercial testing service Igenity, for 2,976

commercially-fed cattle from a single feedlot in Iowa. Cattle represented year-round placements in

the years 2007 and 2008. At placement, animals were weighed and a hair sample or tissue punch from

ear tag application was collected for genetic testing. Genetic information was provided in the form of

MBVs for the following seven traits: marbling, yield grade, rib-eye area (in^2), hot-carcass weight

(lbs.), average daily gain (lbs./day), tenderness (lbs. of Warner-Bratzler shear force [WBSF]), and

days-on-feed (days). Each of these markers, except hot-carcass weight and days-on-feed, have been

found to be significantly correlated with the traits they are designed to predict in independent

validations (DeVuyst et al., 2011; National Beef Cattle Evaluation Consortium, 2015). Molecular

breeding values are a continuous representation of an animal's genetic potential to express a given trait. Similar to expected progeny differences (EPDs), MBVs are reported in the units of the trait they represent. However, they are interpreted as the "relative differences expected in animals across breeds compared to their contemporaries" (Igenity, 2013, p. 2). For example, if two animals exposed to the same environmental and management conditions have marbling MBVs of -100 and 100, respectively, we would expect, on average, that these two animals' marbling scores would differ by 200 units (100 - [-100] = 200). Additional live-animal characteristics for days-on-feed, sex, and hide color were also provided, and carcass performance measurements, including calculated yield grade, marbling score, and hot-carcass weight, were collected at slaughter. Summary statistics for carcass performance, live-animal characteristics, and MBVs are reported in table IV-1.

The data consist of 101 contemporary groups, which are defined as groups of animals that had an equal opportunity to perform: same sex, managed alike, and exposed to the same feed resources. These groups ranged in size from 11 to 69 animals with an average group size of 29 animals. While most of the groups are expected to be from a single producer, the extent to which some cattle were comingled from different herds was not recorded. Therefore, the results of our analysis are conditional on the data that we use, and may underestimate the value of testing for cattle that are known to have homogeneous genetics. Sensitivity analysis is done to provide some context for the results presented here.

Procedures

Using the data described above we estimate the parameters needed to obtain the optimal sample size in equation (13) and the returns from sampling in equation (12). A brief description of each of the parameters along with their baseline values and a range of parameter values for sensitivity analysis are reported in table IV-2. The procedures for how these parameters and their ranges were estimated from the data are discussed below.

Expected Profit

The intercept and slope coefficients in the buyer's profit equation, α and $\boldsymbol{\beta}$, are estimated using a mixed model regression of feedlot profit on the MBVs. Prior to estimating these parameters an estimate of profit for each animal in the sample was generated using grid pricing:

$$(16) \qquad \pi = P(YG, QG, HCW) \times HCW - PC(PWT, SEX) - FC(DOF) - YC(DOF)$$
$$- IC(PC, DOF),$$

where P is the grid price which is a function of actual yield grade (YG), quality grade (QG), and hot-carcass weight (HCW), PC is the purchase cost of feeder cattle which is a function of placement weight (PWT) and sex (SEX), FC is feed cost, YC is yardage cost, and IC is interest cost on the purchase of feeder cattle which are all a function of days-on-feed (DOF). Fed cattle prices, including grid premiums and discounts, and feeder cattle prices were simple averages of the weekly prices reported by the USDA Agricultural Marking Service (AMS) for the 2014 marketing year and were obtained from the Livestock Marketing Information Center (LMIC) spreadsheets (LMIC, 2015; USDA AMS, 2015). The prices used in this analysis are reported in table IV-3. Observations of feed intake were not available. Therefore, a standardized estimate of feed intake was generated for each animal in the sample using the dry matter intake model from the National Research Council's (NRC) *Nutrient Requirements of Beef Cattle* (NRC, 2000). For examples of the National Research Council's dry matter intake model see Lusk (2007) or Thompson et al. (2014). Additional information needed to evaluate profit includes a dry matter feed cost of $230/ton ($0.12/lb.), yardage cost of $0.40/day, and a 7% interest rate on the purchase of feeder cattle (Lardy, 2013).

Using equation (16), estimates of profit for the animals in our sample are generally negative. This is contradictory to Tonsor (2015), which reported that feedlot net returns in Kansas were positive for most of 2014. However, negative returns to cattle feeding are common with average net returns over the past 13 years being -$26.77 and -$15.44/head for steers and heifers, respectively (Tonsor, 2015). The discrepancy between our estimates of profit and those reported by Tonsor (2015) are

likely due to differences in the input and output prices used in this analysis and those observed when cattle in our sample were actually being fed.

A mixed model regression equation of profit on MBVs and other live-animal characteristics is then estimated as:

$$(17) \quad \pi_{ij} = \alpha_0 + \alpha_1 PWT_{ij} + \alpha_2 DOF_{ij} + \alpha_3 DOF_{ij}^2 + \alpha_4 PWT_{ij}DOF_{ij} + \alpha_5 STR_{ij}$$

$$+ \alpha_6 BLK_{ij} + \boldsymbol{\beta X}_{ij} + v_j + \varepsilon_{ij},$$

where π_{ij} is the estimated feedlot profit for the ith animal in the jth contemporary group, PWT_{ij} is placement weight, DOF_{ij} is days-on-feed, STR_{ij} is a dummy variable equal to one if the animal was a steer and zero otherwise, BLK_{ij} is a dummy variable equal to one if the animal was black-hided and zero otherwise, $\boldsymbol{X}_{ij}$ is a 7×1 vector of MBVs characterizing marbling, yield grade, rib-eye area, hot-carcass weight, average daily gain, tenderness, and days-on-feed, $v_j \sim N(0, \sigma_v^2)$ is a contemporary group random effect, and $\varepsilon_{ij} \sim N(0, \sigma_\varepsilon^2)$ is a random error term.

The model is estimated using Proc Mixed in SAS (SAS Institute Inc., 2013). D'Agostino-Pearson K^2 omnibus test for skewness and kurtosis and a conditional variance test identified evidence of nonnormality and static heteroskedasticity. Sandwich estimators of the standard errors were estimated to obtain estimates of standard errors that were consistent in the presence of nonnormality and static heteroskedasticity (White, 1982). Given the large sample size, asymptotic properties are relevant, and the small sample biases common with generalized method of moments estimators should be of little concern.

Results from the estimation of equation (17) are reported in table IV-4. Live-animal characteristics generally exhibited the expected relationships with the only notable result being that, on average, fed cattle profit for steers was $75/head less than heifers. While previous research has discussed the potential for heifers to generate higher returns (Williams et al., 1993; Tonsor, 2015), steers are usually expected to generate higher fed cattle profit. In this case, the discrepancy between feedlot profit for steers and heifers is a result of the prices used. Although feeder cattle prices include

a premium for steers regardless of the weight class, the average dressed fed cattle prices used as the base for the grid were nearly identical for steers and heifers. Fixed effects for live-animal characteristics are not of interest in this study, so these variables are set to their mean values and absorbed into the intercept, $\alpha = \alpha_0 + \alpha_1 \overline{PWT} + \alpha_2 \overline{DOF} + \alpha_3 \overline{DOF^2} + \alpha_4 \overline{PWT} \times \overline{DOF} + \alpha_5 \overline{STR} + \alpha_6 \overline{BLK}$. Thus, the profit equation can be written as a linear function of the MBVs, $\pi = \alpha + \boldsymbol{\beta X}$.

Each of the MBV effects, except for the rib-eye area MBV, is positive. This is consistent with expectations given that higher MBVs correspond with more favorable outcomes for the traits they characterize. The marbling and hot-carcass weight MBVs were the only markers to significantly influence fed cattle profitability. The negative effect of the rib-eye area MBV is likely due to genetic correlations among the MBVs included in our model. Specifically, the known inverse relationship between rib-eye area and marbling is likely the primary driver of this result (DeVuyst et al., 2011). That is, more favorable rib-eye area outcomes are often accompanied by less favorable outcomes for marbling. Therefore, for the grid used in this analysis, the premiums associated with more favorable rib-eye area (yield grade) outcomes are not enough to offset the lower premiums, or higher discounts, associated with less favorable marbling (quality grade) outcomes.

Buyer and seller expectations of profit are estimated from the data using equation (17). We assume that the buyer's expected value of profit, $\alpha + \boldsymbol{\beta \mu_b}$, is equal to the mean profit observed in our data. Given linearity of the profit function, this is equivalent to profit at the mean values of the seven MBVs. If the seller's expectation of profit is less than or equal to the buyer's prior expectation of profit then the optimal sample size is zero. That is, there is no incentive to test if sellers know that their cattle will have below-average profitability. However, for any combination of MBVs that $\alpha + \boldsymbol{\beta \mu_s} > \alpha + \boldsymbol{\beta \mu_b}$ there is a potential benefit to testing. Therefore, the baseline value for the seller's expectation of profit is arbitrarily assumed to be equal to the 75th percentile of profit observed in our sample, and sensitivity analysis is conducted for values of $\alpha + \boldsymbol{\beta \mu_s}$ ranging from the mean to

the maximum profit observed in the sample to determine the effect of the quality of a particular set of cattle on optimal sample size and the returns from sampling.

Variance of Profit Between and Within Pens

The variances of the MBVs *between* and *within* lots of cattle (i.e., the diagonal elements of V_b and Σ, respectively) can be estimated using a random effects model for each of the seven MBVs:

(18) $$MBV_{ijk} = \mu_k + g_{jk} + e_{ijk},$$

where the dependent variable is the kth MBV for the ith animal in the jth contemporary group, μ_k is the mean for the kth MBV, $g_{jk} \sim N(0, \tau_k^2)$ is a contemporary group random effect where τ_k^2 is the variance of the kth MBV *between* groups of cattle, and $e_{ijk} \sim N(0, \sigma_k^2)$ is a random error term where σ_k^2 is the variance of the kth MBV *within* groups. Models for each of the seven MBVs were estimated independently using Proc Mixed in SAS (SAS Institute Inc., 2013).

Estimates of the between and within variance from the random effects models are reported in table IV-5. The variance of the MBVs within contemporary groups was generally higher than the variance between groups. As discussed earlier, this result could indicate that some of the cattle in our sample were comingled for feeding. That is, cattle from different sources with differing genetics were fed in the same contemporary group resulting in higher within pen variability than may be experienced by a single producer with a lot of cattle with homogenous genetics. Nonetheless, the estimated variances, along with the correlation matrix of the seven MBVs, can be used to calculate the covariances, or off-diagonal elements, of V_b and Σ using the known relationship between them, $Cov(x, y) = \rho_{x,y}\sigma_x\sigma_y$. Variance-covariance matrices of genetics are then converted to scalar estimates of the variance of profit within and between lots of cattle using the vector of parameter values $\boldsymbol{\beta}$.

In addition to their baseline values, the variance of profit between ($\boldsymbol{\beta}V_b\boldsymbol{\beta}'$) and within ($\boldsymbol{\beta}\Sigma\boldsymbol{\beta}'$) lots of cattle is subjected to sensitivity analysis to determine how the homogeneity or

heterogeneity of a particular lot of cattle influences optimal sample size and the returns from sampling. The upper and lower bounds for the sensitivity analysis of both $\boldsymbol{\beta V_b \beta'}$ and $\boldsymbol{\beta \Sigma \beta'}$ were approximately set to equal the maximum and minimum variance of profit observed for the contemporary groups in our data.

Cost of Genetic Testing

The final component to evaluating the optimal sample size in equation (13) is the per-head cost of genetic testing, $\frac{c}{m}$. The current cost of commercially available genetic testing services is $c = \$40$/head (Igenity, 2015). Therefore, assuming the data collected is applied to a pen of $m = 100$ animals, the cost of testing an additional animal is $0.40/head. In addition to this baseline value, sensitivity analysis is conducted for costs of testing ranging from $0.10/head to $1.00/head. These values are evaluated to account for differing costs of testing due to smaller or larger lots of cattle and to account for the potential decreasing cost of genetic testing services.

Results

The optimal sample size and returns from sampling are first evaluated at the baseline parameter values in table IV-2. A plot of the expected value of sample information (EVSI), total cost, and expected net gain (ENG), as a function of sample size (n), are reported in figure IV-1. The EVSI is increasing sharply for small sample sizes as the genetic information collected from each additional animal contains valuable information. However, as sample size increases above $n = 20$ the EVSI levels off at values of $16-$18/head. Given that the cost of testing each additional animal is the same, $0.40/head, the total cost function is linear with respect to sample size. The difference in the EVSI and total cost is the ENG, or the returns from sampling. Results indicate that in this case an optimal sample size of $n^* = 10$ maximized the ENG. Despite only testing 10% of the animals, the returns from sampling are $9.79/head compared with not testing any animals and accepting the buyer's prior expectation of the genetic makeup of the pen. Aggregating across the assumed pen size of $m = 100$

animals, that is a net return of approximately $1,000 from a $400 investment, or a 250% return-on-investment. These results indicate that random sampling has the potential to provide a context in which the benefits of genetic testing outweigh the costs, which has not generally been the case in previous research where each individual animal was tested and the results were used to sort cattle into management groups.

Sensitivity analysis is conducted to evaluate the robustness of these results with respect to the parameters $\alpha + \boldsymbol{\beta}\boldsymbol{\mu}_s$, $\boldsymbol{\beta}\boldsymbol{\Sigma}\boldsymbol{\beta}'$, $\boldsymbol{\beta}\boldsymbol{V}_b\boldsymbol{\beta}'$, and $\frac{c}{m}$. As expected, holding all else constant, optimal sample size and the returns from sampling are both increasing with respect to the seller's expectation of profit ($\alpha + \boldsymbol{\beta}\boldsymbol{\mu}_s$; figure IV-2, panel i). That is, sellers with higher quality (more profitable) cattle have an incentive to test more animals. However, consider that the optimal sample size for a lot of cattle with a genetic makeup similar to the most profitable animals in our sample is only about $n^* = 24$. Although the returns from testing for such animals are quite high, nearly $60/head, the marginal return to testing additional animals beyond $n = 24$ is not enough to offset the marginal cost of obtaining additional information. Therefore, at the baseline values for the variance of profit between and within lots of cattle and the cost of testing, the benefits of genetic testing can be captured by testing a relatively small portion of a lot of feeder cattle (less than 25 out of 100 animals for a set of very high-quality cattle).

Optimal sample size is also increasing with the variance of profit *within* a lot of cattle ($\boldsymbol{\beta}\boldsymbol{\Sigma}\boldsymbol{\beta}'$; figure IV-2, panel ii). However, the returns from sampling are simultaneously decreasing. That is, the additional noise associated with more heterogeneous lots of cattle make it more difficult to identify improvements in the actual quality of a particular set of cattle. As a result, more animals must be tested in order to "convince" buyers that a particular set of cattle is actually higher quality. In addition, the marginal return to testing each additional animal is decreased relative to more homogeneous lots of cattle resulting in decreased returns from sampling. For example, a set of cattle with variability similar to the most heterogeneous lot of cattle observed in our sample has an optimal

sample size of $n^* = 12$, but the returns from sampling are only about \$4/head. On the other hand, producers selling feeder cattle that are known to have very homogeneous genetics may be able to capture a large portion of the additional value by testing a relatively small percentage of the cattle. For example, the returns from sampling for a set of cattle with variability similar to the most homogeneous group of cattle in our sample is \$15/head with an optimal sample size of just $n^* = 5$.

In the case that the buyer is completely uninformed, the variance of profit *between* lots of cattle is used to characterize the variance of the buyer's subjective prior distribution of expected profit for a lot of feeder cattle. Contrary to within variability described above, optimal sample size is decreasing with the variance of the buyer's prior distribution of expected profit ($\boldsymbol{\beta V_b \beta'}$), and the returns from sampling are increasing (figure IV-2, panel iii). This indicates that as the buyer's prior distribution of expected profit becomes more uninformed (i.e., more diffuse), it is easier to persuade their opinion away from their prior expectation towards the seller's expectation of the actual profitability of the pen. As a result, fewer animals need to be tested to "convince" the buyer that the cattle are actually higher quality, and the marginal returns from testing each additional animal becomes more valuable. For example, if the buyer is completely uninformed (high variance for the prior distribution of profit) the optimal sample size is $n^* = 4$, and the returns from sampling are over \$16/head. However, for buyers with very narrow prior distributions of expected profit the optimal sample size is $n^* = 11$ and the returns from sampling are just \$8/head.

Lastly, as would be expected, the per-head cost of testing $\left(\frac{c}{m}\right)$ is inversely related to optimal sample size and the returns from sampling (figure IV-2, panel iv). That is, as the marginal cost of testing increases, the ENG of testing each additional animal is reduced, and as a result, optimal sample size will decrease. The cost of testing is made up of two components: the cost of genetic testing services (c) and the size of the pen to which the information collected is being applied (m). Therefore, a lower per-head cost of testing could be the result of either a reduction in the cost of the test due to technological advancements or an increase in the number of animals to which the decision

is applied. Either way, results indicate that the ability to reduce the cost of testing would enable

sellers to test more animals allowing them to achieve closer to the full value of their cattle. For

example, the ability to cut the baseline value of per-head testing cost in half, $0.20/head, increases the

optimal sample size to $n^* = 15$ and the returns from testing to $12/head. Conversely, doubling the

per-head cost of testing, $0.80/head, leads to an optimal sample size of $n^* = 6$ animals and returns

from sampling of less than $7/head.

Conclusions

In this article, we introduce an economic approach to sample size determination utilizing a Bayesian

decision theoretic framework (Grundy, Healy, and Rees, 1956; Riffa and Schlaifer, 1961; Lindley,

1997). To date, few economic studies explicitly consider the endogeneity of sample size and so this

method is scarcely used in economic research. However, this method is a theoretically sound

approach to determining sample size for many economic problems and should be considered in a

wide range of economic modeling problems. For example, consider a generic scenario in which a new

policy is to be implemented for the betterment of society. Prior to its implementation, the policy

maker must determine the optimal level of the policy through an assessment of its effect on the

population. In most cases, it would be too costly to take a census. However, there is significant value

associated with obtaining a sufficient sample to determine the level of the policy that will maximize

the overall benefits. Therefore, sample size is an endogenous variable that needs to be considered

jointly with other decision variables by utilizing an objective function to balance the expected costs

and benefits of sampling.

To demonstrate the method for a relevant applied economics problem, we turn to the problem

of asymmetric information in the market for feeder cattle. A theoretical model is developed

characterizing a scenario in which sellers (producers) who know that their feeder cattle have high-

value genetics are trying to convince buyers (feedlots) that their cattle are higher quality in order to

receive a premium above the prevailing market price. However, in order to establish the actual

genetic makeup of a lot of feeder cattle, the seller must incur the cost of genetic testing. Using the Bayesian sampling model we determine the economically-optimal sample size and the returns from sampling.

Results from this example indicate that the marginal benefit to testing is high for small sample sizes as the genetic information collected from each additional animal contains valuable information. However, as the sample size increases the marginal expected value of sample information diminishes quickly, indicating that a large portion of the additional value for higher-quality cattle can be estimated by testing a relatively small percentage of a lot of feeder cattle. For example, at the baseline parameter values the optimal sample size is $n^* = 10$ animals out of a lot of 100 feeder cattle and the returns from sampling are nearly $10/head. Aggregating across the assumed pen size of 100 animals, that is a net return of approximately $1,000 from a $400 investment, or a 250% return-on-investment. Sensitivity analysis was conducted to provide some context, and results indicated that the optimal sample size and returns from sampling may increase or decrease depending on the actual quality (or profitability) of a particular pen of cattle, the homogeneity within the pen, the variance of the buyer's subjective prior distribution of expected profit, and the per-head cost of genetic testing. The only scenario evaluated in which the returns from sampling were not positive was if the seller's expectation of profit was less than or equal to the buyer's prior expectation of profit, in which case the optimal sample size is $n^* = 0$.

Nonetheless, results suggest that random sampling has the potential to provide a context in which the benefits of genetic testing outweigh the costs, which has not generally been the case in previous research. Previous research demonstrates that genetic differences generate measurable differences in fed cattle profitability. However, the per-head difference in profit has been shown to be less than genetic testing costs. So prior to this research, genetic testing of feeder cattle for feedlot placement decisions has not been considered economically advisable. Our sampling method demonstrates that economically-optimal sampling of feeder cattle can improve profitability. This is the first research to demonstrate the potential for genetic testing of feeder cattle to improve net return

from testing. So, this research represents an important contribution to the literature evaluating the economic value of genetic testing for beef cattle and potentially more importantly to the beef cattle industry. While demonstrated for a feeder calf sale, the method can be similarly applied for a fed calf sale to packers or boxed beef sale to high-end retailers.

When interpreting the results presented here consider that we only include the direct cost of genetic testing. However, there may be additional management and handling costs associated with collecting samples for genetic testing. As indicated in previous research, these additional costs could be mitigated, or even eliminated, if samples were collected at a point when animals are already being handled (Koontz et al., 2008). Perhaps the more troublesome issue is that if the seller is the one making the sampling decision, will they truly select a "random sample?" That is, there is an incentive for the seller to selectively sample animals known to be higher quality. This raises the question of whether third-party verification would be needed to ensure the cattle being tested are really a random sample. This is similar to the third-party verification associated with value-added feeder cattle sales (Chymis et al., 2007; Williams et al., 2012), and brings about the potential for some additional costs that may need to be considered in order for the application described here to succeed. However, using third-party verified value-added feeder calf sales as the metric, this cost is likely much less than estimated returns from genetic sampling.

It is also important to note that the static context described here does not lead to changes in the product form, and as a result, does not appear to generate any additional value. Instead, value is redistributed between buyers and sellers. However, by better aligning prices received by feeder calf producers with traits desired by feedlot operators, economically-optimal genetic testing has the potential to reduce misaligned incentives and improve the overall profitability of the beef industry. By reducing asymmetric information, cow-calf producers with genetics valued by feedlot operators are compensated for those genetics. This provides the incentive to produce more cattle that perform better in feedlots with higher value carcasses, so profits for the beef sector improve. While the model presented here assumes that profits accrue to the cow-calf producer for tractability, the likely outcome

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is a division of profits from sampling to both buyer and seller. In addition, if feedlot operators were subsequently able to use the genetic information provided by sellers to improve feedlot management decisions, including how cattle are fed, how technologies such as implants and beta agonists are used, and how cattle are marketed (Van Eenennaam and Drake, 2012), they could generate additional value by changing the product form (Koontz et al., 2008). This additional information would lead to reduced inefficiencies associated with cattle feeding and could potentially create social welfare gains through improved quality and consistency of beef products.

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Table IV-1. Summary Statistics for Carcass Performance, Live-Animal Characteristics, and Molecular Breeding Values (n = 2,976)

Variable	Mean	Standard Deviation	Minimum	Maximum
Carcass performance				
Marbling score	414.43	70.87	250.00	830.00
Yield grade	2.97	0.58	0.31	5.10
Hot-carcass weight, cwt.	7.20	0.70	4.58	9.83
Live-animal characteristics				
Placement weight, cwt.	6.55	1.24	2.94	11.16
Days-on-feed, days	171.51	29.09	106.00	238.00
Steer[a]	0.74			
Black[b]	0.78			
Molecular breeding values (MBV)				
Marbling MBV	-16.44	26.94	-119.37	68.26
Yield grade MBV	-0.06	0.07	-0.28	0.20
Rib-eye MBV, in^2	-0.78	0.47	-2.16	1.38
Hot-carcass weight MBV, lbs.	28.43	9.06	-15.57	55.91
Average daily gain MBV, lbs./day	0.20	0.10	-0.12	0.48
Tenderness MBV, lbs. of WBSF[c]	-1.49	1.52	-5.90	2.92
Days-on-feed MBV, days	-2.83	2.95	-14.28	8.35

Note: Molecular breeding values (MBVs) are reported in the units of the trait and reflect the differences expected in animals across breeds compared to their contemporaries (Igenity, 2013). Therefore, mean MBVs offer little insight. Instead, the range of MBVs is more informative. For example, the range of average daily gain MBV suggests that the animal with the highest genetic potential for average daily gain in the sample would be expected, on average, to gain approximately 0.60 lbs./day more than the animal with the lowest genetic potential for average daily gain (0.48 - [-0.12] = 0.60).

[a] Steer is a dummy variable equal to one if the animal was a steer and zero otherwise.
[b] Black is a dummy variable equal to one if the animal was black-hided and zero otherwise.
[c] Warner-Bratzler shear force.

Table IV-2. Parameter Definitions, Baseline Values, and Ranges for Sensitivity Analysis

Parameter	Definition	Baseline Value	Range for Sensitivity Analysis
$\alpha + \beta\mu_s$	Seller's expectation of profit (\$/head)	-\$63.16	-\$82.30 to -\$3.74
$\alpha + \beta\mu_b$	Buyer's expectation of profit (\$/head)	-\$82.30	—
$\beta\Sigma\beta'$	Variance of profit *within* a lot of cattle	608.57	100 to 2000
$\beta V_b\beta'$	Variance of the buyer's subjective prior distribution of expected profit (variance of profit *between* lots of cattle)	157.01	100 to 2000
$\dfrac{c}{m}$	Cost of genetic testing (\$/head)	\$0.40	\$0.10 to \$1.00

Table IV-3. Average 2014 Base Price and Yield Grade, Quality Grade, and Hot-Carcass Weight Premiums and Discounts for Grid Pricing

Grid Component	Premium/(Discount)
	$/cwt.
Base price	
Steers	$244.22
Heifers	$244.21
Quality grade adjustment	
Prime	$19.26
Choice	$0.00
Select	($8.63)
Standard	($20.84)
Yield grade adjustment	
1.0-2.0	$4.58
2.0-2.5	$2.25
2.5-3.0	$2.13
3.0-4.0	$0.00
4.0-5.0	($8.63)
>5.0	($13.64)
Hot-carcass weight adjustment	
400-500	($25.42)
500-550	($22.19)
550-600	($2.93)
600-900	$0.00
900-1000	($0.24)
1000-1050	($2.27)
>1050	($23.24)

Source: USDA Agricultural Marketing Service (AMS) reports LM_CT150 and LM_CT169 obtained from the Livestock Marketing Information Center (LMIC) spreadsheets (LMIC, 2015; USDA AMS, 2015).

Table IV-4. Feedlot Profit Mixed Model Regression Estimates (n = 2,976)

Variable	Coefficient	Standard Error[a]
Intercept	-1151.33***	353.24
Placement weight	103.82***	25.15
Days-on-feed	8.08**	3.35
Days-on-feed squared	-0.01	0.01
Placement weight × days-on-feed	-0.60***	0.14
Steer[b]	-75.25***	10.88
Black[c]	2.08	7.58
Marbling MBV[d]	0.44***	0.12
Yield grade MBV	17.54	55.70
Rib-eye area MBV	-23.40**	9.58
Hot-carcass weight MBV	1.55***	0.31
Average daily gain MBV	27.21	32.32
Tenderness MBV	1.86	2.10
Days-on-feed MBV	0.30	0.84
quasi-R^{2}[e]	0.29	

Note: Dependent variable is estimated feedlot profit ($/head) from equation (16). Single, double, and triple asterisks (*, **, ***) indicate significance at the 10%, 5%, and 1% level.

[a] Standard errors are estimated using "sandwich estimators" to obtain estimates of standard errors that are consistent in the presence of nonnormality and static heteroskedasticity (White, 1982).

[b] Steer is a dummy variable equal to one if the animal was a steer and zero otherwise.

[c] Black is a dummy variable equal to one if the animal was black-hided and zero otherwise.

[d] Molecular breeding value.

[e] The quasi-R^{2} is calculated as the squared correlation of the actual and predicted values including the contemporary group random effect.

Table IV-5. Random Effects Model Estimates of Variance of Molecular Breeding Values Between and Within Lots of Cattle (n = 2,976)

Molecular Breeding Value	*Between* Variance	*Within* Variance
Marbling	191.730***	543.420***
Yield grade	0.001***	0.004***
Rib-eye area	0.046***	0.173***
Hot-carcass weight	11.184***	72.080***
Average daily gain	0.001***	0.008***
Tenderness	1.072***	1.332***
Days-on-feed	0.297***	8.425***

Note: Single, double, and triple asterisks (*, **, ***`) indicate significance at the 10%, 5%, and 1% level.
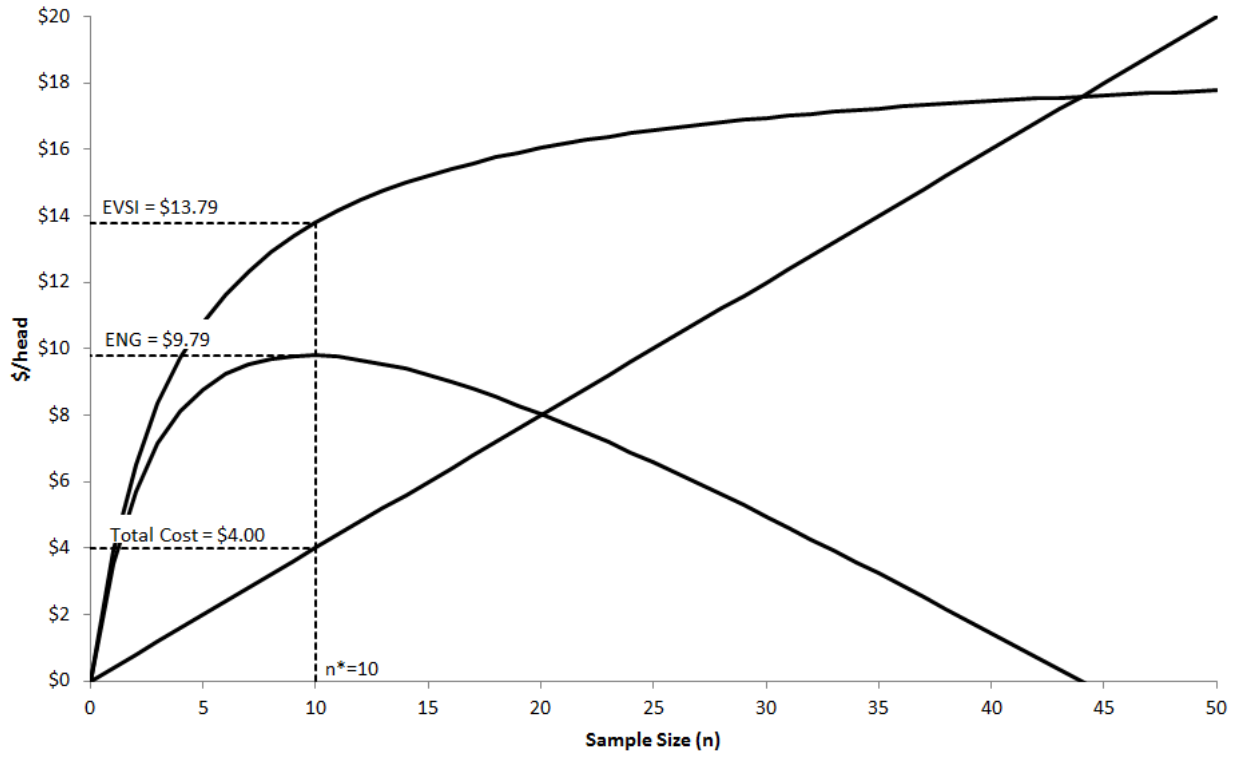
Figure IV-1. Expected value of sample information (EVSI), expected net gain (ENG), and total cost as a function of sample size (*n*) at the baseline parameter values
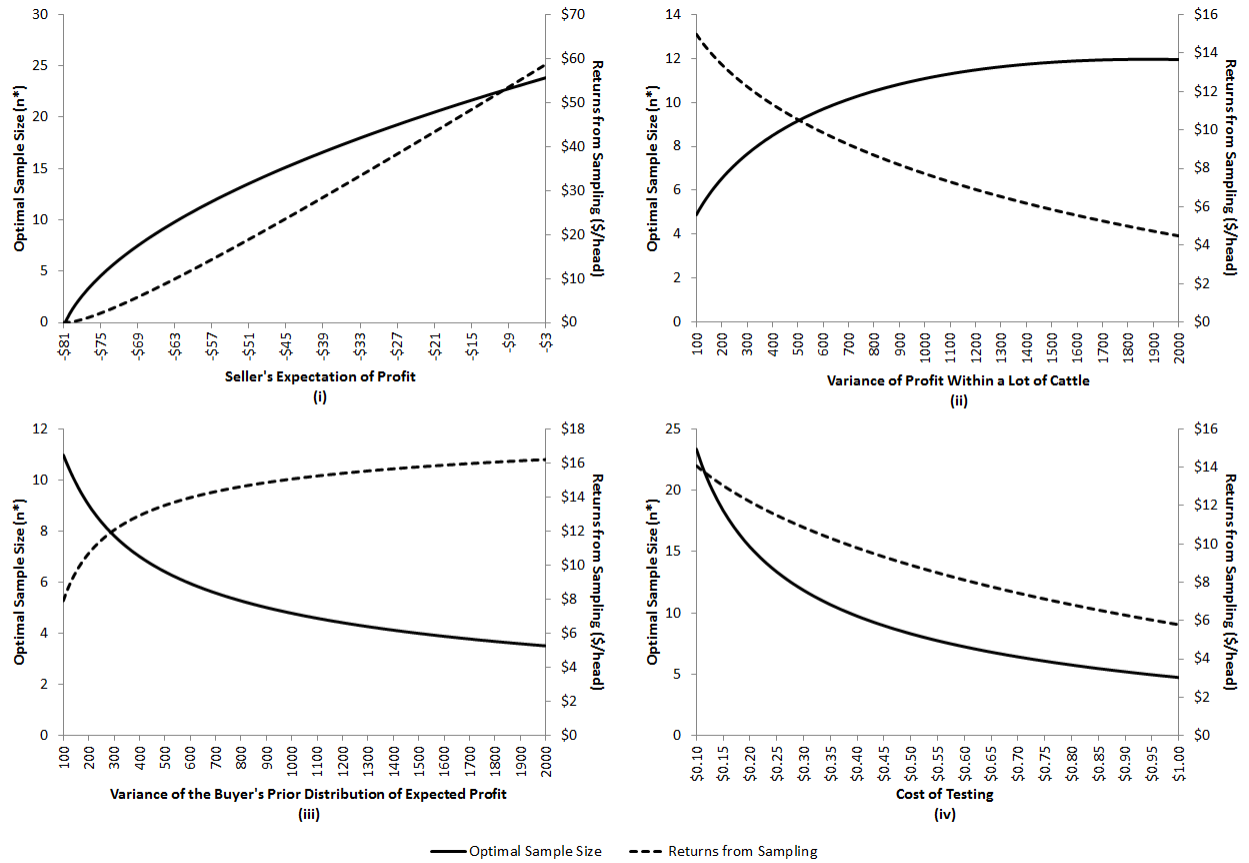
Figure IV-2. Sensitivity analysis of optimal sample size and the returns from sampling with respect to (i) the seller's expectation of profit $(\alpha + \beta\mu_s)$, (ii) the variance of profit within a lot of cattle $(\beta\Sigma\beta')$, (iii) the variance of the buyer's prior distribution of expected profit$(\beta V_b \beta')$, and (iv) the per-head cost of genetic testing $\left(\frac{c}{m}\right)$

VITA

Nathanael Mark Thompson

Candidate for the Degree of

Doctor of Philosophy

Thesis: ESSAYS ON THE ECONOMIC VALUE OF GENETIC TESTING IN BEEF
CATTLE PRODUCTION

Major Field: Agricultural Economics

Biographical:

Education:

Completed the requirements for the Doctor of Philosophy in Agricultural
Economics at Oklahoma State University, Stillwater, Oklahoma in December,
2015.

Completed the requirements for the Master of Science in Agricultural
Economics at the University of Tennessee, Knoxville, Tennessee in 2012.

Completed the requirements for the Bachelor of Science in Economics at the
University of South Florida, Tampa, Florida in 2010.

Experience:

Graduate Research Assistant, USDA National Needs Fellow
Oklahoma State University

Research Associate
University of Tennessee

Graduate Research Assistant
University of Tennessee

Professional Memberships:

Agricultural and Applied Economics Association

Southern Agricultural Economics Association