ASSOCIATION OF GENETIC PRODUCTION INDEXES WITH PRODUCTION OUTCOMES OF FEEDLOT STEERS

by

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ABSTRACT

Genetic knowledge is increasingly utilized within the beef seedstock sector, yet uncertainty remains on how to maximize these inputs at the commercial level. The objectives of this study were to evaluate the effect of sorting natural and conventionally marketed fed beef cattle according to a genetic prediction index on performance and carcass traits, and determine the association of genetic indices to economically important production outcomes. The study hypothesis was that sorting beef cattle by genetic index would not influence the outcome of economically important traits. Two cattle sources were utilized, Angus and Angus × Hereford steers that did not receive growth promoting technologies or antimicrobials to comply with a natural marketing program (NAT; n=98; initial BW = 362 ± 11 kg) and Angus steers that were fed conventionally (CONV; n=81; initial BW = 364 ± 11 kg). Cattle were assigned to pens within source and stratified according to a feeder advantage (FA1) index from least to greatest by pen (NAT=10 steers/pen and 9 pens/treatment; CONV=10 or 11 steers/pen and 7 pens/treatment). All cattle were managed similarly and fed the same basal diet with the exception that NAT diets did not contain antimicrobial (monensin or tylosin) or growth promoting technologies (implants or beta-agonist). Individual cattle were harvested upon achieving a target shrunk (4%) BW of 635 kg. Genomic indices for WW and gain increased quadratically ($P < 0.01$) as the FA1 index increased for both cattle types. For conventionally finished cattle, genomic indices for heifer pregnancy ($P \leq 0.02$) decreased whereas milk ($P < 0.01$), gain ($P < 0.01$), carcass weight ($P = 0.03$), marbling ($P < 0.01$), and ribeye area ($P = 0.02$) increased as the FA1 index increased. Daily dry matter feed

offered (DDMFO) increased quadratically ($P < 0.01$) as FA1 index increased for both NAT and CONV. Within the NAT cattle, FA1 index was correlated to DOF ($r = -0.39$; $P < 0.001$), DDMFO ($r = 0.35$; $P < 0.01$), SUMDMO ($r = -0.32$; $P < 0.01$), day 0 BW ($r = 0.30$; $P < 0.01$), and ADG ($r = 0.23$; $P < 0.05$). Among CONV cattle, FA1 index was positively correlated ($r = 0.44$; $P < 0.001$) to DDMFO. The FA1 index score means did not differ ($P = 0.08$) amongst USDA QG's, or USDA YG's ($P = 0.25$). Numerically, NAT cattle in FA group 75 to 82 were greatest in HCW ($P < 0.01$), dressed yield ($P < 0.01$), and total carcasses value ($P < 0.01$). Net return carcass basis ($P = 0.02$) was numerically greatest for FA group 32 to 41.

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CHATPER 1
INTRODUCTION

Advancements in applicable genomics technology have been made since the discovery and mapping of the bovine genome. One such advancement is the identification of single nucleotide polymorphisms (SNPs) that correlate with economically important traits, such as maternal, growth and carcass characteristics. Using these different SNPs, several companies have designed genetic tests geared towards specific traits of interest to help producers determine the genetic potential of cattle. Genetic potential using ADG and marbling indices has been demonstrated effectively categorized cattle for placement in the feedlot according to growth prediction has resulted in profit of approximately $38/animal (Amen et al., 2016).

In fed cattle, efficient gain is a primary driver for profitability. Sorting cattle into marketing groups using genetic technology, compared to traditional methods, (live weight, hide color, and frame score) improves the opportunity for profit (Thompson et al., 2015). In addition to improving the returns to cattle feeding, genetic sorting can also reduce the variability or risk associated with value-based marketing (Thompson et al., 2016).

Consumers are increasingly concerned about where their food comes from, resulting in opportunities for producers to feed cattle geared towards niche-markets, such as all-natural beef (Sawyer et al., 2003). To be classified as “all-natural”, cattle may be prohibited to receive any growth promotants or antimicrobials for up to the duration of

life of the cattle, depending on the specific requirements of a specific natural marketing program (USDA, AMS, 2009).

Eluding variation in cattle by knowing the genetic makeup can alleviate several challenges, such as cattle having excessive DOF causing over finished cattle. The objectives of this study were to evaluate the effect of sorting beef cattle according to a genetic prediction index on performance and carcass traits, and determine the association of various genetic indices to economically important production outcomes.

CHAPTER 2

LITERATURE REVIEW

2.1. History

The discovery of deoxyribonucleic acid (DNA) in 1869 by Friedrich Miescher led to today's understanding of the differences in genetic makeup between individuals. In 1953, Watson and Crick discovered that DNA is a double-stranded helix structure. Within a polymer of DNA, each nucleotide includes an inorganic phosphate which is connected to a sugar deoxyribose, and one of the four nitrogenous bases: adenine, guanine, cytosine, and thymine (Hartwell et al., 2000). Of the nitrogenous bases, adenine and guanine are purine-based and cytosine and guanine are pyrimidine-based (Watson and Crick, 1953).

Jay L. Lush, the modern-day father of animal breeding, worked with coworkers Hazel and Dickerson to define the concept of the "selection index" and "breeding values" (Green, 2008). Selection index is defined as measuring the net merit of breeding animals versus breeding values that are determined by the value of the gene to the progeny (Hazel, 1943). In 1935, Lush stressed that phenotypic improvement is limited by the current variation within a trait and that variation differs between traits (Hazel, 1943). To test this hypothesis, a study was conducted on young boars and gilts evaluating selection indices for growth performance, market suitability, and litter size. Relative history of the herd was documented for the Iowa Experiment Station swine herd from 1937 to 1940. Using this data Hazel and Lush (1943) developed equations for a selection index to give proper weight to each trait. Hazel and Lush (1943) reported weighted indexes were more efficient than selection of a single trait or several traits with an independent culling level

for each trait (Hazel, 1943). Limitations of this study included: environmental effects, dominance, and epistasis; causing difference in phenotypic appearances, not genetic makeup.

In the 1950s, artificial insemination techniques were developed allowing implementation by the cattle industry. It wasn't until the 1980s when the livestock breeding industry was revolutionized so that statistical methodology could be applied to large pedigreed performance databases, also referred to as best linear unbiased prediction (BLUP) methodology (Green, 2008). Scientists were able to use BLUP technology to calculate what are now referred to as expected progeny differences (EPDs). Expected progeny differences grant producers the ability to predict which genes will be transmitted within breeds using statistical methodology (Green, 2008). With the innovative technologies discovered, the new science of genomics began.

Genomics was first coined as a term in 1986 to describe the scientific discipline of mapping, sequencing, and analyzing genomic level DNA information (Green, 2008). Analysis of the genome allows researchers to better study inherited genes including those causing abnormalities and/or diseases. Further understanding occurred in humans by creating the National Human Genome Research Institute (NHGRI) in the late 1990s, now known as the Human Genome Project. Initially it focused all efforts and funding towards sequencing the human genome. Both physical and genetic linkages were used to determine which chromosome and specific location on the chromosome caused abnormalities and/or diseases within the human. By 2005, a detailed haplotype map was completed (Green, 2008). To broaden knowledge of human health, in 2002 the NHGRI decided to begin funding the genetic mapping of other mammalian species to discover

genetic differentiations within species. This led to the discovery of more markers for use in the detection of health issues in humans. A prime example is muscular hyperplasia, commonly observed in Belgian Blue cattle and humans displaying a phenotypic appearance of double muscling. Myostatin has been verified to be the cause of this abnormality from cattle and human chromosome 2 (Womack, 2005). This discovery was made possible because of the multiple genetic maps available from different mammalian species. Muscular hyperplasia was detected in mice because of the deletion of the *Gdf8* gene for encoding myostatin.

2.1.1. Techniques used to map the bovine genome

In bovine, there are 29 autosomal chromosomes from each parent and 2 sex chromosomes; consisting of approximately 50 trillion somatic cells, each containing 5.6 billion base pairs of DNA (Seidel, 2011). Within DNA, base pairs are sequenced to code for a specific protein, known as genes (Hartwell et al., 2000). Genes are responsible for phenotypic traits inherited from the sire and dam. When DNA is being translated, the sequencing can cause differences to occur because of base-pair substitutions, deletions, insertions, or translocation. Furthermore, these differences allow a way to pinpoint exactly which chromosome the mutation occurs on and identify the quantitative trait loci (QTL) that was inherited by the offspring. Mutations occur in several different forms such as, restriction fragment length polymorphism (RFLP), microsatellites, and SNPs. These different forms make it simpler to identify which genes were inherited from the sire and dam. The detection of an elimination site or recognition of a restriction site are discovered by RFLPs, which are produced during replications of a gene. When this transpires, DNA fragments are cut by a restriction enzyme, causing the DNA to vary in

size, thus making the restriction fragments easily detectable. Restriction enzymes originate in and can be purified from bacterial cells (Hartwell et al., 2000). Hundreds of restriction enzymes are in the body, the majority of recognition sites are between 4 to 6 base pairs in length and the DNA reads identical from the 5' to 3' direction (Hartwell et al., 2000).

There are two distinct ways that restriction fragments cut DNA, 1) straight through both DNA strands, creating fragments with blunt ends, or 2) unequally through the top and bottom strand, leaving single-stranded ends known as sticky ends. Sticky end fragments leave a base-pair available to be attached to a complementary sequence of DNA from any organism cut by the same restriction enzyme (Hartwell, et al., 2000).

Once the DNA is cut into pieces, the fragments are placed onto an electrophoresis gel plate to sort the DNA by size. At the top of the gel plate DNA is inserted, because DNA is negatively charged, the positive charge causes it to be pulled through the electrophoresis gel to the bottom. Thus, the fragments separate according to size, resulting in a unique banding pattern for each individual. Pulse field gel electrophoresis (PFGE) has the same concept as conventional gel electrophoresis, but multiple charges are applied to the gel at different directions to elongated large fragments of DNA to determine the size (Birren and Lai, 1993). Fragments that are 15 to 20 kilobases (kb) in length are ideal for PFGE (Birren and Lai, 1993). For the RFLPs to be informative, it must be able to distinguish between the two chromosomes of an individual (Hartwell et al., 2000). When a modification to the DNA strand happens, RFLPs are used as a marker for a particular site on a chromosome. The reason that RFLPs are important in

determining genetic differences is because the analysis can track the inheritance of a specific genomic segment.

Restriction fragments are used to make DNA clones to conduct research or to keep in libraries for future reference. There are two steps in cloning DNA fragments. First, fragments are sorted by size to find specialized chromosome-like carriers known as vectors. Vectors are used to ensure that transport, replication, and purification of individual DNA fragments takes place (Hartwell et al., 2000). Vectors enter the living cell, allowing replication to take place for the vector and the foreign DNA within it. To help connect the foreign DNA to the vector, DNA ligase is used. Physical traits of the vector allow for replication independently of the host cell's genome. Several different vectors differ depending on origin, construction, and carrying capacity. Examples of vectors include plasmids, bacteriophage lamda, cosmid, phagemid, bacteriophage P1, bacterial artificial chromosome (BAC), and yeast artificial chromosome (YAC). The second step of cloning DNA involves allowing the vector to transport individual fragments into living cells, causing replication of both the vector and genomic DNA.

Differences in vectors include: carrying capacity, origin, and makeup of the vector. Most vectors are hosted by a bacterial plasmid known as, *Escherichia coli*, except YAC host cells are yeast. Plasmids are double-stranded circular DNA that gain access to and replicate within the cytoplasm of bacterial cells. They are self-sufficient, meaning plasmids do not use the nuclear chromosomes to replicate. Valuable types of plasmids are ones that carry multiple restriction enzymes, thus allowing more opportunity for the chromosomes to insert the DNA in the vector. Once DNA is inserted, the origin of replication allows for the plasmid to replicate inside the bacterium. Plasmids carry an

antibiotic resistant gene, this gene communicates with the host cell to signal its presence and has the ability to survive in medium containing antibiotics (Hartwell et al., 2000). Carrying capacity of plasmids are 15 kb. Some DNA need larger capacity vectors in order to replicate. Bacteriophage lambda vectors are built from the genome of phage lambda to have a larger carrying capacity of up to 25kb of DNA in length. Phage lambda consist of double-stranded DNA virus that infects *E. coli*. Using the phage lambda genome as well, cosmids are hybrids between plamids and phage vectors (Hartwell et al., 2000). Construction of a cosmid begins with plasmid-derived selectable markers and two specific segments of phage lambda DNA known as cohesive ends (*cos*), allowing for their packaging into viral shells. Once in the viral capsule, the cosmid is introduced into the host cell allowing the DNA molecule to replicate. Unlike the other vectors, cosmids can hold up to 45 kb of inserted DNA. A plasmid foundation containing yeast DNA sequences is what makes up a YAC (Hartwell et al., 2000). Yeast DNA is unique because it enables YACs to separate properly inside eukaryotic yeast cells, as if they are natural occurring chromosomes. A significant advantage YAC have over all other vectors is the carrying capacity of 1000 kb of inserted DNA. The two bacterial vectors that hold the most inserted DNA are bacteriophage P1 of 90 kb and BAC of 500 kb.

The second step of DNA cloning involves implanting the foreign DNA into the host cells, selecting cells that have received a DNA molecule, and distinguishing insert-containing recombinant molecules from vectors without inserts. Ultimately, the host cell must be transformed so the foreign DNA will be accepted. First, the plasmid vector is ligated to insert DNA from any source (Hartwell et al., 2000). In order to ligate the plasmid the recombinant DNA is mixed with *E. coli* by either suspension of the bacterial

cells in a cold $CaCl_2$ solution or by treating the solution with high-voltage electric shock, also known as electroporation (Hartwell et al., 2000). Once either method is used to mix the two solutions, the plasmids will enter about 1 in 1000 cells. This process is very inefficient because when the DNA gains access to the bacterial cell, the methodology is creating temporary pores through the cell membrane and ensures that only one molecule of DNA is taken up by one cell. This process is used for YACs as well. However, lambda and cosmid molecules have a slightly more efficient process because the molecules are packaged within the lambda virus particles *in vitro.* As the molecules enter the host cells via specific receptors for the virus and the viral injection apparatus, the molecules achieve 10 to 1000 times as many transformations per unit of DNA as the nonviral systems (Hartwell et al., 2000). Once the DNA in question is in the vector of choice, the host cells are placed on an agar plate that includes nutrients for growth and an antibiotic. Antibiotics are added to the agar plate because few DNA of interest gain access into the host cell. Therefore, many scientists will also include an antibiotic resistance gene to the vector to ensure that the colonies that are grown on the agar plate contain the desired recombinant DNA.

Another technique that many researchers have used for linkage mapping of the genome for both humans and animals are microsatellites. Microsatellites, also known as simple sequence repeats (SSRs), are arranged with 15 to 100 tandem repeats of one-, two-, or three-base sequence. They are highly polymorphic, meaning the DNA locus has two or more sequence variations, each present at a frequency of 1% or more in a population (Hartwell et al., 2000). As DNA is being replicated, polymerase impediment causes the dinucleotide to be skipped completely or duplicated. Occasionally, one mutation in every

thousand gametes will occur and normally, will not happen again within a few generations (Hartwell et al., 2000), thus making stable markers for genomic outcomes.

Genes have hundreds of thousands of DNA sequences and cloning overcomes the overwhelming number of sequences by reproducing copious amounts of a specific DNA fragment. However, this is tedious and time-consuming work. In 1985, polymerase chain reaction (PCR) was developed to achieve the same overall goal as cloning but is much easier to perform and is more cost efficient. Once the sequence is known, or even partially known, PCR can be used to complete the amplification of a unique gene sequence. Using PCR, genomic DNA is selected from the object of concern, then specialized oligonucleotide primers are selected from a short single-stranded chain of 16 to 26 nucleotides with the target sequence present. Both the genomic DNA and primers are placed in a test tube with 4 deoxynucleotides and *Thermus aquaticus* (Taq) DNA polymerase. The reason Taq is most commonly used is because it is a specialized polymerase obtained from bacteria living in hot springs (Hartwell et al., 2000), and is therefore heat resistant during the PCR procedure.

Once prepared, the test tube is place in a thermal cycler which regulates the temperate during the incubation period. First, the DNA is denatured by heating for 5 minutes at 94°C, causing the DNA to separate into single strands. Next, the temperature decreases to 50 to 60°C for 2 minutes allowing the base pairs and primers to form sequences in the single-strand genomic DNA. The primers will attach to the 3’ end of each stand. The temperature varies in this step depending on the length and GC:AT ratio of the primer sequences (Hartwell et al., 2000). Subsequently, the temperature is increased to 72°C for 2 to 5 minutes, allowing for Taq polymerase to work at maximum

potential to elongate from the 5' to 3' direction. At the end of this cycle, DNA synthesis is complete and the first round of PCR is complete. Depending on how many copies of DNA the researcher requires, additional rounds of PCR may be used. The second round of PCR increases the temperature to 94°C for only 20 seconds, again allowing for the denaturation of the short stretches of DNA to consist of one of the original stands of genomic DNA and a newly synthesized complementary strand initiated by a primer (Hartwell et al., 2000). For the second round, short single strands become the templates for the replication because the synthesized primers can anneal to them. This allows for multiple copies of DNA to be produced in a short amount of time. However, because PCR can only occur when a targeted region is available, it cannot be used as a starting point for the analysis of genes or genomic regions that have not yet been cloned (Hartwell et al., 2000).

2.1.2. Single nucleotide polymorphisms

Cattle have very similar DNA, but there are variations within the DNA known as SNPs. The occurrence of SNPs happen when at least one base pair from the DNA is changed, which generally occurs during meiosis, but the adjacent base pairs do not differ. The amount of genetic variation within a breed can be measured by how often SNPs occur within the base pairs of DNA. *Bos taurus* cattle have SNPs occurring about every 700 base pairs versus every 300 base pairs in *Bos indicus* cattle (Seidel, 2011). However, the presence of SNPs do not indicate that there will always be a difference in the phenotypic appearance. Researchers have been trying to map the bovine whole-genome dating back to 1983 with Soller and Beckerman and was successfully mapped in 2009 (Tellam et al., 2009). Soller believed that economically important traits, including

quantitative trait loci (QTL), could be genetically mapped to improved herd selection by marker-assisted technology.

2.2. Beef cattle genomics

Currently, several companies have commercially available genetic tests for both the beef and dairy cattle industries. Illumina is one of the founding genetic tests in the bovine genome (Illumina, 2015). Four tests are offered to genotype cattle DNA against the entire bovine genome. The primary difference between the tests is how in-depth the customer desires to understand about the cattle being tested. The more SNPs available to be tested, the greater the cost of the test.

The difference between the four tests are the amount of SNPs used to determine the genetic makeup of the animal. GoldenGate Bovine3K Genotyping BeadChip uses 2,900 SNPs that provide high capacity for prediction of the genetic merit of cattle (Illumina, 2015). Minor allele frequency was used to ensure equal distribution and representation of the bovine genome with the limited number of SNPs. Content included on the chip are 100 parentage SNPs, 154 X-linked markers, and 14 Y-chromosome markers for gender determination (Illumina, 2015). BovineLD v2.0 BeadChip uses 7,931 SNPs and of those, 2,162 SNPs are overlapping from the Bovine3K BeadChip to ensure backward compatibility. Of the overlapping SNPs, all 200 SNPs from the International Society for Animal Genetics panel for bovine parentage are used (Illumina, 2015). BovineLD v2.0 BeadChip is costing approximately $25/animal (Illumina, 2015). Parameters and number of SNPs taken from BovineSNP50 v2 are as followed: parentage, 121; chromosomal ends, 433; breed identification, 98; other autosomal, 6000; and X chromosome, 219; Parameters for BovineHD include: X chromosome, 18; Y

chromosome, 9; and mitochondrial, 13. Additional content incorporated includes parentage SNPs, SNPs for imputation to microsatellite alleles, causative mutations, and milk protein polymorphisms, totaling 1020 SNPs (Illumina, 2015).

The BovineSNP50 v3 is a novel chip that was used to help determine the *Bos taurus* genome. High-density indicates that the test shows every gene or marker for each centimorgan of a genome (Hartwell et al., 2000). The BovineSNP50 v3 is assembled with 53,714 SNPs including a variation of genome-wide-enabled selection, identification or quantitative trait loci, evaluation of genetic merit of individuals, and comparative genetic studies with imputation power (Illumina, 2015). Due to the amount of SNPs, the BovineSNP50 v3 is approximately $50/animal. All SNPs have been validated against 19 different beef and dairy breeds. Another high-density test is the BovineHD with a total of 777,962 SNPs and costing approximately $100/animal. A majority of the SNPs were novel content derived from 20 different cattle breeds, Holstein BAC sequence data, iBMAC reduced representation libraries sequencing project, parentage, whole-genome shotgun reads, SNPs from Baylor genome build Btau2.0, bovine Hapmap data set, and a few from uncited sources (Illumina, 2015). The reason for such a dense SNP population is because scientists wanted to develop an informative test that could be used on both *Bos taurus* and *Bos indicus* cattle of the entire bovine genome. Companies such as Zoetis and Neogen based their genetic tests on the BovineSNP50 and determined which SNPs were most beneficial to producers to generate insightful test results.

Zoetis offers many genetic tests for breeding heifers, bulls, and dairy cattle. Sire match is available with GeneMax Advantage and GeneMax Focus to help link registered Angus sires to tested heifer progeny. This feature benefits bull producers that used HD

50K and i50K to proactively manage inbreeding when mating tested heifers, flexibility to a multi-sire breeding system, and combined used of artificial insemination and natural service breeding (Zoetis, 2016). Many ranchers have different traits that they focus on when selecting replacement heifers, such as maternal, growth or feeder traits. Zoetis offers two genetic tests for commercial Angus replacement females that contain 75% or greater Black Angus breed composition, GeneMax Advantage and GeneMax Focus. When evaluating the traits offered to predict an outcome, the SNPs used to determine the index scores are proprietary to Zoetis.

GeneMax Advantage quantifies maternal, feedlot, carcass, and consumer eating satisfaction traits (Zoetis, 2016). The primary economic index scores used to determine those traits are: total advantage (TA), feeder advantage (FA), and cow advantage (CA). All index scores are ranked from 1 to 100 with higher index values being more desirable. The mean value is equal to a score of 50 in a reference population of 37,519 commercial Angus females (Zoetis, 2016). Prediction differences in profitability from genetic merit across all economically relevant traits captured in the CA and FA index scores is known as TA (Zoetis, 2016). Selection of the highest valued heifer from weaning to produce a Certified Angus Beef (CAB) carcass is FA. Terminal traits such as dry matter intake (DMI), carcass weight (CW), marbling, and yield grade (YG) are scores used to determine the feeder advantage score. The CA score selects heifers that are superior at calving and developing the most valuable calves through weaning (Zoetis, 2016). Traits used for maternal selection include calving ease maternal (CEM), weaning weight (WW), heifer pregnancy (HP), milk, and mature weight (MW). An option offered with this test is smart reporting of outliers, which includes cow cost, docility (DOC), and tenderness

(TEND). Outliers are traits that cause negative impact towards economic return and traits for selection or mating (Zoetis, 2016). Cow cost predicts females that will have high maintenance and production feed costs associated with genetics for mature cow size and milk (Zoetis, 2016). Females with less than desirable temperament is quantified through the DOC index. Prediction of genomic associations for Warner-Bratzler shear force is clarified as TEND (Zoetis, 2016).

GeneMax Focus helps producers select and breed to consistently qualify for carcass premiums and value-added feeder cattle marketing programs (Zoetis, 2016). The scoring system is 1 to 100, higher indexes are more desirable, which is identical to GeneMax Advantage. Scores and indexes for individual traits are compared against a reference population of more than 37,000 genotyped commercial Angus cattle (Zoetis, 2016). This test evaluates WW, post-weaning feedlot gain, CW, and USDA marbling score. For the economic selection index, animals are ranked for net returns due to combined genetic merit for growth, CW, and quality grade (QG). Zoetis is currently marketing this test to help alleviate the uncertainty of how cattle will perform within a feedlot setting, thus estimating whether the cattle will have a premium or discount when taken to market. This test may also allow customers to enroll in value-added feeder cattle programs such as, AngusSource, Top Dollar Angus, and Reputation Feeder Cattle.

PredicGEN is designed to assist with selection of *Bos taurus* influenced heifers via genomic predictions for carcass traits. Traits of interest include marbling score, USDA YG, TEND, and an index that predicts carcass grid value. Scores range from 0 to 100 with 50 being the average of the reference groups. Higher scores are deemed more desirable for all traits. PredicGEN was developed from a proprietary resource population

of more than 10,000 animals with recorded carcass outcomes and Illumina BovineSNP50 genotypes that evaluate the targeted phenotypic traits, calculated YG was derived from hot carcass weight (HCW), ribeye area (REA), percent kidney-pelvic-heart fat and backfat measurements (Zoetis, 2015). Warner-Bratzler shear force was used to determine TEND. However, values were not cited on how TEND scores were established. A subset of markers from Illumina BovineSNP50 were selected based on an algorithm from a compound covariate predictor feature. This helped to identify SNP markers associated with the strongest, independent effects on the selected traits. Resulting marker effects from selected SNPs were estimated using Bayes C in GenSel (Zoetis, 2015). Development of the prediction values, recorded a strong correlation for marbling (r = 0.45), YG (r = 0.34), and TEND (r = 0.31) associated with phenotypes of the cattle. (Zoetis, 2015). Zoetis has conducted multiple studies using this genomic test on commercial steers as well. The first external trial consisted of 2,500 crossbred steers in a commercial feedlot. Per feedlot protocol, cattle were implanted and received beta adrenergic agonists (BAA). Cattle were on feed approximately 198 days on average. Correlation between PredicGEN and observed phenotypes were 0.39 for marbling score and 0.43 for YG (Zoetis, 2015). Using a general linear effects model to account for clustering by pen, PredicGEN values were significant in predicting marbling score, USDA QG, and USDA YG (Zoetis, 2015). The grid merit index results are reported on the same scale and represent underlying economic index values for combined marbling and YG (Zoetis™, 2015). To guarantee there was no interaction between implant and BAA to the genetic test, a 1,100 crossbred steer study was conducted. Steers were allocated to one of 5 groups dependent on predicted genetic merit for marbling and YG:

1) high marbling and high YG; 2) average marbling and average YG; 3) low marbling and low YG; 4) high marbling and low YG; and 5) low marbling and high YG. The statistical design was a 2x2 factorial with BAA and implants being the 2 treatments. The study compared ractopamine hydrochloride fed for 28 days versus zilpatoral hydrochloride fed for 20 days with a 4-day withdrawal period. Implants included Synovex Choice versus Synovex Plus. Steers were fed 97 to 123 days prior to harvest. Data was analyzed using a generalized linear mixed effects model to account for fixed effects of treatments, first-order interactions, and clustering by assigned group (Zoetis, 2015). Predicted values were associated with observed carcass outcomes, verifying accuracy of the PredicGEN predictions. There were no significant interactions between PredicGEN values and either BAA or implant treatments (Zoetis, 2015). With these essential genetic tests, feedlots know how the cattle will perform and the optimal time for harvest.

When looking for the next replacement bull or the best breeding bull, many things come into play when trying to make the best decision for the type of cattle the producer wants to raise. Black and Red Angus cattle can use the HD 50K to help producers alleviate the uncertainty of what will be best for their herd. This high-density genomic test is using over 50,000 different genetic markers combined with 19 different traits: calving ease direct (CED), birth weight (BW), WW, yearling weight (YW), residual feed intake (RFI), DMI, yearling height (YH), scrotal circumference (SC), DOC, HP, CEM, milk, MW, mature height (MH), CW, marbling score, REA, fat thickness (FAT, and TEND to determine the genetic potential of the cattle. These traits are also known as genomic enhanced EPDs (GE-EPDs). These traits are scored in a percentile ranking

based on a test population of 50,000 animals (Zoetis, 2017). The top performers have lower percentage values, indicating higher and more favorable genetic merit for most traits (Pfizer Animal Health, 2012). Traits of exception include: milking ability, YW, MW, mature cow weight, and FAT. Thus, lower ranked values indicate genetic merit of higher levels of milk, size, feed requirements, and less maternal adaptability (Pfizer Animal Health, 2012). This genomic test is equivalent to having the tested animals produce dozens of progeny.

Red Angus HD 50K is very similar to the Black Angus test; however it only tests for 14 traits: CED, BW,WW, YW, Milk, YW maintenance energy (ME), HP, CEM, stayability (STAY), marbling score, YG, CW, REA, and FAT. Traits of reproduction, weight, carcass value, and bull selection from 8,500 reference animals were used for development of the test. Reproduction is very important because without bred heifers, there would be no opportunity to build the herd, and it is the major determinant of profitability in the cow calf sector. Five reproductive traits that are predicted include CEM, CED, HP, ME, and STAY. Prediction of the probability of calves born unassisted from two-year-old heifers is referred to as CEM. Ultimately, this trait is looking for the ease of calving for both the heifer and cattle owner. The probability of conception for two-year-old heifers is a prediction index for HP. Prediction of the probability a cow's offspring to calve unassisted when they are two-year-old is known as CED. Looking for differences in the future daughters' maintenance energy requirements is predicted by ME. This will help producers to determine which bull is more desirable to breed to so that cowherd feed costs are reduced and the cows are more efficient. The probability of a bull's daughter remaining productive until they are at least six-year-olds is estimated by

STAY. The sixth year of age threshold is used because that is typically when a cow will breakeven, given the expenses of development (Red Angus Association, 2015).

Within weight category, there are four different traits considered: BW, WW, YW, and Milk. To derived at an index for BW, differences in the birth weight plus the ease to calf unassisted. Weaning weight predicts the differences in weight of the calves by adjusting to the age of the dam and standard 205 days calf age, indicating the growth from birth to weaning (Red Angus Association, 2015). Evaluation of expected difference in weight is adjusted to 365 days of age, indicating growth from birth to yearling is known as YW. Milk predicts the difference in maternal production of an individual animal's daughters as expressed by the weaning weight of their calves (Red Angus Association, 2015). Carcass values are significant as they can increase profitability to the producers. The demand of consistent performance, combined with premiums from value-based grids, led to five traits targeted to predict carcass value (marbling score, YG, CW, REA, and FAT). Herd builder is an index looking at both replacement heifer traits and non-replacement marketed traits. Maternal traits such as STAY, HP, and calving ease are used on replacement heifers retained in the herd. For remaining progeny sold on a quality-based carcass grid, marbling score, YG, and growth EPDs influence the index score (Red Angus Association, 2015). Grid master is used to maximize profitability of feeders and carcass traits. Thus, traits that influence the index score are marbling score, YG, and all growth EPDs.

Zoetis also offers a lower density genomic test for bull selection known as i50K. The "i" stand for imputation, which is a process that uses a strategically smaller subset of the HD 50K markers and pattern recognition to very accurately predict the full range of

50,000 marker genotypes (Zoetis, 2016). However, fewer markers are used equating to lower costs for producers. This is offered for both the HD 50K Black Angus consisting of 19 traits and HD 50K Red Angus test consisting of 14 traits.

Zoetis protocol for collecting DNA samples is either hair for the switch of the tail that include the follicle or an ear scrap to draw blood to place on a FTA micro card® (model WB120210, Whatman®, Buckinghamshire, UK). The DNA is then sent to Zoetis Genetics Kalamazoo, MI, to decipher the DNA and send results of each individual animal back to the owner. According to Zoetis (2016), the cost of these different tests per animal are: GeneMax Advantage, $26; GeneMax Focus, $17; PredicGEN, $19.50; Black/Red Angus HD 50K, $79; and Black/Red Angus i50K, $37.

Neogen has produced several different genomic tests to help producers increase performance within their herd. The tests offered are Igenity Silver and Igenity Gold, which each profiles for both crossbred and Angus bred cattle. Up to 5,000 genetic markers are used for each of the four tests and the scoring system is different from other tests. Cattle are given a score from 1 to 10, with higher scores being more desirable. The appropriate units of either pounds, percent, USDA marbling units, square inches or inches are represented dependent on trait. When comparing animals' scores, the producer takes the difference between the two animals to see which animal will outperform the other. All tests offer a parentage test (SireSeek) for traceability back to a sire and to keep records of his performance. Igenity Silver for crossbred cattle is a baseline profiler that predicts maternal, performance, and carcass traits with the addition of parentage. Six genomic traits include CEM, STAY,RFI, average daily gain (ADG), TEND, and marbling. Igenity Gold for crossbred cattle predicts 13 traits that include: BW, CED,

CEM, STAY, HP, DOC, Milk, RFI, ADG, TEND, MARB, REA, and FAT. Due to Angus cattle being a predominant breed, there are an increased amount of genetic markers available to use in predicating more accurate genetic outcomes. Both tests are designed for cattle with ≥75 % Angus breed composition. Igenity Silver for Angus cattle measures six different traits: CEM, HP, DOC, Milk, ADG, and marbling. Igenity® Gold for angus cattle predicts 15 different traits: BW,CED, CEM, HP DOC, Milk, ADG, residual average daily gain (RADG), WW, TEND, Marbling, REA, FAT, and CW.

Neogen also offered several seedstock and artificial insemination sire genetic tests. These include, GeneSeek Genomic Profiler Ultra Low-Denisty (GGP uLD), GeneSeek Genomic Profiler Low-Density (GGP LD), GeneSeek Genomic Profiler 50K (GGP 50K), GeneSeek Genomic Profiler High-Density 150K (GGP HD150K), and GeneSeek Genomic Profiler F-250 (GGP F-250). Assisted selection of seedstock replacement heifers is possible at lower cost with the low-density testing, GGP uLD. A breed association profiler for sale bull GE-EPDs, which also contains over 100 genetic markers to determine genetic conditions in cattle is the GGP LD. According to Neogen (2017), GGP 50K will take the place of GGP LD. This test will produce GE-EPDs for purebred cattle and causative markers for relevant genetic health conditions. Neogen offers a high density test that uses up to 150,000 genetic markers for DNA testing known as GGP HD150K, which is ideal for elite seedstock, donor dams, artificial insemination (AI) studs, and high-impact cattle (Neogen, 2015). This test also quantifies 100 genetic causative markers for animal diseases. Tests which include all use of parentage markers, Y chromosome test, and PLAG1, which is a marker for growth rate and stature, are the: GGP LD, GGP 50K, and GGP HD150K. The GGP F-250 was developed for researchers

to use to determine more genetic markers to be discovered in the bovine genome to improve fertility, health, growth, and performance. Thus far, 220,000 genetic markers have been collected from the use of this test to enhance the bovine genome (Neogen, 2015).

Samples collected either hair or blood samples and placed on cards, then shipped to Neogen Gemonics Lincoln, NE. According to Neogen (2015), the cost per animal of these tests are: Igenity Silver, $25; Igenity Gold, $40; Igenity Angus Silver, $25; Igenity Angus Gold, $40; GGP uLD, $40; GGP LD, $55; GGP 50K, $80; GGP150K, $90; and GGP F-250, $125.

Quantum Genetix three genetic tests: Q-Sort, Q-Link, and Leptin testing. Very little information is available on Q-Sort and Q-Link and which traits are used to predict the values, due to the information being proprietary. Also, it is unclear what unit the predictions are in and if low or high numbers are more desirable. As described in the name, Q-Sort is a genomics based sorting system used to sort feedlot cattle to improve efficiency of feeding and help individuals reach their full growth potential (Quantum Genetix, 2017). This is achieved using genetic variants, visual criteria, weight, ultrasound backfat, and coat color. Q-Link is a parentage and herd improvement tool for commercial and purebred operations (Quantum Genetix, 2017). This test would be primarily used in multi-sire breeding systems to determine which bull is the sire of the calf. Then the calf's performance data is linked back to the sire.

Leptin testing is a new way to predict cattle performance and quality traits that are of economic importance for the beef industry. Leptin is of interest because it is a protein hormone secreted by white adipocytes that acts upon the central and peripheral tissues to

regulate feed intake, energy expenditure, and whole-body energy balance (Houseknecht et al., 1998). Thus, leptin plays a role in metabolic regulation which has been observed through its action on the hypothalamic-pituitary-adrenal axis and its role in the growth process (Delavaud et al., 2002). Leptin secretion can also be stimulated by feed intake, fasting, pregnancy, sex, physical activity, infection, and ambient temperature (Altman and Von Borell, 2007). Leptin is located on chromosome 4 and has 3 different exons. The first exon is not transcribed into the leptin protein (Altman and Von Borell, 2007). Exon 2 is the transition of cytosine to thymine and causes a change of arginine and cysteine at the 25^{th} amino acid in the α-helix of the leptin molecule. It was assumed by Buchanan et al. (2002) that the addition of cysteine can alternate the disulfide bonding of the leptin molecule. Di-sulfide bonds are critical for biological function and may influence the binding of leptin to its receptor, which affects feed intake, growth, and fat deposition. Exon 3 is the transition of thymine to cytosine, but this is unlikely because the polymorphism does not alter the amino acid sequence in the leptin molecule (Altman and Von Borell, 2007). Cattle are genotyped for being homozygous CC, CT, and homozygous TT. In recent research (Altman and Von Borell, 2007), it was noted that animals that are homozygous CC will produce more lean yield, lower fat levels, and increase ribeye area. However, McEvers et al. (2014) reported that ribeye area was not different among the 3 genotypes. Cattle that have a T allele are associated with increased backfat thickness and/or marbling (Altman and Von Borell, 2007). However, McEvers et al. (2014) concluded that no difference in backfat existed among the 3 genotypes; however, there was a shift in marbling score from CC to TT genotypes, with TT alleles possessing increased degrees of marbling.

Sorting cattle at feedlot arrival is commonly done already to create more heterogeneous outcome groups based on their growth potential. When selling cattle on the grid, producers can ensure a higher net return for consistent grading or leaner cattle. Quantum Genetix has produced a test that specifically looks at the 3 different genotypes of leptin in cattle. These include, CC are animals that are lean, CT animals are economically intermediate, and TT are animals that have more intermuscular fat. The leptin gene has been shown to be influential on weaning weight, cow milk production, dry matter intake, days on feed, accumulation of backfat, marbling, yield and quality grade, and feed intake.

Samples collected is a 2mm diameter ear tissue biopsy is collected by using a QGI ear tagger (Quantum Genetix, Saskatoon, SK) and placed in a QGI ear tag (Quantum Genetix, Saskatoon, SK). Tissues need to stay frozen/cool upon arrival at the laboratory for testing where Quantum Genetix Saskatoon, SK, completes the genetic testing phase. The purchase of the desired test already included the cost of the QGI ear tag, but for an additional fee the CCIA tags can be purchased to use the barcode system for more reliable tracking. According to Quantum Genetix (2017), Cost per animal to complete genetic testing: QGI ear tagger, $75; QGI ear tag, $1; CCIA tags, $4; Q-Sort, $5; Q-Link, $12; and Leptin, $15.

2.3. Economic Implications of Genetic Evaluation Tools

Genetic evaluation of cattle is a relatively young technology with many advancements yet to be discovered. By improving breeding stock among the beef industry, there is potential for improved meat quality by utilizing other industry developments more efficiently. The question is, “Are producers using genetics to help

improve their herds?" Vestal et al. (2013) conducted a study to assess the value of genetic profiles to producers when purchasing bulls. Data was collected from the Oklahoma Beef Inc. (OBI) Bull Test Station in Stillwater, Oklahoma. Two bull sales per year are conducted by OBI; they have incorporated EPDs and DNA profiles into their sales catalog. Even though EPDs and DNA profiles were available, it was unclear what producers were using to select their next bull. A survey was mailed out to all producers that had purchased bulls from OBI in the past. The survey instructed producers to select characteristics they would use to select a bull, including what they thought the bull was worth. This data was known as stated preferences (SP) and was used to compare to the data from OBI called revealed preferences (RP). Even though the parameter consistency between RP and SP data was rejected, by examining the correlation between common parameters, specific bull characteristics are of great importance to bull buyers and should be presented in the information set as they are highly correlated (Vestal et al., 2013). The characteristics shown to be of importance to bull buyers were birth weight EPD, marbling EPD, and intramuscular fat ultrasound. It is also important to producers that some type of information is presented rather than no information. Producers place high value on a bull's ability to produce progeny with improved carcass-quality traits, coinciding with results for ribeye area EPD in the RP model which were statistically significant (Vestal et al., 2013), thus yielding a premium. Vestal et al. (2013) reported that cow-calf producers have been slow to adapt to new technologies and feel confident in the EPDs, test performance, and ultrasound data, therefore, the use of genetic information could be disregarded. Van Eenennaam et al. (2010) suggested that the viability of DNA testing in

the seedstock sector will be dependent upon increased vertical integration or more efficient price signaling throughout the beef production chain.

Fed cattle producers are always trying to increase the profitability of their finished cattle. In the 1990s grid pricing was incorporated into the industry to encourage finished cattle with more uniformity and consistency. Traditional price discovery enabled the communication between beef consumers and beef producers to determine what is in high demand. Therefore, grid pricing eliminated the lost communication between the two. Grid pricing has increased for the amount of fed cattle sold from 15% in 1995 to 34% in 2005 (National Cattlemen's Beef Association, 2006) and 40% to 45% in 2010 (Fausti et al., 2010) to 60% to 65% in 2016 (Lawrence, 2016). We can speculate that the use of grid pricing will increase in future years. It has been noted that using genetic information to purchase feeder cattle for placement in the feedlot can have an economic value of up to $60 per head (Thompson et al., 2016). However, genetic information in not generally provided during the purchase of feeder cattle. Thompson et al. (2016), conducted a study to estimate the expected value of genetic information for improving fed cattle marketing decisions, including decisions of both marketing method (live weight, dressed weight, or grid pricing) and time to market (days-on-feed). Cattle were sorted into groups by their expected performance. In order to do this, expected net returns for each of the marketing methods and molecular breeding values (MBV) for yield grade and marbling were developed using a random set of 1,000 animals. Days-on-feed for traditional marketing was estimated by the expected net return for each group. Grid pricing for optimal days-on-feed was determined by grid search data. Animals with greater genetic potential for marbling would be marketed for grid prices, if the animal had a lower genetic potential in

marbling it would be marketed via either live weight or dressed weight pricing, thus, returning a larger net profit when sold off dressed weight pricing. However, cattle with higher yield grade MBVs will have a higher net return when marketed base off live weight pricing. According to Debertin (1986), there are three stages of the production function that are used to explain the net return for MBVs. Total physical product (TPP) represents a normally distributed bell shaped curve. Once the curve escalates to the highest peak, it has reached elasticity of production (E_p). Marginal physical product (MPP) and E_p will equal zero at the start of stage III and will continue as long as E_p and MPP are negative. Once E_p is equal to one, stage II begins. However, MPP is now equal to average physical product (APP) rather than zero. Within this region, maximum profit is utilized. When E_p is greater than one and MPP is greater than APP, Stage I begins. In conclusion, Thompson et al. (2016) reported that individual marketing groups 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 cattle that with poor genetic performance and pull them off the grid increased the expected net return by more than $11/head (Thompson et al., 2016). There was an overall increase of -$26.68/head when genetically marketing cattle. 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 (Thompson et al., 2016). The results suggest that genetic information used to sort cattle by yield grade and marbling score into marketing groups

and determine optimal days-on-feed increased expected net return by $1-13/animal depending on marketing strategy and grid structure. Currently, this is not enough net return to overcome the costs of the genetic tests. The low-density imputation chips cost $39 to $50 and for high-density chips $75 to $90 per animal (Van Eenennaam, 2016).

2.3.1. Live animal production system

In the cattle industry, there are five different sectors that play primary roles in producing beef for human consumption: seedstock, cow-calf, stocker/feeder calves, feedlots, and processors. Seedstock cattle are breeding stock that are typically purebred and registered with desirable genetic pedigrees. Most cow-calf operations are small and use the income as a supplemental source to the household. Cow-calf operations with 1 to 49, 50 to 99, 100 to 199, and 200 or more beef cows account for 79.4, 11.0, 5.7, and 3.9 percent, respectively, of all 764,984 farms with beef cows in the United States (NASS 2007 Census of Agriculture). In 2012, there was a decline of 37,078 farms with beef cows in the United States thus reducing the number from 764,984 to 727,906 farms (NASS 2012 Census of Agriculture). Cow-calf producers must ensure that cows are bred and calve every year because calves are the majority of their income. Calves are typically weaned from 175 to 215 days of age, and age at weaning is dependent on the cows' body condition score to ensure that the cows are not too thin to rebreed. Other factors that influence weaning are weather, location of the cows, and the estimated harvest date (Patterson, 2007). Depending on the herd and operation, calving/weaning seasons can happen twice a year; spring and fall. Approximately two months prior to calving, cows should be fed a high-quality forage to ensure weight gain, rebreed quickly, and produced sufficient milk supply to yield heavy calves at weaning (Comerford et al., 2013). A few

weeks prior to weaning, calves should be vaccinated, bulls castrated, de-wormed, and identified. Directly after weaning, calves should be re-vaccinated. Once the calves are weaned, some are kept for replacement stock, sold as stockers to be backgrounded, or sent straight to the feedlot. Calves can also be marketed to stockers. Breed-influenced programs are used to label and market beef products by cattle breed and generally require specific management practices that include identification of the cattle. Age-and-source verification programs allow the buyer to verify the source and age throughout the lifetime of the cattle to target certain marketing channels (USDA, APHIS, 2011). Nearly 30 percent of cow-calf operations targeted natural cattle and only 1 percent targeted certified organic beef (USDA, APHIS, 2011). Natural and certified organic marketing refers to product statements and labels indicating to consumers how the animal was raised. Organic beef has to be raised on 95 to 100 % certified organic ingredients and processing aids, no GMOs, and comply with the National List of Allowed and Prohibited Substances (USDA, APHIS, 2011). According to USDA, APHIS (2011), to be classified at natural, cattle are minimally processed and no added ingredients. Conventional marketing is marketing a standard commodity and not targeting a specific market. About 62.8 percent of cow-calf operations use production practices to target conventional markets (USDA, APHSIS, 2011). The main difference in stocker and feeder calves is quite simple, stocker calves are generally younger or lighter and that need a few more months on grass to enhance growth before being sent to a feedlot. Feeder calves are generally the older and/or heavier calves. Once they leave the cow-calf operation, calves are taken to a feedlot and are fed high-energy rations for approximately four to six months before harvest. The optimal harvest weight currently ranges from 1,200 to 1,600 pounds

(National Cattleman's Beef Association, 2009). This weight could also vary if animals were finished on grass instead of an energy dense ration.

2.4. Marketing differentiations in beef cattle programs

Future food availability is of concern because in 2050 the global population is estimated to be 9.5 billion people (Capper, 2012). Along with increased population, Tilman et al. (2002) have predicted increased income. As income increases, the demand for high-quality animal protein such as meat, milk, and eggs increases as well. Therefore, the Food and Agriculture Organization of the United Nations (FAO) suggests that food requirements will increase by 70% by 2050. In agriculture, technologies to improve cattle performance have been used since the 1950s when diethystilbestol was approved to be fed to cattle. The first growth implant used in cattle in 1969 was zeranol and then in 1980s and 1990s the use of estradiol/trenbolone acetate (TBA) combination implants became popular (Maxwell et al., 2015). Currently, the U.S. consumer has become more concerned with where and how their food is raised and some negative perceptions exist about the technologies used to improve cattle performance. A recent study found that 50% of consumers said hormones were a serious hazard (Yang et al., 2017). Because of that concern, several cattle owners are marketing to niche-targeted finishing programs such as "all natural".

2.4.1. All natural cattle

The recent USDA guidelines for natural beef production is no added ingredients and minimally processed (USDA, FSIS, 2011). However, the new rule allows the use of ionophores for the control of coccidiosis, parasite control, vaccinations, bloat prevention and treatment products (feed grade probiotics or buffer) (USDA, AMS, 2009). Most

concerning about all natural cattle is that these cattle will not be able to produce meat efficiently due to increased days on feed and feed intake. Recent studies by Cooprider et al. (2011) and Maxwell et al. (2015) reported no difference in dry matter intake for steers receiving technologies to those fed naturally for the entire feeding period. However, average daily gain was increased 37.8% and gain to feed ratios were improved by of 33.3% for conventionally fed cattle supplemented a BAA versus natural cattle (Maxwell et al., 2015). Natural cattle are typically fed past their optimum compositional endpoint thus drastically reducing efficiency at the end of the feeding period (Maxwell et al., 2014).

2.4.2. Conventional cattle

Conventionally raised cattle utilize technologies such as growth implants, beta-adrenergic agonists (BAA), ionophores, and antibiotics to improve cattle performance and health. Growth implants have been consistently shown to increase growth rate by 8 to 28%, improve feed efficiency 5 to 20%, and enhance lean tissue mass of the carcass (3 to 10%) (Duckett and Owens, 1997). Growth implants contain are steroid compounds of estrogens, androgens, and progestins; they may include both naturally occurring and synthetic hormones. Of the hormones used implants, the three naturally occurring are estradiol, progesterone, and testosterone (Stewart, 2013). The three synthetic compounds used in beef cattle production to enhance growth rate and feed efficiency are zeranol, TBA, and melegestrol acetate (MGA) (Johnson et al., 2013). A synthetic implant like TBA is a testosterone analogue with 10 to 50 times the anabolic activity compared to testosterone (Bouffault and Willemart, 1983). Today, the beef industry commonly uses growth implants that contain TBA and a form of estrogen, normally estradiol (E_2) or

estradiol benzoate (Johnson et al., 2013). In order to maximize growth rate and feed efficiency, TBA and E_2 work best together (Johnson et al., 2013). This is done by inducing muscle growth by increasing the local production of muscle insulin-like growth factor (IGF) that in turn, enhances satellite cell activity and consequently increases skeletal muscle growth (Johnson et al., 2013). The use of MGA is approved for feedlot heifers to suppress estrus and enhance growth (Johnson et al., 2013). It is made up of exogenous synthetic progestin and is most effective when fed to heifers at 0.40 mg/head/day.

Phenethanolamine compounds are also known as BAA, which are similar to norepinephrine and epinephrine that are catecholamines found in all animals and humans. The U.S. Food and Drug administration approved are ractopamine hydrochloride (RH) in 2003 and zilpaterol hydrochloride (ZH) in 2006 for the use in cattle. These products are intended for use at the end of the feeding period for $\leq$ 20 days for ZH and $\leq$ 42 days for RH prior to slaughter. Zilpaterol has a 72-hour withdrawal time before harvest and ractopamine has a 12-hour withdrawal (Johnson et al., 2013). Either type of BAA causes existing muscle fibers to display muscle hypertrophy very proficiently without the need for additional nuclei (Johnson et al., 2013). This is caused by direct binding of the BAA to its receptor on skeletal muscle tissue. Following receptor activation, key pathways regulating protein accretion are upregulated resulting in an increased protein accumulation in the muscle fiber (Johnson et al., 2013). Many studies have concluded that cattle fed ZH have improved average daily gain by 43.5%, 26.6%, and 42.8% (Montgomery et al., 2009; McEvers et al.,2014; Maxwell et al., 2015) and improved feed efficiency by 46.6%, 30.8%, and 45.6% (Montgomery et al., 2009; McEvers et al.,2014;

Maxwell et al., 2015). On August 7, 2013, Tyson Fresh Foods, Inc. announced they would no longer be taking cattle fed ZH due to animals being unable to walk. Following this event, the other major meat packets sided with Tyson to not accepted ZH fed cattle. Eventually, Merck Animal Health withdrew ZH for sales in U.S. and Canada to implement a five step program ensuring responsible beef and to further test the usage and safety of the product.

Ionophores are classified as carboxylic polyether antibiotics that disrupt the ion concentration gradient of calcium, potassium, hydrogen, and sodium across bacterial cell wall, which causes them to enter a futile ion cycle (Hersom and Thrift, 2015). Ionophores increase feed efficiency and body weight gain by altering rumen fermentation patterns. Commercially available ionophores include monesin, lasalocid, and laidlomycin; they are classified as feed additives and are carried via another feed source to ensure administration. Ionophores function when the ion concentration is disrupted, thus preventing certain bacteria from maintaining normal metabolism and causing the microorganisms to expend extra energy (Hensom and Thrift, 2015). The main target species in the rumen are gram-positive bacteria and protozoa because they decrease energy of ruminal digestion of feedstuffs and efficiency of rumen digestion physiology (Hensom and Thrift, 2015). By controlling the gram-positive bacteria and protozoa, less waste products, such as methane are produced (Guan et al., 2006). Ruminal protein breakdown in decreased, thus decreasing ammonia production. The shift of ruminal bacteria population and metabolism allows beneficial bacteria to be more efficient through an increase in the amount of propionic acid and a decrease in the production of

acetic acid and lactic acid (Hensom and Thrift, 2015). Thus, an overall increase in energy and the use of feedstuffs more efficiently is realized.

Antibiotics used in beef production to help control liver abscesses and improve the health of a sick animal. The incidence of liver abscesses is highly variable, but ranging from 10 to 20% (Amachawadi and Nagaraja, 2016). To control the occurrence of acidosis and subsequent ruminitis, leading to liver abscesses, tylosin is combined with the feed and a nutritional sound management practice (Amachawadi and Nagaraja, 2016). Many feedlots have protocols on which antibiotic to use depending on diagnosis of bovine respiratory disease, other infections, pinkeye, etc. All use of antibiotics must be logged by animal to ensure that withdrawal times are met before sending the animal to harvest. The FFD&C Act states that a food is adulterated if it has been "prepared, packed or held under insanitary conditions" (FDA, 2017). All antibiotics are required by federal law to include the withdrawal period to ensure the level of residues within edible tissues are minimal and pose little risk to people (FDA, 2017). During the approval process for a drug used in food-producing animals, the FDA sets the drug's tolerance level. As of January 1, 2017, all food grade antibiotics have to be prescribed by a licensed veterinarian that authorizes the use of a veterinary feed directive (VFD) drug or combination of VFD drug in or on an animal feed (Beef Quality Assurance, 2017). Currently, the antibiotics that require a VFD are chlortetracycline, chlortetracycline with sulfamethazine, neomycin with oxytetracycline, oxytetracycline, tylosin, and virginiamycin.

2.5. USDA beef carcass grading

In 1902 Herbert Mumford from the University from Illinois produced a series of bulletins discussing market and grade classes with suggestions for interpreting market quotations (Harris et al., 1996). Mumford classified the different grading classes as Prime, Choice, Good, Medium, Common, Cutter, and Canner. The purpose behind the bulletins were to try to standardize the grading system for cattle and to report the market conditions to the public. In 1914, the USDA was funded to convey a national market livestock report. By 1917, daily market reports had begun and the first USDA bulletin that incorporated grades of beef and market class was released in August of 1924 (Harris, et al. 1996). A series of hearing began in 1925 to involve packers, producers, and anyone else with an opinion to improve the beef grading system. Implemented in 1926 was the Official United States Standards for Grades of Carcass Beef, allowing a one year trial period to determine if the grades would be a workable program (Harris et al., 1996). In 1941, carcass beef standards were changed to establish grade terminology for all beef: Prime, Choice, Good, Commercial, Utility, Cutter, and Canner (Harris et al., 1996). Incorporating a dual grading system was implemented in 1965, using cutability along with grades. The following changes were made in 1975: 1) maturity of the animal was eliminated in the determination of the quality grade for all bullock beef, steer, heifer, and cow beef included in the A maturity group 2) marbling requirements were increased for the Good grade in A maturity 3) maximum maturity was reduced for steer, heifer, and cow beef in the Good and Standard grade to the same as Prime and Choice 4) conformation was eliminated from all quality grade standards (Harris et al., 1996). November 1987, revision for name change for Good to Select for steer, heifer, cow, and bullock carcass (UDSA, AMS, 2016). In 1997, grade classifications were changed to

restrict the Select grade to A maturity only and raise the marbling degree required for Choice to a minimum modest throughout B maturity (USDA, AMS, 2016). The last revisions made to the grading system in 1997, is what is currently being used within packing plants.

2.5.1. Quality grading

For cattle to be considered Prime, the ribeye must have slightly abundant to abundant marbling, Choice cattle are required to have small to moderate marbling score within the ribeye. Select quality graded cattle require slight amount of marbling. Standard cattle must have a marbling score of practically devoid to slight. Within these quality grades, cattle have to be determined 30 months of age or younger either by dentition or documentation of actual age (USDA, AMS, 2017). Unless the cattle are D or E skeletal maturity, dentition and documentation of age is null.

Cattle that are greater than 30 months of age, the maturity of the cattle is determined by their skeletal maturity. Commercial carcasses have small to moderate amount of marbling depending if the carcasses is C, D, or E maturity. Utility carcasses are practically devoid to moderate marbling and can be B, C, D, or E maturity. Cutter carcasses are practically devoid to slight marbling and C, D, or E maturity. Canner carcasses include only those carcasses that are inferior to the minimum requirements specified for the cutter grade (USDA, AMS, 2016).

2.5.2. Yield grading

The characteristics that determine the yield grade of a carcass are the amount of external fat, kidney-pelvic-heart fat (KPH), the area of the longissimus muscle, and carcass weight. External fat is measured perpendicular to the outside surface at a point

three-fourths of the length of the longissimus from its chine bone end and is evaluated for the thickness of the fat over the longissimus. This score can be adjusted up or down if there is excess fat or lack of fat deposits in the brisket, plate, flank, cod or udder, inside round, rump, and hip. The excess amount of KPH fat is removed when making closely trimmed retail cuts (USDA, AMS, 2016). The amount of KPH fat is examined subjectively and expressed as a percent of the carcass weight. The longissimus muscle area is measured after the carcass has been ribbed, estimated subjectively, or objectively by camera (USDA, AMS, 2016). The formula the USDA uses to calculate the yield grade of carcasses is as follows: (2.50 + (2.50 x adjusted fat thickness, inches) + (0.20 x percent kidney, pelvic, heart fat) + (0.0038 x HCW, pounds) – (0.32 x longissimus area, square inches). Yield grades are applied as a categorical value from 1 to 5, with 1 being the highest cutability carcasses and 5 being the least cutability. Yield grade 1's have a thin layer of external fat and bluing of the muscles is visible. Yield grade 2's are nearly completely covered with fat, but the lean is plainly visible through the fat over the outside of the rounds, the tops of the shoulders, and the necks (USDA, AMS, 2016). Yield grade 3 are covered in fat, but can still see lean visibly in part of the necks and bottoms of the rounds. The cod or udder and flank have large amounts of fat deposited in these areas. Yield grade 4 the only muscles that are visible are the shanks, plates, and flanks; it will show a moderately thick layer of fat will be present over the loin, ribs, inside rounds, rumps, hips, and clods. Yield grade 5 has the most fat on all the various parts, a smaller area of longissimus muscle, and more KPH fat compared to yield grade 4 (USDA, AMS, 2016).

2.6. Overall Conclusions

The ability to determine variation within DNA is commonly found in the base pairs, also known as SNPs. Using SNPs for genomic testing helps to evaluate different characteristics, such as performance and carcass traits. Black et al. (2015) sorted cattle based off their genetic potential (GP) for gain and marbling and placed them in either a high or low group depending on their genetics. No differences were observed between GP groups in BW, ADG, DMI, or gain to feed, even though steers within the high group had greater GP for gain than the low group (Black et al. 2015). DeVuyst et al. (2011) also observed no correlation between Igenity (Neogen Corporation, Lansing, MI) scores for gain and actual performance in steers fed for 135 to 257 days. The use of genetics in different aspects of the cattle industry has been shown to improve the quality of today's cattle. However, there are still some grey areas on how effective the genetic predictions are against the actual breeding value of the cattle. Furthering the knowledge base of exactly how genetic predictions can be beneficial to the cattle industry, especially in feedlots, could enhance the overall performance of the cattle.

CHAPTER 3

ASSOCIATION OF GENETIC PRODUCTION INDEXES WITH PRODUCTION OUTCOMES OF FEEDLOT STEERS

3.1. Abstract

Genetic knowledge is increasingly utilized within the beef seedstock sector, yet uncertainty remains on how to maximize these inputs at the commercial level. The objectives of this study were to evaluate the effect of sorting natural and conventionally marketed fed beef cattle according to a genetic prediction index on performance and carcass traits, and determine the association of genetic indices to economically important production outcomes. The study hypothesis was that sorting beef cattle by genetic index would not influence the outcome of economically important traits. Two cattle sources were utilized, Angus and Angus × Hereford steers that did not receive growth promoting technologies or antimicrobials to comply with a natural marketing program (NAT; n=98; initial BW = 362 ± 11 kg) and Angus steers that were fed conventionally (CONV; n=81; initial BW = 364 ± 11 kg). Cattle were assigned to pens within source and stratified according to a feeder advantage (FA1) index from least to greatest by pen (NAT=10 steers/pen and 9 pens/treatment; CONV=10 or 11 steers/pen and 7 pens/treatment). All cattle were managed similarly and fed the same basal diet with the exception that NAT diets did not contain antimicrobial (monensin or tylosin) or growth promoting technologies (implants or beta-agonist). Individual cattle were harvested upon achieving a target shrunk (4%) BW of 635 kg. Genomic indices for WW and gain increased

quadratically ($P < 0.01$) as the FA1 index increased for both cattle types. For conventionally finished cattle, genomic indices for heifer pregnancy ($P \leq 0.02$) decreased whereas milk ($P < 0.01$), gain ($P < 0.01$), carcass weight ($P = 0.03$), marbling ($P < 0.01$), and ribeye area ($P = 0.02$) increased as the FA1 index increased. Daily dry matter feed offered (DDMFO) increased quadratically ($P < 0.01$) as FA1 index increased for both NAT and CONV. Within the NAT cattle, FA1 index was correlated to DOF ($r = -0.39$; $P < 0.001$), DDMFO ($r = 0.35$; $P < 0.01$), SUMDMO ($r = -0.32$; $P < 0.01$), Day 0 BW ($r = 0.30$; $P < 0.01$), and ADG ($r = 0.23$; $P < 0.05$). Among CONV cattle, FA1 index was positively correlated ($r = 0.44$; $P < 0.001$) to DDMFO. The FA1 index score means did not differ ($P = 0.08$) amongst USDA QG's, or USDA YG's ($P = 0.25$). Numerically, NAT cattle in FA group 75 to 82 were greatest in HCW ($P < 0.01$), dressed yield ($P < 0.01$), and total carcasses value ($P < 0.01$). Net return carcass basis ($P = 0.02$) was numerically greatest for FA group 32 to 41.

3.2. Introduction

Advancements in applicable genomics technology have been made since the discovery and mapping of the bovine genome. One such advancement is the identification of single nucleotide polymorphisms (SNPs) that correlate with economically important traits, such as maternal, growth and carcass characteristics. Using these different SNPs, several companies have designed genetic tests geared towards specific traits of interest to help producers determine the genetic potential of cattle. Genetic potential using ADG and marbling indices has been demonstrated effectively categorized cattle for placement in the feedlot according to growth prediction has resulted in profit of approximately $38/animal (Amen et al., 2016).

In fed cattle, efficient gain is a primary driver for profitability. Sorting cattle into marketing groups using genetic technology, compared to traditional methods, (live weight, hide color, and frame score) improves the opportunity for profit (Thompson et al., 2015). In addition to improving the returns to cattle feeding, genetic sorting can also reduce the variability or risk associated with value-based marketing (Thompson et al., 2016).

Consumers are increasingly concerned about where their food comes from, resulting in opportunities for producers to feed cattle geared towards niche-markets, such as all-natural beef (Sawyer et al., 2003). To be classified as "all-natural", cattle may be prohibited to receive any growth promotants or antimicrobials for up to the duration of life of the cattle, depending on the specific requirements of a specific natural marketing program (USDA, AMS, 2009).

Eluding variation in cattle by knowing the genetic makeup can alleviate several challenges, such as cattle having excessive DOF causing over finished cattle. The objectives of this study were to evaluate the effect of sorting beef cattle according to a genetic prediction index on performance and carcass traits, and determine the association of various genetic indices to economically important production outcomes.

3.3. Materials and Methods

3.3.1. Cattle receiving

On December 2 and December 10, 2015, Angus and Angus x Hereford certified natural steers (NAT; n=98; initial BW = 362 ± 11 kg; previously received no growth promotants or antibiotics) were transported 568 km from Menard, TX, and Angus conventional steers (CONV; n=81; initial BW = 364 ± 11 kg) were transported 459 km

from Breckenridge, TX to the West Texas A&M University Research Feedlot in Canyon. Upon arrival, steers were placed in holding pens by source, and allowed access to water. A receiving ration without monensin or tylosin was fed to the NAT steers and a receiving ration with monensin was fed to conventional steers.

3.3.2. Genetic index determinations

On December 10, 2015, cattle were weighed (Daniels Chute, model AH-10S, Daniels Manufacturing Company, Ainsworth, NE) and had blood sampled either via jugular venipuncture or from the posterior aspect of the ear and retained with an FTA micro card (model WB120210, Whatman, Buckinghamshire, UK) and/or approximately 25 hair follicles from the tail switch.

Blood and hair samples were sent to Zoetis Genetics (Kalamazoo, MI), where individual outcomes for calving ease maternal (CEM), weaning weight (WW), heifer pregnancy (HP), milk, mature weight (MW), cow advantage original (CA1), cow advantage updated (CA2), gain, carcass weight (CW), marbling (MARB), ribeye area (RE), fat thickness (FAT), feeder advantage original (FA1), feeder advantage updated (FA2) and total advantage original (TA1), and total advantage updated (TA2) were determined using the GeneMax Advantage single nucleotide polymorphism (SNP) panel.

3.3.3. Genetic scoring parameters

The original CA1, FA1, and TA1 scores were developed from the high density (HD) 50k platform of over 39,000 genotypes integrated into the American Angus Association (AAA) (Zoetis™, 2014). As for the updated CA1, FA1, and TA1 indices used the same genetic platform of the HD 50k; however, this updated panel included 108,000 genotypes were integrated into the AAA (Zoetis™, 2016). With the larger population

genotyped, recalibration of the markers and updated economic indices assumptions were made. Commercially, 37,519 Angus females were used as a reference population in the updated scores versus 2,913 Angus females for the original scores.

3.3.4. Assignment to pens

Prior to SNP panels being returned (77 d), cattle were kept separate depending on cattle type, but allowed to commingle amongst the herd. On d 0, all cattle were weighed and sorted to study pens depending on the genetic results of the FA score and cattle type (9 pens NAT with 10 steers/pen; 7 pens CONV with 10 or 11 steers/pen). Within cattle type (NAT or CONV), cattle were stratified by FA score and pens were filled from the lowest FA scores to the highest.

3.3.5. Feed and health management

Cattle were housed in 6.1 x 27.4 m soil surfaced pens with 6.1 m fence-line concrete feed bunks and a 15.9-L water tank (Model WaterMetric 100/150 #18166, Ritchie, Oskalossa, IA) within each pen. Cattle were allowed 0.61 m or 0.55 m bunk space per animal depending on pen stocking density.

Cattle were transitioned to a finishing diet (Table 1) on d18 using a three-step program that entailed feeding a portion of a grower, transition and finisher ration. Cattle were on a 50/50 grower/transition ration for 4 days, then on full transition ration for 8 days. Transition and finisher were fed 50/50 for 5 days, then on full finisher ration for the remainder of the feeding period. All rations were formulated to meet or exceed NRC (2000) requirements. Through the finishing stages of the CONV cattle, within the ration 35.83 g/907 kg of monensin sodium (Rumensin, Elanco Animal Health, Greenfield, IN) and 9.76 g/907 kg of tylosin phosphate (Tylan, Elanco Animal Health) was fed

throughout the entirety of the study; NAT cattle were not supplemented with either feed additive. Feed bunks were managed using a slick bunk program. Bunk reads were completed at 0700h, and cattle were fed once daily at 0800h. Residual feed (ORTS) at 0700h bunkread were subtracted from the current day's feed call; orts were shoveled to one side of the bunk, feed was then delivered, then orts were placed on top. Feed was mixed (model 274-12B, mixer wagon, Roto-Mix, Dodge City, KS) and delivered to each pen with delivery accuracy to the nearest 0.907 kg. Feeding order was NAT followed by CONV at each feeding. Flushing of the mixer before feeding or batching NAT finisher ration was done daily by two people carefully physically entering the mixer and pushing all feedstuff out of the mixer by hand. This ensured that no residue of monensin sodium (Rumensin™, Elanco Animal Health, Greenfield, IN) or tylosin phosphate (Tylan™, Elanco Animal Health) remained.

Natural cattle were not allowed to receive any antibiotics, growth implants, or beta adrenergic agonists (BAA) during the duration of the study. None of the animals from either NAT or CONV were treated for morbidity. One mortality from the NAT group occurred due to heart failure. One mortality within the CONV cattle occurred from euthanasia due to a broken jaw.

3.3.6. Harvest selection

Individual cattle within pens were harvested at a target shrunk BW of 635 kg. Natural cattle were harvest in 6 groups {10May2016 (n=7; shrunk BW 577 kg), 23Aug2016 (n=16; shrunk BW 675 kg), 20Sep2016 (n=16; shrunk BW 663 kg), 27Sep2016 (n=7; shrunk BW 647 kg), 11Oct2016 (n=7; shrunk BW 652 kg), 18Oct2016 (n=43; shrunk BW 599 kg)} at Caviness Beef Packers, Hereford, TX. On the last

shipping date (18Oct2016), the remaining 43 head of cattle were harvested all at once, therefore, not all the cattle reached the harvest weight of 635 kg. Conventional cattle were harvested in 5 groups {16Jun2016 (n=17; shrunk BW 648 kg), 20Jul2016 (n=24; shrunk BW 663 kg), 12Aug2016 (n=20; shrunk BW 661 kg), 19Sep2016 (n=13; shrunk BW 662 kg), 26Oct2016 (n=6; shrunk BW 665 kg)} at Tyson Fresh Meats, Amarillo, TX.

3.3.7. Carcass evaluation

Conventional cattle were allowed to chill for 28h prior to grading. Conventional carcasses were evaluated by a camera grading system (VBG 2000; E+V, Oranienburg, Germany) for yield grade assessment and by a USDA grader for quality grade assessment. Natural cattle were allowed to chill for 48h prior to grading. Natural carcasses were evaluated by a USDA grader for both yield and quality assessment. However, caution needs to be taken when interrupting the results of HCW and dressed yield in comparison because Tyson Fresh Meats retains KPH in the carcasses, unlike Caviness Beef Packers which removes all KPH from all carcasses.

3.3.8. Financial implications

Day 0 feeder calf value was derived from a nationwide weighted average of feeder calf report from the USDA market news service (St Joseph, MO). To determine the total feed cost per pen, the total pounds of each ration were calculated, then multiplied by the rations costs per pound to equal the total feed cost for each pen. Ration prices were derived from the 2015 West Texas A&M Research Feedlot ration costs. Yardage was charged $0.25 per animal per day. Carcass value per 45.5 kg base price was derived from the 2016 5 area daily weighted average direct slaughter cattle report from the USDA

market news service (St Joseph, MO). To calculate the total carcass value, using the carcass value per 45.5 kg to determine the base price, divided by 45.5 to calculate the price per kg, then multiplied by the HCW for the total. Return on investment is necessary for GeneMax Advantage strategy to be adopted in commercial feeding operations. Currently, the GeneMax Advantage test, cost $26 per animal. Net return on a carcass basis is calculated by taking the total carcass value minus the feeder calf value, feeding expenses, and yardage costs.

3.3.9. Statistical analysis

All genetic indices were analyzed (SAS 9.4, SAS Inst. Inc., Cary, NC) as a completely randomized design using PROC MIXED and all performance data except d 0 weight (DAY0WT) were analyzed using PROC GLM with a covariate of pay weight (PAYWT). Animal was considered the experimental unit; model included the fixed effects of: FA1, hot carcass weight (HCW), quality grade (QG), yield grade (YG), average daily gain (ADG), and cattle type (NAT or CONV). Distributions of USDA quality grade (QG) and yield grade (YG) were analyzed using PROC GLIMMIX. The Tukey-Kramer adjustment was used to separate means. Differences were considered significant when $P < 0.05$ and a trend when $0.05 \geq P \leq 0.10$.

3.4. Results and Discussion

3.4.1. Cattle type

Descriptive statistics of SNPs contained within the GeneMax panel were initially evaluated between CONV and NAT cattle (Table 2). Maternal traits including heifer pregnancy (51; $P < 0.01$) and updated cow advantage (51; $P < 0.01$) scores were greater

for the NAT cattle. In contrast, HCW was greater (53; $P = 0.01$) and fat thickness tended (60; $P = 0.07$) to be greater for the CONV cattle. All other indices did not differ between cattle types ($P \geq 0.22$). Ranchers will select for different characteristics depending on the goals they want to accomplish with their breeding program. These differences offer insight into selection differences between two different cattle breeding programs.

Animal performance during the feedlot finishing phase was determined for CONV finished cattle and those finished under the NAT program (Table 3). As expected, the lack of a growth promoting implant led to a longer feeding period ($P < 0.01$; 207 vs 154 days on feed) and reduced efficiency for feed to gain ($P < 0.01$; 3.84 kg vs 3.13 kg) for cattle fed to fit the NAT. Moreover, CONV cattle had greater ADG ($P < 0.01$; 1.85 vs 1.31 kg), concomitant with more DM offered daily ($P < 0.01$; 12.8 vs 10.7 kg). However, the CONV cattle had the least total DM per animal (1960 kg vs 2164 kg; $P < 0.01$). Previous results reported by others (Bartle et al., 1992; Johnson et al., 1996; Bruns et al., 2005; Black et al., 2015) were similar, with greater ADG and feed efficiency for steers that were implanted compared to nonimplanted steers.

Pay weight ($P < 0.01$; 660 vs 628 kg) and HCW ($P < 0.01$; 406.8 vs 384.1 kg) was heavier for CONV finished. Maxwell et al. (2015) reported similar results that naturally fed cattle had lighter HCW. Dressed yield was also greater for the CONV finished cattle (64.26 vs 60.71 %; $P < 0.01$). The HCW and dressed yield outcomes are confounded by processing facility and are not a true reflection of a repeatable outcome. Kidney-pelvic-heart fat were included for HCW of CONV cattle whereas the HCW of NAT did not include the internal kidney-pelvic-heart fat. This likely represents an average difference of 1.9% and likely change in HCW of 7.3 kg (Boykin et al., 2017).

The percentage of cattle that were yield grade 3 tended ($P = 0.08$) to be increased for the CONV finished cattle. Maxwell et al. (2015) reported no difference of USDA yield grades between conventional and natural fed cattle. This result may also be confounded by measurement bias; the CONV cattle were evaluated by via camera grading system whereas the NAT cattle were yield graded by a human grader. The percentage of cattle that graded USDA choice tended ($P = 0.08$) to be greater for CONV finished cattle. This result should also be interpreted with caution because the CONV cattle were graded after 24h of chill whereas the NAT label cattle were graded after a 48h chill. Kreikemeier et al (1998) determined there was no effect on percentage of carcasses grading Choice or better between 24h and 48h chill times.

The feeding expense for ($695.08 vs $620.13; $P < 0.01$) was greater for the NAT cattle. However, carcass value per cwt. ($221.87/cwt. vs $184.64/cwt.; $P < 0.01$), total carcass value ($1876.55 vs $1644.43; $P < 0.01$) and net return on a carcass basis ($56.21 vs $-72.47; $P < 0.01$) was greatest for the NAT cattle, primarily due to the premium for qualifying under the natural label.

3.4.2. Feeder advantage score

The original statistical design was arranged to evaluate growth and carcass performance of cattle sorted by FA score of CONV fed (Tables 4, 5) and NAT label (Tables 6, 7) finished animals. In CONV cattle, CEM tended ($P = 0.09$) to increase from 46 to 65 as FA scores increased across the 7 pens. Mean WW indices differed ($P < 0.01$) and generally increased from 33 to 67 across the FA groupings. According to the FA index standards, heavier WW have an enhanced opportunity to gain faster, greater feed efficiency, and heavier HCW. Genetic estimates for mean HP decreased ($P < 0.01$) from

52 to 32 as FA pen score increased, suggesting an inverse relationship between fertility and finishing performance. As FA group scores increased, genomic estimates for Milk ($P < 0.01$), Gain ($P < 0.01$), CW ($P < 0.01$), Marbling ($P < 0.01$), FA1 ($P < 0.01$), and TA2 ($P = 0.01$) increased. The Tukey-Kramer adjustment did not detect differences ($P \geq 0.05$) among the pens for RE, even though the model indicated differences ($P = 0.02$) existed. These results are expected because, majority of these significant traits are a part of the equations to calculate the FA index.

A difference ($P < 0.01$) was detected for DDMFO but did not follow a linear increase as FA increased, rather a more quadratic approach (Table 5). The highest DDMFO was 13.66 kg with a mean FA score of 44 within the pen. Interestingly, the lowest DDMFO were 11.43 kg with a FA mean of 26 within the pen. Other researchers reported no differences (DeVuyst et al., 2011; Black et al., 2015) for cattle with higher gain estimates versus actual performance data of steers.

Within NAT fed cattle, as FA score increased amongst the pens, WW ($P < 0.01$) and Gain ($P < 0.01$) increased with a quadratic effect. Concluding that an increase in WW is correlated to having an increased gain in cattle. As expected, FA1 and FA2 increased ($P < 0.01$) as FA score increased due to the fact this is how the cattle were sorted for the study. Scores for FA within 47 to 53 tended ($P = 0.10$) to have the highest TA1 score, however this wasn't continued in TA2 ($P < 0.01$) score with group 75 to 82 having the highest score.

Even though FA group scores increase, DDMFO ($P < 0.01$) did not show a direct correlation to increasing with the FA group score (Table 7). Numerically, FA group 75 to 82 had the greatest ($P < 0.01$) dressed yield with a linear effect. This also coincides with

FA group 75 to 82 having the greatest ($P < 0.01$) HCW numerically, but the lowest ($P = 0.02$) percentage of YG 2 cattle. No differences ($P \geq 0.05$) were detected with the Tukey-Kramer adjustment amongst pens for YG percentage in cattle. Interestingly, cattle within FA group 32 to 41 tended ($P = 0.10$) to have the greatest percentage of YG 3. As expected, FA group 75 to 82 had the greatest ($P = 0.01$) total carcass value numerically. However, FA group 32 to 41 had the greatest ($P = 0.02$) net return carcass basis numerically. Caution needs to be taken when deciphering these differences because not all NAT label cattle were harvested at the same ending weight.

3.4.3. Correlation outcomes

Correlation between genetic indices and performance data were determined for CONV fed (Tables 8, 10) and NAT label (Tables 9, 11) animals. Among the different tables, CEM had a positive correlation ($r = 0.23$; $P < 0.05$) to DDMFO, but a negative correlation ($r = 0.27$; $P < 0.01$)) to HCW for CONV fed cattle. However, the NAT cattle did not have any correlation within the CEM index. Conventional fed cattle exhibited a positive (r = 0.24; $P < 0.05$) association between WW and DDMFO. As for NAT cattle, correlated variables to WW included: DDMFO ($r = 0.26$; $P < 0.01$), Day 0 BW ($r = 0.20$; $P < 0.05$), DOF ($r = -0.26$; $P < 0.01$), QG ($r = -0.24$; $P < 0.05$), and Feed to Gain ($r = -0.23$; $P < 0.05$). Physiologically, cattle with higher WW tend to be on feed for less time because they reach their desired body weight faster. Thus, less time is allowed for the animal to deposit intramuscular fat within the longissimus muscle (LM) likely decreasing the QG potential of the animal.

Neither CONV nor NAT cattle yielded outcomes that were correlated ($P \geq 0.05$) to HP. Within the CONV cattle, Milk was positively correlated with ADG ($r = 0.39$; $P < 0.01$) and DDMFO ($r = 0.31$; $P < 0.01$) and negatively correlated with Dressed Yield ($r = -0.43$; $P < 0.001$), Feed to Gain ($r = -0.28$; $P < 0.01$), HCW ($r = -0.25$; $P < 0.05$), and DOF ($r = -0.24$; $P < 0.05$). The negative correlation to dressed yield was also notable in NAT cattle ($r = -0.27$; $P < 0.01$).

No correlations ($P \geq 0.05$) were detected for MW within the CONV fed cattle. However, for the NAT cattle, as MW increased, ($r = 0.25$; $P < 0.01$) Day 0 BW increased while YG ($r = -0.22$; $P < 0.05$), DOF ($r = -0.21$; $P < 0.05$), and total DM ($r = -0.21$; $P < 0.05$) decreased.

The only variable that was positively correlated to CA1 in CONV cattle was Feed to Gain ($r = 0.26$; $P <0.05$). However, in the NAT cattle, as CA1 increased ($r = 0.22$; $P < 0.05$) total DM increased. Conventionally fed cattle had CA2 score negatively correlated to Dressed Yield ($r = -0.29$; $P < 0.01$) and HCW ($r = -0.29$; $P < 0.01$). Natural fed cattle CA2 index scores increased as DDMFO ($r = 0.21$; $P < 0.05$) increased, meaning cattle with a higher CA2 score, consumed more feed. Gain index for CONV cattle increased ($r = 0.29$; $P < 0.01$) as DDMFO increased, meaning the larger the Gain index, the more the cattle consumed. The NAT cattle had more performance variables correlated to Gain than the CONV fed cattle: ADG ($r = 0.41$; $P < 0.001$), Day 0 BW ($r = 0.30$; $P < 0.01$), Pay weight ($r = 0.25$; $P < 0.01$), Feed to Gain ($r = -0.36$; $P < 0.001$), DOF ($r = -0.34$; $P < 0.01$), Total DM ($r = -0.29$; $P < 0.01$), DDMFO ($r = -0.26$; $P < 0.01$), and QG ($r = -0.22$; $P < 0.05$). Cattle that had a high Gain index had a higher Day 0 BW, resulting in fewer DOF because it took less time for cattle to reach targeted end weight. Interestingly, the

cattle that were offered less Total DM throughout the study had a higher ADG and DDMFO for the natural cattle.

No correlation ($P \geq 0.05$) for any performance data within the CONV cattle was detected for CW. However, for NAT cattle, CW was correlated to ADG ($r = 0.41$; $P < 0.001$), Day 0 BW ($r = 0.33$; $P < 0.001$), Pay weight ($r = 0.31$; $P < 0.01$), Feed to Gain ($r = -0.36$; $P < 0.001$), and Total DM ($r = -0.29$; $P < 0.01$). In the NAT cattle, as CW increased, ADG, Day 0 BW, and Pay weight increased. Total DM decreased ($P < 0.01$) as CW increased for the NAT cattle, therefore, less total feed was offered during the study, but they had a heavier CW.

In CONV cattle, as MARB increased DDMFO ($r = 0.39$; $P < 0.001$) and YG ($r = 0.24$; $P < 0.05$) increased. DeVuyst et al. (2011) reported no significant correlation between the Igenity (Neogen Corporation, Lansing, MI) marbling index and YG. Interestingly, for the CONV cattle, there was no correlation ($P \geq 0.05$) between QG and MARB, thus, as the marbling score increased, the QG did not increase or decrease. Igenity (Neogen Corporation, Lansing, MI) panels showed a positive correlation between the marbling prediction and QG (DeVuyst et al. 2011). Natural fed cattle MARB index increased ($r = 0.24$; $P < 0.05$), QG and YG increased, causing the cattle to have more external fat.

No correlations ($P \geq 0.05$) were present for RE for either cattle type. Correspondingly, the same results were reported by (DeVuyst et al., 2011).

Conventionally fed cattle FAT index increased as QG ($r = -0.26$; $P < 0.05$) and Feed to Gain ($r = -0.27$; $P < 0.05$) decreased. Expectantly, as the FAT index increased,

YG decreased for CONV (r = -0.31; $P < 0.01$) and NAT (r = -0.31; $P < 0.01$) fed cattle. Therefore, the greater the FAT index, the less fat at the 12th rib will be acquired to adjust for YG.

A positive correlation ($P < 0.001$) between FA1 and DDMFO (r = 0.44) was observed in the CONV fed cattle. Natural cattle revealed correlations between FA1 to DDMFO (r = 0.35; $P < 0.01$), Day 0 BW (r = 0.30; $P < 0.01$), ADG (r = 0.23; $P < 0.05$), DOF (r = -0.39; $P < 0.001$), and Total DM (r = -0.32; $P < 0.01$). The positive associative effect was shown for Day 0 BW, ADG, and DDMFO and negative associative effect for DOF and Total DM for the NAT label cattle. As the FA2 index increased for CONV cattle, DDMFO (r = 0.35; $P < 0.01$) and Pay weight (r = 0.23; $P < 0.05$) increased. Natural cattle FA2 score increased as ADG (r = 0.28; $P < 0.01$) and DDMFO (r = 0.26; $P < 0.01$) increased, but DOF (r = -0.22; $P < 0.05$) and Feed to Gain (r = -0.23; $P < 0.05$) decreased.

Both CONV and NAT cattle had no correlation for TA1 ($P \geq 0.05$) for any outcomes. Conventionally fed cattle TA2 index increased, thus having a positive associative effect (r = 0.30; $P < 0.01$) towards DDMFO, but a negative associative effect (r = -0.25; $P < 0.05$) causing a decrease towards Dressed Yield. Natural label fed cattle TA2 index increased (r = 0.27; $P < 0.01$) as DDMFO increased, concluding that as the TA2 score increased, the cattle consumed more DDMFO.

3.4.4. Quality grade

Carcass merit, such as quality grade, yield grade, and hot carcass weight are important factors in finished beef cattle due to current marketing arrangements. Thus,

genomic predictions and performance data (Tables 12) were compared across quality grades. Mean genomic indices for Milk and CW tended ($P = 0.06$; $P = 0.09$) to be greater for cattle that graded USDA Select and lowest for these grading USDA Choice. As expected, the genetic estimate for mean Marbling increased ($P < 0.01$) from 55 to 65 as the quality grades increased. Mean TA1 tended ($P = 0.09$) to increase from 55 to 65 as quality grades increased. No other differences were reported for remaining traits ($P \geq 0.17$).

Cattle that graded USDA Select had the greatest Day 0 weight (408 kg; $P < 0.01$), followed by USDA Choice (360 kg), and USDA Prime (343 kg) (Table 13). Cattle that graded USDA Prime (215 days) required the greatest number of DOF, followed by USDA Choice (192 days), and USDA Select (141 days). Heavier cattle are expected to consume more feed, which concurs with increased ADG (1.69 kg vs. 1.36 kg; $P < 0.01$) and DDMFO (11.9 kg vs. 11.4 kg; $P < 0.01$) for cattle that graded USDA Select cattle compared to these grading USDA Prime. Feed to Gain resulted to be the most efficient ($P = 0.01$; 3.32 kg) for USDA Select cattle, but no different than USDA Choice cattle ($P = 0.01$; 3.57). However, total dry matter offered increased ($P < 0.01$) as the quality grades increased. Dressed yield ($P < 0.01$) and HCW ($P < 0.01$) was lowest for USDA Select cattle, but greatest for USDA Choice and Prime cattle. Carcass value per cwt. ($P < 0.01$) and total carcass value ($P < 0.01$) was greatest for USDA Prime cattle. This is primarily due to the premiums allotted to higher grading cattle and the discounts for the USDA Select cattle.

3.4.5. Yield grade

Genomic indices and performance data were also compared across USDA yield grades (Tables 14). Genomic index for MARB increased ($P = 0.01$) and Fat thickness decreased ($P < 0.01$) as yield grade increased. These data agree with the biological expectation and indicate that selection for marbling will also net an increase in fat thickness. Mean TA1 tended ($P = 0.09$) to increase as yield grade increased.

Cattle that had lower yield grades tended ($P = 0.10$) to have a greater feeder value at Day 0 (Table 15). No difference ($P = 0.51$) was reported for DOF. However, ADG ($P = 0.02$) and DDMFO (10.9 kg vs 12.3 kg; $P < 0.01$) increased as yield grades increased. Yield grade 4 carcasses had a heavier HCW (399.8 kg; $P < 0.01$) and dressed higher (63.12; $P < 0.01$). Thus, carcass value per cwt. ($184.64/cwt.; $P < 0.01$), total carcass value ($1608.30; $P < 0.01$), and net return on a carcass basis (-$160.72; $P < 0.01$) was least for yield grade 4 carcasses due to the discounts applied to the carcass.

3.4.6. Hot carcass weight

Genetic indices and performance data were also compared amongst predetermined HCW groups (Tables 16). Genetic estimates for CA2 ($P = 0.01$) and TA2 ($P = 0.01$) were greatest for carcasses weighing < 362.4 kg (HCW 2), smallest for carcasses 362.9 to 407.8 kg (HCW 3), but carcasses < 408.2 kg (HCW 1) was not different. Gain ($P = 0.04$) and FA2 ($P < 0.01$) estimates were greatest for HCW 2, smallest for HCW 1, but not different from HCW 3. Mean CW predictions tended ($P = 0.06$) to increase as HCW increased.

Cattle in HCW 2 had the greatest ($P = 0.04$) ADG but not different from HCW 3 (Table 17). Moreover, HCW 3 ($P < 0.01$) had the greatest DDMFO and the lowest ($P =$

0.05) Feed to Gain ratio, but not different from HCW 1. Pay weight was greatest ($P <$ 0.01) for HCW 3, concomitant with the greatest ($P < 0.01$) dressed yield and a tendency ($P = 0.10$) to have the greatest percentage of USDA Choice carcasses. Boykin et al. (2017) reported a similar trend for carcasses that weighed 363.6 to 409.0 kg were graded USDA 710 or Choice. DeVuyst et al. (2011) reported a positive correlation between percentage Choice Igentiy (Neogen Corporation, Lansing, MI) score and HCW. Thus, the higher the HCW, the greater chances of the carcass grading USDA Choice. Heavier carcasses had the greatest percentage ($P < 0.01$) of yield grade 4. The lightest carcass weight group had the greatest ($P < 0.01$) percentage of USDA Select cattle. This is expected because the smaller the animal, the less total feed offered. Cattle within HCW 1 had the highest percentage ($P < 0.01$) of yield grade 2, which coincides with findings from Boykin et al. (2017). Cattle in HCW 3 tended ($P = 0.10$) to have the lowest Day 0 Feeder Calf Value and carcass value per cwt. ($196.24/cwt.; $P < 0.01$), but the total carcass value ($1599.79; $P < 0.01$) and net return on a carcass basis (-$232.26; $P < 0.01$) was least for HCW 1.

3.4.7. Average daily gain

Average daily gain quartiles were used to compare genetic estimates (Table 18) and performance data (Table 19). Genetic estimates for MW ($P < 0.01$) were greatest for 1.28 to 1.48 kg (ADG 2), but not different from 1.48 to 1.85 kg (ADG 3) and >1.85 kg (ADG 4). Mean genomic predictions for Gain ($P = 0.05$) and CW ($P < 0.01$) increased as ADG increased, however, Tukey-Kramer detected no difference among the groups for Gain. Interestingly, FA1 decreased ($P < 0.01$) as ADG increased with the lowest score being for ADG 4.

As expected, ADG 1 had the lowest DAY0WT ($P < 0.01$), thus cattle with lighter body weight on d 0 will have the greatest DOF ($P < 0.01$) in order to reach the expected finish weight (Table 19). However, this resulted in ADG 1 cattle having the lowest pay weight ($P < 0.01$). Cattle in ADG 4 had the least (130; $P < 0.01$) DOF, thus lowest feed and yardage ($538.14; $P < 0.01$) expense. However, for carcass value per cwt. ($185.04; $P < 0.01$) and total carcass value ($1616.62; $P < 0.01$) was least for ADG 4. Cattle in ADG 3 had the lowest (12.50; $P < 0.01$) percentage of YG 2, but the greatest (39.20; $P < 0.01$) percentage of YG 4 with no differences detected between ADG 4. In ADG 4, the percentage of USDA Prime was lowest ($P < 0.02$). This is expected because these cattle were not on feed long enough to deposit intramuscular fat. Cattle in the ADG 1 consumed less feed daily DM ($P < 0.01$), but the greatest total feed offered ($P < 0.01$) over the entirety of the study. However, ADG 1 was the most inefficient feeders ($P < 0.01$) as assessed by Feed to Gain ratio.

3.5. Conclusion

After comparing all significant outcomes among the different cattle types, the study concludes that sorting CONV cattle by FA scores would not be beneficial within a feedyard. Due to growth technologies being implemented more often than not in feedyards, this helps to enhance any poor doing cattle to become more efficient growers and allows for more uniformity within the cattle. Thus, CONV cattle did not yield a high enough return to justify the use of genetically testing in commercial feedyard steers.

When looking at NAT cattle that were not allowed to receive any growth promotants and only perform based on genetic potential, thus seeing differences among the different FA scores. The main difference among the cattle were seen with the higher

performing cattle within the range of 63 to 82 FA scores. This could be used to the advantage of a cattle producer to sell the highest scoring cattle to guarantee high performance within the feedyard without growth technologies. Due to the premiums the NAT cattle receive at harvest, the net return will be high enough to potentially cover the costs for the genetic test. For cattle that scored lower than 63, it would be best to utilize growth technologies to increase the performance and efficiency of the cattle.

Further research should be conducted to verify of the high genetic scores, which scores would be best utilized within a feedyard.

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Table 1. Ingredient and analyzed nutrient composition (percent DM basis) of diets fed.

	Experimental Diet[1]					
Ingredients	NAT Grower	NAT Transition	NAT Finisher	CONV Grower	CONV Transition	CONV Finisher
Sweet Bran[2]	58.52	49.00	44.50	58.82	49.35	44.50
Corn Stalks	19.20	12.00	4.50	19.20	12.00	4.50
Flaked Corn	15.28	30.00	40.00	15.29	30.00	40.00
Molasses	3.00	3.00	3.00	3.05	3.00	3.00
Corn Oil	---	2.00	4.00	---	2.00	4.00
Natural Supplement[3]	4.00	4.00	4.00	---	---	---
Grower Supplement[4]	---	---	---	3.65	3.65	---
Finisher Supplement[5]	---	---	---	---	---	4.00
DM, %[6]	66.37	69.03	70.03	66.24	68.92	70.03
CP, %[6]	16.29	15.18	14.72	16.37	15.26	14.72
ADF, %[6]	14.23	5.97	3.02	14.26	5.97	3.02
NDF, %[6]	31.58	10.44	6.22	31.67	10.44	6.22
Fat, %[6]	11.27	4.91	2.59	11.30	4.91	2.59
Ca, %[6]	1.20	1.16	1.12	1.14	1.10	1.16
P, %[6]	0.72	0.60	0.58	0.72	0.60	0.58
Mg, %[6]	0.40	0.37	0.33	0.39	0.37	0.33
K, %[6]	1.33	1.11	0.98	1.32	1.11	0.98
S, %[6]	0.33	0.06	0.06	0.33	0.06	0.06

[1]Natural (NAT) cattle – no antibiotics, ionophores, growth implants, or beta-agonists. Conventional (CONV) cattle – fed tylosin, monensin, and received growth implant.

[2]Corn gluten feed product made from wet corn milling, Cargill, Inc., Minneapolis, MN.

[3]Formulated to contain (DM Basis): 68.37% limestone, 19.18% salt, 5.25% potassium chloride, 2.66% manganese oxide, 2.00% lecithin, 0.83% iron oxide, 0.57% zinc sulfate, 0.34% manganese sulfate, 0.30% vitamin A (20M/lb), 0.27% sodium selenite, 0.12% vitamin E (500), 0.11% copper sulfate, 0.0015% ethylenediamine dihydroiodide, and 0.0005% cobalt carbonate.

[4]Formulated to contain (DM Basis): 72.10% limestone, 0.27% Rumensin-90, 19.18% salt, 5.48% potassium chloride, 0.58% zinc sulfate, 0.56% vitamin E (44 IU/g), 0.18% manganese oxide, 0.18% vitamin A (30,000 IU/g), 0.14% selenium premix (0.4% se), 0.11% copper sulfate, 0.0006% cobalt carbonate, and 0.002% ethylenediamine dihydroiodide.

[5]Formulated to contain (DM Basis): 72.10% limestone, 19.18% salt, 5.48% potassium chloride, 0.58% zinc sulfate, 0.56% vitamin E (44 IU/g), 0.45% Rumensin-90, 0.18% manganese oxide, 0.18% vitamin A (30,000 IU/g), 0.11% Tylan-100, 0.11% copper sulfate, 0.05% selenium premix (1.0% se), 0.0006% cobalt carbonate, and 0.002% ethylenediamine dihydroiodide.

[6]All values are on a 100% DM basis. Samples were chemically analyzed at University of California, Davis.

Table 2. Least square means of genomic indices for conventional and natural cattle.

	Cattle Type					
Genomic Indices[1]	Conventional	Natural	Minimum	Maximum	SEM	*P*-Value
Calving Ease Maternal	53	52	16	83	2.22	0.57
Weaning Weight	52	49	16	87	4.00	0.68
Heifer Pregnancy	41	51	10	76	1.73	<0.01
Milk	52	52	18	87	2.31	0.94
Mature Weight	54	51	16	94	2.21	0.43
Cow Advantage Original[2]	58	58	30	83	1.65	1.00
Cow Advantage Updated[2]	44	51	9	81	1.63	<0.01
Gain	51	49	14	90	4.13	0.73
Carcass Weight	53	44	14	83	2.35	0.01
Marbling	58	54	18	90	2.85	0.27
Ribeye Area	55	55	12	93	2.30	0.98
Fat Thickness	60	55	13	88	1.77	0.07
Feeder Advantage Original[3]	54	54	10	93	6.16	0.99
Feeder Advantage Updated[3]	52	53	12	96	0.32	0.90
Total Advantage Original[4]	47	53	23	83	2.24	0.22
Total Advantage Updated[4]	48	53	10	83	3.18	0.33

[1]Genomic prediction based on GeneMax® Advantage™ (Zoetis™, Madison, NJ)

[2]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used from the older and updated version of GeneMax® Advantage™ (Zoetis™, Madison, NJ).

[3]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA Quality and Yield Grades). Scores used from the older and updated version of GeneMax® Advantage™ (Zoetis™, Madison, NJ).

[4]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the Cow and Feeder Advantage scores. Scores used from the older and updated version of GeneMax® Advantage™ (Zoetis™, Madison, NJ).

Table 3. Least square means of performance data for conventional and natural cattle.

	Cattle Type					
Performance Data	Conventional	Natural	Minimum	Maximum	SEM	*P*-Value
Day 0 Weight, kg	364	362	247	490	11.12	0.83
Day 0 Feeder Calf Value, $[1]	1096.77	1125.26	855.2	2093.4	15.79	0.16
Days on Feed	154	207	75	244	4.85	<0.01
Average Daily Gain, kg/d	1.85	1.31	0.85	2.33	0.06	<0.01
Daily DM Feed Offered, kg	12.8	10.7	9.5	14.5	0.30	<0.01
Sum DM/Hd, kg	1960	2164	795	3052	115.49	<0.01
Feed to Gain, kg	3.13	3.84	2.28	7.40	0.31	<0.01
Pay Weight, kg	660	628	520	729	9.07	<0.01
Dressed Yield	64.26	60.71	48.00	68.00	0.40	<0.01
Hot Carcass Weight, kg	406.8	384.1	288.5	455	5.71	<0.01
Yield Grade						
2, %	9.46	16.85				0.17
3, %	75.68	62.92				0.08
4, %	14.86	20.22				0.38
Quality Grade						
Prime, %	13.75	20.83				0.22
Choice, %	76.25	62.53				0.08
≤ Select, %	10.19	16.62				0.33
Feed and Yardage/Animal, $[2]	620.13	695.08	253.8	978.8	16.81	<0.01
Carcass Value/cwt, $/Animal[3]	184.64	221.87	165.3	235.4	1.10	<0.01
Total Carcass Value, $/Animal[4]	1644.43	1876.55	1413.9	2161.2	17.49	<0.01
Net Return Carcass Basis, $[5]	-72.47	56.21	-829.3	424.2	20.28	<0.01

[1]Feeder calf value derived from a nationwide weighted average feeder calf report from the USDA market news service (St Joseph, MO).

[2]Feed cost was determined by 2015 ration costs from WTAMU Research Feedlot with 0.25/hd/day yardage fee.

[3]Carcass value/cwt base price was derived from the 2016 5 area daily weighted average direct slaughter cattle report from the USDA market news service (St Joseph, MO).

[4]Total carcass value used the carcass value base price divided by 100 then multiplied by the hot carcass weight.

[5]Calcuated from subtracting feeder calf value, feed and yardage from Total Carcass Value.

Table 4. Least square means of genomic indices by feeder advantage score pen for conventionally finished cattle (n=81).

	Feeder Advantage Score Pen Sort										
Genomic Indices	10 to 28	28 to 36	36 to 46	46 to 53	53 to 63	64 to 70	72 to 93	SEM	*P*-Value	LIN	Quad
Calving Ease Maternal	46	47	58	46	55	51	65	5.38	0.09	---	---
Weaning Weight	33^{c}	39^{bc}	36^{bc}	52^{ab}	57^{a}	64^{a}	67^{a}	3.75	<0.01	0.29	<0.01
Heifer Pregnancy	52^{a}	49^{a}	41^{ab}	40^{ab}	37^{ab}	38^{ab}	32^{b}	4.16	0.02	0.90	<0.01
Milk	39^{b}	44^{b}	54^{ab}	49^{ab}	50^{ab}	58^{ab}	64^{a}	4.61	<0.01	0.90	<0.01
Mature Weight	55	45	44	56	59	63	55	5.16	0.12	---	---
Cow Advantage Original[1]	53	57	54	57	53	66	65	4.91	0.28	---	---
Cow Advantage Updated[1]	44	45	46	38	44	43	49	4.31	0.75	---	---
Gain	33^{d}	39^{cd}	38^{d}	48^{bcd}	54^{bc}	61^{ab}	69^{a}	3.58	<0.01	0.26	<0.01
Carcass Weight	43^{b}	50^{ab}	50^{ab}	52^{ab}	48^{ab}	58^{ab}	64^{a}	4.51	0.03	0.52	<0.01
Marbling	37^{c}	45^{bc}	59^{ab}	55^{abc}	61^{ab}	72^{a}	70^{a}	4.59	<0.01	0.98	<0.01
Ribeye Area	48	46	55	57	44	65	66	5.53	0.02	0.70	<0.01
Fat Thickness	60	56	51	62	62	64	61	4.90	0.55	---	---
Feeder Advantage Original[2]	23^{f}	31^{e}	41^{d}	50^{c}	58^{b}	64^{b}	78^{a}	1.57	<0.01	<0.01	<0.01
Feeder Advantage Updated[2]	27^{e}	35de	38de	49^{cd}	57^{bc}	68^{ab}	75^{a}	3.84	<0.01	0.16	<0.01
Total Advantage Original[3]	54	52	52	61	57	69	65	6.18	0.31	---	---
Total Advantage Updated[3]	34^{d}	40^{cd}	41^{bcd}	43^{bcd}	53^{abc}	56^{ab}	64^{a}	3.77	<0.01	0.22	<0.01

^{a,b,c,d,e,f,g}Least squares means within a row means without common superscript differ (P < 0.05)

[1]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used older and updated version GeneMax® Advantage™ (Zoetis, Madison, NJ).

[2]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA Quality and Yield Grades). Scores used GeneMax® Advantage™ (Zoetis, Madison, NJ).

[3]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the Cow and Feeder Advantage scores. Scores used GeneMax® Advantage™ (Zoetis, Madison, NJ).

Table 5. Least square means of cattle performance by feeder advantage score pen for conventionally finished cattle (n=81).

	Feeder Advantage Score Pen Sort								*P*-		
Performance Data	10 to 28	28 to 36	36 to 46	46 to 53	53 to 63	64 to 70	72 to 93	SEM	Value	LIN	Quad
Day 0 Weight, kg	362	365	376	352	366	363	359	28.24	0.93	---	---
Day 0 Feeder Calf Value, $[1]	1156.4	1137.3	1136.2	1127.1	1142.2	1061.9	1061.6	41.90	0.61	---	---
Days on Feed	180	143	140	166	161	164	162	14.12	0.41	---	---
Average Daily Gain, kg/d	1.64	1.98	1.99	1.77	1.86	1.97	1.92	0.23	0.23	---	---
Daily DM Offered, kg	11.43[c]	12.74[b]	13.66[a]	11.92[c]	13.08[b]	13.12[ab]	13.22[ab]	0.28	<0.01	<0.01	<0.01
Sum DM/Hd, kg	2108	1823	1958	1961	2090	2139	2151	370.83	0.71	---	---
Feed to Gain, kg	3.30	2.97	3.13	3.08	3.29	3.07	3.14	6.92	0.84	---	---
Pay Weight, kg	651.4	658.1	655.9	662.8	658.5	669.5	661.9	13.02	0.49	---	---
Dress Yield	64.36	63.95	64.00	65.19	64.14	63.55	63.47	0.84	0.83	---	---
Hot Carcass Weight, kg	425.7	423.4	422.0	430.5	422.9	418.2	418.8	12.21	0.76	---	---
Yield Grade											
2, %	22.22	9.09	9.09	0.00	9.09	9.09	9.09		0.85	---	---
3, %	55.56	54.55	36.36	60.00	54.55	27.27	45.45		0.74	---	---
4, %	22.22	36.36	54.55	40.00	36.36	63.64	45.45		0.63	---	---
Quality Grade											
Prime, %	22.22	36.36	54.55	40.00	36.36	63.64	45.45		0.62	---	---
Choice, %	55.56	50.55	36.36	60.00	54.55	27.27	45.45		0.74	---	---
Select, %	22.22	9.09	9.09	0.00	9.09	9.09	9.09		0.85	---	---
Feed and Yardage/Animal, $[2]	671.3	575.6	616.0	624.0	660.8	676.1	679.4	53.77	0.71	---	---
Carcass Value/cwt, $/Animal[3]	185.3	184.3	186.9	184.5	185.6	182.4	185.9	3.60	1.00	---	---
Total Carcass Value, $/Animal[4]	1740.6	1718.5	1739.5	1749.7	1730.4	1680.3	1715.1	44.35	0.97	---	---
Net Return Carcass Basis, $[5]	-87.1	5.6	-12.6	-1.4	-72.6	-57.6	-25.8	44.84	0.69	---	---

[a,b,c,d,e]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Feeder calf value derived from a nationwide weighted average feeder calf report from the USDA market news service (St Joseph, MO).

[2]Feed cost was determined by 2015 ration costs from WTAMU Research Feedlot with 0.25/hd/day yardage fee.

[3]Carcass value/cwt base price was derived from the 2016 5 area daily weighted average direct slaughter cattle report from the USDA market news service (St Joseph, MO).

[4]Total carcass value used the carcass value base price divided by 100 then multiplied by the hot carcass weight.

[5]Calcuated from subtracting feeder calf value, feed and yardage from Total Carcass Value.

Table 6. Least square means of genomic indices by feeder advantage score pen for naturally finished cattle (n=98).

	Feeder Advantage Score Pen Sort												
Genomic Indices	21 to 31	32 to 41	41 to 46	47 to 53	53 to 59	59 to 62	63 to 67	68 to 75	75 to 82	SEM	*P*-Value	LIN	Quad
Calving Ease Maternal	45	44	57	55	58	53	44	49	56	4.80	0.23	---	---
Weaning Weight	33^{c}	38^{bc}	50^{ab}	53^{ab}	49^{ab}	54^{a}	60^{a}	58^{a}	60^{a}	3.62	<0.01	0.33	0.05
Heifer Pregnancy	51	49	53	52	49	46	53	52	54	4.50	0.94	---	---
Milk	46	53	53	52	52	62	53	56	48	4.48	0.38	---	---
Mature Weight	53	43	45	45	59	51	54	48	60	5.60	0.27	---	---
Cow Advantage Original[1]	62	55	56	63	59	64	55	55	54	3.90	0.56	---	---
Cow Advantage Updated[1]	40	45	58	56	51	49	51	54	57	4.69	0.16	---	---
Gain	31^{d}	37^{cd}	45^{bcd}	50^{abc}	53^{ab}	53^{ab}	61^{ab}	61^{a}	60^{ab}	3.55	<0.01	0.58	0.02
Carcass Weight	42	38	45	47	42	45	52	55	45	5.32	0.43	---	---
Marbling	54	51	53	53	52	58	48	60	53	4.21	0.70	---	---
Ribeye Area	46	55	55	55	56	57	61	55	57	4.81	0.68	---	---
Fat Thickness	54	61	54	60	56	49	56	55	49	5.55	0.82	---	---
Feeder Advantage Original[2]	26^{i}	37^{h}	44^{g}	49^{f}	56^{e}	61^{d}	65^{c}	70^{b}	79^{a}	0.74	<0.01	<0.01	<0.01
Feeder Advantage Updated[2]	29^{e}	40de	48^{cd}	53^{bc}	61^{ab}	58^{abc}	66^{ab}	66^{a}	70^{a}	2.82	<0.01	0.30	<0.01
Total Advantage Original[3]	64	55	58	71	61	66	59	49	53	4.34	0.10	---	---
Total Advantage Updated[3]	36^{c}	43^{bc}	57^{ab}	57^{a}	53^{abc}	54^{a}	57^{a}	59^{ab}	63^{a}	4.04	<0.01	0.34	0.02

^{a,b,c,d,e,f,g,h,i}Least squares means within a row means without common superscript differ (P < 0.05)

[1]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used GeneMax® Advantage™ (Zoetis, Madison, NJ).

[2]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA Quality and Yield Grades). Scores used GeneMax® Advantage™ (Zoetis, Madison, NJ).

[3]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the Cow and Feeder Advantage scores. Scores used GeneMax® Advantage™ (Zoetis, Madison, NJ).

Table 7. Least square means of cattle performance by feeder advantage score pen for naturally finished cattle (n=98).

	Feeder Advantage Score Pen Sort												
Performance Data	21 to 31	32 to 41	41 to 46	47 to 53	53 to 59	59 to 62	63 to 67	68 to 75	75 to 82	SEM	*P*-Value	LIN	Quad
Day 0 Weight, kg	345	332	352	370	365	368	367	379	387	35.81	0.37	---	---
Day 0 Feeder Calf Value, $[1]	1081.1	1129.5	1042.1	1104.1	1081.1	1135.7	1102.7	1154.2	1113.4	46.49	0.85	---	---
Days on Feed	241	183	207	196	223	206	199	176	235	17.99	0.35	---	---
Average Daily Gain, kg/d	1.16	1.42	1.39	1.36	1.25	1.26	1.33	1.39	1.12	0.15	0.14	---	---
Daily DM Offered, kg	9.57^{f}	9.89^{ef}	11.13^{a}	10.56^{bc}	10.03^{de}	10.32^{cd}	10.41^{c}	10.85^{ab}	9.97^{de}	0.17	<0.01	<0.01	<0.01
Sum DM/Hd, kg	2325	1786	2331	2027	2269	2129	2097	1907	2380	399.09	0.46	---	---
Feed to Gain, kg	3.86	3.18	3.68	3.53	3.61	3.81	3.62	3.53	4.20	8.09	0.25	---	---
Pay Weight, kg	610.4	605.9	651.0	635.3	638.6	636.6	635.9	633.4	603.9	29.12	0.16	---	---
Dressed Yield	60.88^{ab}	60.69^{ab}	58.19^{ab}	61.24^{ab}	63.68^{a}	55.63^{b}	61.62^{ab}	61.20^{ab}	65.52^{a}	1.56	<0.01	0.04	0.60
Hot Carcass Weight, kg	379.0^{ab}	380.1^{ab}	363.9^{ab}	383.3^{ab}	397.7^{a}	346.9^{b}	384.7^{ab}	384.0^{ab}	409.5^{a}	21.93	<0.01	0.42	0.87
Yield Grade													
2, %	0.00	0.00	0.00	30.00	10.00	50.00	20.00	30.00	11.11		0.02	0.39	0.15
3, %	70.00	90.00	80.00	50.00	60.00	40.00	50.00	40.00	88.89		0.10	---	---
4, %	30.00	10.00	20.00	20.00	30.00	10.00	30.00	30.00	0.00		0.68	---	---
Quality Grade													
Prime, %	10.00	0.00	10.00	0.00	0.00	10.00	0.00	10.00	11.11		0.84	---	---
Choice, %	60.00	50.00	40.00	50.00	50.00	30.00	50.00	80.00	44.44		0.65	---	---
Select, %	30.00	50.00	50.00	50.00	50.00	60.00	50.00	10.00	44.44		0.53	---	---
Feed and Yardage/Animal, $[2]	752.4	576.7	745.7	651.4	730.8	684.1	672.2	610.3	766.9	58.45	0.45	---	---
Carcass Value/cwt, $/Animal[3]	223.6	223.5	226.4	224.0	225.5	211.1	221.4	221.4	219.0	3.73	0.22	---	---
Total Carcass Value, $/Animal[4]	1870^{ab}	1871^{ab}	1817^{ab}	1891^{ab}	1973^{a}	1612^{b}	1881^{a}	1870^{ab}	1981^{a}	64.60	0.01	0.41	0.92
Net Return Carcass Basis, $[5]	36.2^{ab}	164.4^{a}	28.9^{ab}	135.5^{a}	161.6^{a}	-208.2^{b}	106.1^{a}	105.0^{ab}	100.6^{ab}	73.26	0.02	0.37	0.35

[a,b,c,d,e,f]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Feeder calf value derived from a nationwide weighted average feeder calf report from the USDA market news service (St Joseph, MO).

[2]Feed cost was determined by 2015 ration costs from WTAMU Research Feedlot with 0.25/hd/day yardage fee.

[3]Carcass value/cwt base price was derived from the 2016 5 area daily weighted average direct slaughter cattle report from the USDA market news service (St Joseph, MO).

[4]Total carcass value used the carcass value base price divided by 100 then multiplied by the hot carcass weight.

[5]Calcuated from subtracting feeder calf value, feed and yardage from Total Carcass Value.

Table 8. Pearson square correlation coefficients (r) for genomic indices and performance data for conventionally finished cattle (n=81).

	Genomic Indices[1]							
Performance Data	CEM	WW	HP	MILK	MW	CA1[2]	CA2[2]	GAIN
Day 0 Weight	-0.20	0.06	0.007	0.07	0.13	0.01	-0.14	0.007
Days on Feed	0.02	-0.08	-0.02	-0.24*	-0.13	0.14	-0.03	-0.07
Average Daily Gain	0.12	0.11	-0.005	0.39**	0.15	-0.17	0.11	0.16
DDMFO	0.23*	0.24*	-0.22	0.31**	0.004	0.11	0.08	0.29**
SUMDMO	0.09	-0.01	-0.04	-0.18	-0.15	0.19	0.05	0.01
Feed to Gain	-0.02	0.001	-0.10	-0.28**	-0.18	0.26*	-0.05	-0.04
Pay Weight	-0.10	0.15	0.02	0.15	0.19	0.13	-0.06	0.19
Dressed Yield	-0.21	-0.04	-0.10	-0.43***	0.02	-0.03	-0.29**	-0.12
Hot Carcass Weight	-0.27**	0.07	-0.06	-0.25*	0.15	0.10	-0.29**	0.03
Yield Grade	0.11	0.06	-0.11	-0.01	-0.01	0.20	0.02	0.08
Quality Grade	0.04	0.06	0.01	0.05	0.13	0.23	-0.0001	0.13

[1]Genomic prediction based on Genemax® Advantage™ (Zoetis™, Madison, NJ). Molecular breeding values are calving ease maternal (CEM), weaning weight (WW), heifer pregnancy (HP), mature weight (MW), cow advantage (CA), daily dry matter feed offered (DDMFO), sum dry matter offered (SUMDMO).

[2]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used from older or updated version of Genemax® Advantage™ (Zoetis™, Madison, NJ).

**significance levels where α <0.05; **significance levels where α <0.01; ***significance levels where α <0.001.*

Table 9. Pearson square correlation coefficients (r) for genomic indices and performance data for naturally finished cattle (n=98).

	Genomic Indices[1]							
Performance Data	CEM	WW	HP	MILK	MW	CA1[2]	CA2[2]	GAIN
Day 0 Weight	-0.06	0.20*	0.005	0.16	0.25**	-0.11	-0.03	0.30**
Days on Feed	-0.09	-0.26**	-0.08	-0.11	-0.21*	0.18	-0.03	-0.34**
Average Daily Gain	-0.05	0.30	0.05	0.18	0.19	-0.10	0.05	0.41***
DDMFO	0.15	0.27**	0.05	0.07	0.006	0.14	0.21*	0.26**
SUMDMO	0.14	-0.20	-0.07	-0.09	-0.21*	0.22*	0.02	-0.29**
Feed to Gain	0.09	-0.23*	-0.05	-0.16	-0.19	0.12	-0.002	-0.36***
Pay Weight	0.05	0.15	-0.07	0.18	0.18	0.06	-0.03	0.25**
Dress Yield	0.01	0.04	0.07	-0.27**	0.10	-0.08	0.07	-0.08
Hot Carcass Weight	0.05	0.14	0.01	-0.08	0.19	0.01	0.04	0.12
Yield Grade	0.12	-0.10	-0.07	0.07	-0.22*	0.03	0.08	-0.10
Quality Grade	0.11	-0.24*	-0.06	-0.19	-0.03	0.02	-0.04	-0.22*

[1]Genomic prediction based on Genemax® Advantage™ (Zoetis™, Madison, NJ). Molecular breeding values are calving ease maternal (CEM), weaning weight (WW), heifer pregnancy (HP), mature weight (MW), cow advantage (CA), daily dry matter feed offered (DDMFO), sum dry matter offered (SUMDMO).

[2]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used from older and updated version of Genemax® Advantage™ (Zoetis™, Madison, NJ).

**significance levels where α <0.05; **significance levels where α <0.01; ***significance levels where α <0.001*

Table 10. Pearson square correlation coefficients (r) for genomic indices and performance data for conventionally finished cattle (n=81).

	Genomic Indices[1]							
Performance Data	CW	MARB	RE	FAT	FA1[2]	FA2[2]	TA1[3]	TA2[3]
Day 0 Weight	-0.08	-0.11	-0.11	-0.03	0.04	-0.008	0.13	-0.02
Days on Feed	-0.01	0.0008	0.06	-0.12	-0.10	0.06	0.08	-0.07
Average Daily Gain	0.15	0.15	0.06	0.22	0.18	0.17	-0.19	0.20
DDMFO	0.19	0.39***	0.13	-0.06	0.44***	0.35**	-0.07	0.30**
SUMDMO	0.03	0.10	0.11	-0.14	0.0005	0.04	0.08	0.004
Feed to Gain	-0.08	0.01	-0.01	-0.27*	0.02	-0.03	0.20	-0.06
Pay Weight	0.07	0.06	0.16	0.05	0.17	0.23*	0.09	0.10
Dress Yield	-0.12	-0.05	-0.05	-0.09	-0.10	-0.12	-0.06	-0.25*
Hot Carcass Weight	-0.06	-0.05	0.08	-0.02	0.03	0.06	0.03	-0.15
Yield Grade	0.05	0.24*	-0.008	-0.31**	0.15	0.12	-0.08	0.07
Quality Grade	0.08	0.16	0.14	-0.26*	0.09	0.14	0.20	0.06

[1]Genomic prediction based on Genemax® Advantage™ (Zoetis™, Madison, NJ). Molecular breeding values are carcass weight (CW), marbling (MARB), ribeye area (RE), fat thickness (FAT), feeder advantage (FA), total advantage (TA), daily dry matter feed offered (DDMFO), sum dry matter offered (SUMDMO).

[2]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA quality and yield grades). Scores used from older and updated version of Genemax® Advantage™ (Zoetis™, Madison, NJ).

[3]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the cow and feeder advantage scores. Scores used from older and updated version of Genemax® Advantage™ (Zoetis™, Madison, NJ).

**significance levels where α <0.05; **significance levels where α <0.01; ***significance levels where α <0.001.*

Table 11. Pearson square correlation coefficients (r) for genomic indices and performance data for naturally finished cattle (n=98).

	Genomic Indices[1]							
Performance Data	CW	MARB	RE	FAT	FA1[2]	FA2[2]	TA1[3]	TA2[3]
Day 0 Weight	0.33***	-0.09	-0.07	-0.12	0.30**	0.16	0.03	0.01
Days on Feed	-0.31	0.15	0.10	0.06	-0.39***	-0.22*	-0.05	-0.09
Average Daily Gain	0.41***	-0.15	0.06	-0.01	0.23*	0.28**	0.03	0.10
DDMFO	0.18	0.04	0.005	-0.02	0.35**	0.26**	0.21	0.27**
SUMDMO	-0.29**	0.16	0.12	0.05	-0.32**	-0.16	0.01	-0.02
Feed to Gain	-0.36***	0.19	-0.07	-0.008	-0.11	-0.23*	0.02	-0.04
Pay Weight	0.31**	-0.04	0.11	-0.08	0.05	0.15	0.02	-0.008
Dress Yield	-0.11	0.04	-0.03	0.02	0.11	0.05	-0.06	0.11
Hot Carcass Weight	0.12	-0.006	0.05	-0.04	0.12	0.16	-0.002	0.08
Yield Grade	-0.13	0.24*	-0.10	-0.31**	0.05	0.01	0.006	0.09
Quality Grade	-0.19	0.24**	0.02	0.10	-0.18	-0.09	-0.03	-0.10

[1]Genomic prediction based on Genemax® Advantage™ (Zoetis™, Madison, NJ). Molecular breeding values are carcass weight (CW), marbling (MARB), ribeye area (RE), fat thickness (FAT), feeder advantage (FA), total advantage (TA), daily dry matter feed offered (DDMFO), sum dry matter offered (SUMDMO).

[2]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA quality and yield grades). Scores used from older and updated version of Genemax® Advantage™ (Zoetis™, Madison, NJ).

[3]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the cow and feeder advantage scores. Scores used from older and updated version of Genemax® Advantage™ (Zoetis™, Madison, NJ).

**significance levels where α <0.05; **significance levels where α <0.01; ***significance levels where α <0.001.*

Table 12. Least square means of genomic indices by USDA quality grades.

Genetic Indices	≤Select	Choice	Prime	SEM	*P*-Value
	n=24	n=121	n=31		
Calving Ease Maternal	49	52	55	2.29	0.47
Weaning Weight	55	50	49	3.11	0.29
Heifer Pregnancy	48	46	46	5.52	0.78
Milk	59	50	54	2.13	0.06
Mature Weight	56	51	56	2.39	0.29
Cow Advantage Original[2]	61	57	61	1.84	0.17
Cow Advantage Updated[2]	49	47	48	3.70	0.84
Gain	52	49	50	3.19	0.54
Carcass Weight	55	47	49	4.97	0.09
Marbling	55[b]	54[b]	65[a]	3.35	<0.01
Ribeye Area	50	55	56	2.36	0.39
Fat Thickness	58	58	56	2.91	0.88
Feeder Advantage Original[3]	53	54	54	4.27	0.89
Feeder Advantage Updated[3]	51	53	55	3.85	0.44
Total Advantage Original[4]	55	58	65	2.35	0.09
Total Advantage Updated[4]	53	50	52	2.70	0.65

[1]Genomic prediction based on GeneMax® Advantage™ (Zoetis, Madison, NJ)

[2]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

[3]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA Quality and Yield Grades). Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

[4]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the Cow and Feeder Advantage scores. Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

Table 13. Least square means of cattle performance by USDA quality grades.

Performance Data	≤Select	Choice	Prime	SEM	*P*-Value
	n=24	n=121	n=31		
Day 0 Weight, kg	408[a]	360[b]	343[b]	11.86	<0.01
Day 0 Feeder Calf Value, $[1]	1206.89[a]	1104.61[b]	1068.60[b]	15.15	<0.01
Days on Feed	141[c]	192[b]	215[a]	5.96	<0.01
Average Daily Gain, kg/d	1.69[a]	1.50[b]	1.36[b]	0.15	<0.01
Daily DM Feed Offered, kg	11.9	11.4	11.4	0.48	0.42
Sum DM/Hd, kg	1642[c]	2124[b]	2372[a]	114.91	<0.01
Feed to Gain, kg	3.32[b]	3.57[ab]	3.86[a]	7.91	0.01
Pay Weight, kg	638	645	643	34.47	0.68
Dress Yield	59.64[b]	62.47[a]	62.36[a]	0.51	<0.01
Hot Carcass Weight, kg	376.3[b]	395.7[a]	394.1[a]	7.16	<0.01
Yield Grade					
2, %	38.40	27.00	27.38		0.54
3, %	50.00	50.00	44.83		0.88
4, %	11.81	22.21	29.63		0.28
Feed and Yardage/Animal, $[2]	522.52[c]	679.02[b]	759.06[a]	16.88	<0.01
Carcass Value/cwt, $/Animal[3]	194.31[c]	208.08[b]	221.99[a]	2.80	<0.01
Total Carcass Value, $/Animal[4]	1598.83[c]	1804.33[b]	1919.70[a]	22.21	<0.01
Net Return Carcass Basis, $[5]	-130.59[b]	20.70[a]	92.04[a]	22.91	<0.01

[a,b,c]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Feeder calf value derived from a nationwide weighted average feeder calf report from the USDA market news service (St Joseph, MO).

[2]Feed cost was determined by 2015 ration costs from WTAMU Research Feedlot with 0.25/hd/day yardage fee.

[3]Carcass value/cwt base price was derived from the 2016 5 area daily weighted average direct slaughter cattle report from the USDA market news service (St Joseph, MO).

[4]Total carcass value used the carcass value base price divided by 100 then multiplied by the hot carcass weight.

[5]Calcuated from subtracting feeder calf value, feed and yardage from Total Carcass Value.

Table 14. Least square means of genomic indices by USDA yield grades.

Genomic Indices	2	3	≥4	SEM	*P*-Value
	n=49	n=88	n=39		
Calving Ease Maternal	50	52	56	2.36	0.22
Weaning Weight	53	49	51	3.18	0.19
Heifer Pregnancy	47	47	43	4.90	0.38
Milk	51	53	52	2.28	0.89
Mature Weight	56	52	51	3.11	0.28
Cow Advantage Original[1]	55	59	60	1.94	0.30
Cow Advantage Updated[1]	47	48	49	4.21	0.85
Gain	52	48	50	3.25	0.14
Carcass Weight	52	48	46	5.65	0.29
Marbling	51[b]	56[ab]	61[a]	2.52	0.01
Ribeye Area	57	54	54	2.46	0.64
Fat Thickness	66[a]	57[b]	50[b]	5.52	<0.01
Feeder Advantage Original[2]	52	52	53	4.27	0.25
Feeder Advantage Updated[2]	53	52	55	3.86	0.30
Total Advantage Original[3]	58	57	64	2.78	0.09
Total Advantage Updated[3]	50	51	53	2.87	0.69

[a,b,c]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

[2]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA Quality and Yield Grades). Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

[3]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the Cow and Feeder Advantage scores. Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

Table 15. Least square means of cattle performance by USDA yield grades.

Performance Data	2	3	≥4	SEM	*P*-Value
	n=49	n=88	n=39		
Day 0 Weight, kg	362	366	361	13.58	0.81
Day 0 Feeder Calf Value, $[1]	1140.46	1111.00	1079.33	16.97	0.10
Days on Feed	193	187	179	7.16	0.51
Average Daily Gain, kg/d	1.40[b]	1.53[ab]	1.66[a]	0.12	0.02
Daily DM Feed Offered, kg	10.9[b]	11.6[ab]	12.3[a]	0.48	<0.01
Sum DM/Hd, kg	2030	2095	2171	144.88	0.42
Feed to Gain, kg	3.67	3.54	3.49	7.86	0.46
Pay Weight, kg	640	641	654	30.02	0.16
Dressed Yield	60.63[b]	62.57[a]	63.12[a]	0.54	0.01
Hot Carcass Weight, kg	383.6[b]	395.9[ab]	399.8[a]	7.60	0.01
Quality Grade					
Prime, %	18.37	15.91	20.51		0.81
Choice, %	64.14	70.59	70.25		0.73
Select, %	17.76	13.71	8.57		0.49
Feed and Yardage/Animal, $[2]	651.58	669.12	689.69	20.90	0.55
Carcass Value/cwt, $/Animal[3]	220.03[a]	209.27[b]	184.64[c]	2.50	<0.01
Total Carcass Value, $/Animal[4]	1859.63[a]	1817.11[a]	1608.30[b]	23.30	<0.01
Net Return Carcass Basis, $[5]	67.59[a]	37.00[a]	-160.72[b]	22.25	<0.01

[a,b,c]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Feeder calf value derived from a nationwide weighted average feeder calf report from the USDA market news service (St Joseph, MO).

[2]Feed cost was determined by 2015 ration costs from WTAMU Research Feedlot with 0.25/hd/day yardage fee.

[3]Carcass value/cwt base price was derived from the 2016 5 area daily weighted average direct slaughter cattle report from the USDA market news service (St Joseph, MO).

[4]Total carcass value used the carcass value base price divided by 100 then multiplied by the hot carcass weight.

[5]Calcuated from subtracting feeder calf value, feed and yardage from Total Carcass Value.

Table 16. Least square means of genomic indices by hot carcass weights.

Genomic Indices	<362.4 kg	362.9-407.8 kg	<408.2 kg	SEM	*P*-Value
	n=29	n=61	n=86		
Calving Ease Maternal	51	56	50	2.73	0.12
Weaning Weight	47	53	50	3.19	0.13
Heifer Pregnancy	49	47	44	4.84	0.50
Milk	52	54	51	2.31	0.61
Mature Weight	47	52	55	2.49	0.11
Cow Advantage Original[1]	58	57	59	1.86	0.84
Cow Advantage Updated[1]	50[ab]	52[a]	44[b]	2.27	0.01
Gain	45[b]	52[a]	50[ab]	3.25	0.04
Carcass Weight	42	47	51	3.09	0.06
Marbling	56	56	56	3.16	0.98
Ribeye Area	50	55	56	2.49	0.30
Fat Thickness	55	54	60	2.13	0.11
Feeder Advantage Original[2]	53	54	54	4.27	0.73
Feeder Advantage Updated[2]	49[b]	56[a]	52[ab]	3.87	<0.01
Total Advantage Original[3]	59	61	59	2.68	0.78
Total Advantage Updated[3]	52[ab]	55[a]	48[b]	2.75	0.01

[a,b,c]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

[2]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA Quality and Yield Grades). Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

[3]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the Cow and Feeder Advantage scores. Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

Table 17. Least square means of cattle performance by hot carcass weights.

Performance Data	<362.4 kg	362.9-407.8 kg	>408.2 kg	SEM	*P*-Value
	n=29	n=61	n=86		
Day 0 Weight, kg	346.8	366.2	367.2	13.33	0.12
Day 0 Feeder Calf Value, $[1]	1130.57	1140.37	1083.03	21.95	0.10
Days on Feed	207	188	174	9.16	0.15
Average Daily Gain, kg/d	1.50[b]	1.63[a]	1.59[ab]	0.62	0.04
Daily DM Feed Offered, kg	10.7[b]	11.3[b]	12.2[a]	0.64	<0.01
Sum DM/Hd, kg	2185	2015	2083	183.90	0.54
Feed to Gain, kg	3.72[ab]	3.71[a]	3.37[b]	7.81	0.05
Pay Weight, kg	583.3[c]	636.8[b]	666.8[a]	7.93	<0.01
Dressed Yield	54.40[c]	62.46[b]	66.81[a]	0.40	<0.01
Yield Grade					
2, %	46.54[a]	37.49[a]	15.99[b]		<0.01
3, %	44.44	56.36	45.68		0.42
4, %	9.91[b]	6.65[b]	37.41[a]		<0.01
Quality Grade					
Prime, %	13.79	14.75	20.93		0.53
Choice, %	51.37	71.59	72.60		0.10
Select, %	35.60[a]	15.01[b]	5.27[b]		<0.01
Feed and Yardage/Animal, $[2]	701.48	645.63	661.48	27.03	0.56
Carcass Value/cwt, $/Animal[3]	212.53[ab]	218.83[a]	196.24[b]	3.79	<0.01
Total Carcass Value, $/Animal[4]	1599.79[b]	1902.78[a]	1826.94[a]	32.92	<0.01
Net Return Carcass Basis, $[5]	-232.26[b]	116.78[a]	82.04[a]	29.56	<0.01

[a,b,c]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Feeder calf value derived from a nationwide weighted average feeder calf report from the USDA market news service (St Joseph, MO).

[2]Feed cost was determined by 2015 ration costs from WTAMU Research Feedlot with 0.25/hd/day yardage fee.

[3]Carcass value/cwt base price was derived from the 2016 5 area daily weighted average direct slaughter cattle report from the USDA market news service (St Joseph, MO).

[4]Total carcass value used the carcass value base price divided by 100 then multiplied by the hot carcass weight.

[5]Calcuated from subtracting feeder calf value, feed and yardage from Total Carcass Value.

Table 18. Least square means of genetic predictions by average daily gain.

Genomic Indices	<1.28 kg	1.28-1.48 kg	1.48-1.85 kg	>1.85 kg	SEM	*P*-Value
	n=42	n=46	n=42	n=45		
Calving Ease Maternal	53	52	50	55	2.75	0.66
Weaning Weight	49	51	52	50	3.42	0.65
Heifer Pregnancy	44	45	46	57	6.81	0.90
Milk	50	48	53	58	3.77	0.15
Mature Weight	45[b]	57[a]	52[ab]	55[ab]	2.87	<0.01
Cow Advantage Original[1]	61	59	59	53	2.88	0.18
Cow Advantage Updated[1]	47	47	47	50	5.13	0.78
Gain	45	51	52	52	3.42	0.05
Carcass Weight	39[b]	49[a]	53[a]	52[a]	2.64	<0.01
Marbling	59	53	57	55	4.33	0.23
Ribeye Area	54	53	57	55	2.87	0.78
Fat Thickness	53	57	56	62	2.50	0.12
Feeder Advantage Original[2]	57[a]	54[ab]	54[a]	50[b]	4.35	<0.01
Feeder Advantage Updated[2]	52	52	54	54	4.07	0.84
Total Advantage Original[3]	61	61	61	54	3.03	0.23
Total Advantage Updated[3]	53	49	50	52	3.11	0.50

[a,b,c]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Predicts differences in profitability for heifer pregnancy, calving ease total maternal, milk production, growth and costs due to cow size and milk, assuming progeny are sold at or shortly after weaning. Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

[2]Predicts differences in net return of feeder calf progeny due to transmitted genetics for post-weaning growth, feed intake, carcass weight and CAB carcass merit (marbling and traits associated with USDA Quality and Yield Grades). Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

[3]Predicts differences in profitability from genetic merit across all economically relevant traits captured in the Cow and Feeder Advantage scores. Scores used from older and updated version of GeneMax® Advantage™ (Zoetis, Madison, NJ).

Table 19. Least square means of genetic predictions by average daily gain.

Performance Data	<1.28 kg	1.28-1.48 kg	1.48-1.85 kg	>1.85 kg	SEM	*P*-Value
	n=42	n=46	n=42	n=45		
Day 0 Weight, kg	331.0[b]	363.6[a]	376.6[a]	378.6[a]	32.02	<0.01
Day 0 Feeder Calf Value, $[1]	1122.23	1131.12	1098.38	1101.18	20.82	0.56
Days on Feed	231[a]	197[b]	170[c]	130[d]	5.61	<0.01
Daily DM Feed Offered, kg	10.20[d]	11.20[c]	12.15[b]	13.05[a]	0.46	<0.01
Sum DM/Hd, kg	2360.81[a]	2128.23[ab]	2035.90[b]	1704.85[c]	145.30	<0.01
Feed to Gain, kg	4.04[a]	3.76[a]	3.39[b]	2.93[c]	7.77	<0.01
Pay Weight, kg	607.91[b]	648.86[a]	658.73[a]	654.10[a]	14.89	<0.01
Dressed Yield	61.05[bc]	60.79[c]	63.84[a]	63.08[ab]	0.63	<0.01
Hot Carcass Weight, kg	386.3[bc]	384.6[c]	404.4[a]	399.0[ab]	8.90	<0.01
Yield Grade						
2, %	48.78[a]	34.15[ab]	12.50[b]	17.07[b]		<0.01
3, %	46.34	53.66	47.50	48.78		0.92
4, %	7.13[b]	13.71[b]	39.20[a]	30.63[ab]		<0.01
Quality Grade						
Prime, %	26.83[a]	17.07[ab]	25.00[a]	2.44[b]		0.02
Choice, %	66.63	68.30	60.26	79.30		0.33
Select, %	2.37	10.69	17.60	24.57		0.11
Feed and Yardage/Animal, $[2]	759.96[a]	681.88[ab]	647.05[b]	538.14[c]	20.94	<0.01
Carcass Value/cwt, $/Animal[3]	225.56[a]	216.84[a]	195.71[b]	185.04[c]	2.52	<0.01
Total Carcass Value, $/Animal[4]	1916.85[a]	1834.70[a]	1731.75[b]	1616.62[c]	26.77	<0.01
Net Return Carcass Basis, $[5]	34.66	21.70	-13.68	-22.70	31.61	0.54

[a,b,c]Least squares means within a row means without common superscript differ (P < 0.05)

[1]Feeder calf value derived from a nationwide weighted average feeder calf report from the USDA market news service (St Joseph, MO).

[2]Feed cost was determined by 2015 ration costs from WTAMU Research Feedlot with 0.25/hd/day yardage fee.

[3]Carcass value/cwt base price was derived from the 2016 5 area daily weighted average direct slaughter cattle report from the USDA market news service (St Joseph, MO).

[4]Total carcass value used the carcass value base price divided by 100 then multiplied by the hot carcass weight.

[5]Calcuated from subtracting feeder calf value, feed and yardage from Total Carcass Value.