

2013

Evaluation of 54 years of Louisiana bull testing, and SNP affecting growth and performance of yearling bulls on a forage performance bull test

Tabitha Howard

Louisiana State University and Agricultural and Mechanical College

Follow this and additional works at: https://digitalcommons.lsu.edu/gradschool_theses



Part of the [Animal Sciences Commons](#)

Recommended Citation

Howard, Tabitha, "Evaluation of 54 years of Louisiana bull testing, and SNP affecting growth and performance of yearling bulls on a forage performance bull test" (2013). *LSU Master's Theses*. 2521.
https://digitalcommons.lsu.edu/gradschool_theses/2521

This Thesis is brought to you for free and open access by the Graduate School at LSU Digital Commons. It has been accepted for inclusion in LSU Master's Theses by an authorized graduate school editor of LSU Digital Commons. For more information, please contact gradetd@lsu.edu.

EVALUATION OF 54 YEARS OF LOUISIANA BULL TESTING, AND SNP
AFFECTING GROWTH AND PERFORMANCE OF YEARLING BULLS ON
A FORAGE PERFORMANCE BULL TEST

A Thesis

Submitted to the Graduate Faculty of the
Louisiana State University and
Agricultural and Mechanical College
in partial fulfillment of the
requirements for the degree of
Master of Science

in

The Department of
Animal Sciences

by

Tabitha Renea Howard
B.S., Louisiana State University, 2010
May 2013

ACKNOWLEDGEMENTS

Many thanks to all involved with my Masters Project. Most importantly, I would like to thank my major professor, Dr. Matthew Garcia, for all of his patience with me during my time as his graduate student and for all of the support and encouragement over the past two years.

I would like to thank my committee members Dr. Karl Harborth and Dr. Kenneth Bondioli for their contribution to my research. As well as, Dr. Sid DeRouen for the contribution of all 54 years of bull test data. I would also like to thank Dr. Garcia's research associate, Mrs. Anita Canal for her assistance in the genetics lab along with Mr. Mike Canal and the staff at the LSU AgCenter Central Research Station's Purebred Beef Unit for the use of their bulls on performance test.

Lastly, I would like to thank my fellow grad students for their words of wisdom and encouragement throughout my time as a Masters student. Most importantly, I would like to thank God, because without him none of this would have been possible.

TABLE OF CONTENTS

ACKNOWLEDGEMENTS	ii
LIST OF TABLES.....	v
LIST OF FIGURES.....	vii
ABSTRACT	viii
CHAPTER	
I. INTRODUCTION	1
II. REVIEW OF LITERATURE	3
Performance Testing	3
Growth Hormone	5
Genetic Markers	6
SNP	7
<i>Bos taurus</i> vs <i>Bos indicus</i>	8
QTL Associated with Growth	9
Candidate Genes	10
GH (Growth Hormone) Gene	10
IGF-1 Gene	11
CAST Gene	12
Ultrasound Technology for Carcass Traits	12
Marker Assisted Selection	13
Whole Genome Selection	14
III. EVALUATION OF 54 YEARS OF LOUISIANA BULL TESTING	15
Introduction	15
Experimental Animals	16
Statistical Analysis	16
Results	17
Discussion	19
IV. SNP AFFECTING GROWTH AND PERFORMANCE OF YEARLING BULLS ON A FORAGE PERFORMANCE BULL TEST	28
Introduction	28
Experimental Animals	29
Blood Collection and DNA Extraction	29
SNP and Genotyping	30
Statistical Analysis	30
Results	34
Discussion	43
V. SUMMARY	45

LITERATURE CITED	47
APPENDIX A: DNA EXTRACTION – SATURATED SALT PROCEDURE	54
APPENDIX B: BUFFER SOLUTION LABORATORY PROTOCOL	55
VITA	56

LIST OF TABLES

3.1	Breeds evaluated, number of bulls tested per breed in the Dean Lee Bull Research Station Bull Test from 1958-2011	17
4.1	Single nucleotide polymorphisms ID, allele substitution, and forward and reverse primer sequences utilized for amplification and visualization of genotypes for CAST	31
4.2	Single nucleotide polymorphisms ID, allele substitution, and forward and reverse primer sequences utilized for amplification and visualization of genotypes for GH1	32
4.3	Single nucleotide polymorphisms ID, allele substitution, and forward and reverse primer sequences utilized for amplification and visualization of genotypes for IGF1	33
4.4	Level of significance and number of animals from each genotype associated with birth weight	34
4.5	Single nucleotide polymorphisms associated with birth weight and least square means estimate comparisons between reported genotypes	34
4.6	Level of significance and number of animals from each genotype associated with weaning weight	35
4.7	Single nucleotide polymorphisms associated with weaning weight and least square means estimate comparisons between reported genotypes	36
4.8	Level of significance and number of animals from each genotype associated with initial weight	36
4.9	Single nucleotide polymorphisms associated with initial weight and least square means estimate comparisons between reported genotypes	37
4.10	Level of significance and number of animals from each genotype associated with final weight	38
4.11	Single nucleotide polymorphisms associated with final weight and least square means estimate comparisons between reported genotypes	38
4.12	Level of significance and number of animals from each genotype associated with average daily gain	39
4.13	Single nucleotide polymorphisms associated with average daily gain and least square means estimate comparisons between reported genotypes	39

4.14	Level of significance and number of animals from each genotype associated with back fat	40
4.15	Single nucleotide polymorphisms associated with back fat and least square means estimate comparisons between reported genotypes	40
4.16	Level of significance and number of animals from each genotype associated with intramuscular fat %	41
4.17	Single nucleotide polymorphisms associated with intramuscular fat % and least square means estimate comparisons between reported genotypes	41
4.18	Level of significance and number of animals from each genotype associated with ribeye area	42
4.19	Single nucleotide polymorphisms associated with ribeye area and least square means estimate comparisons between reported genotypes	42
4.20	Level of significance and number of animals from each genotype associated with hip height and scrotal circumference	42
4.21	Single nucleotide polymorphisms associated with hip height and scrotal circumference and least square means estimate comparisons between reported genotypes	43

LIST OF FIGURES

3.1	Number of bulls tested in breeds with greater than 500 bulls evaluated in the Dean Lee Research Station Performance bull test from 1958 to 2011	18
3.2	Means of birth weight for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011	20
3.3	Means of initial weight for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011	21
3.4	Means of 112 day weight for all breeds (bottom panel) and the top representing breed (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011	22
3.5	Means of average daily gain (ADG) for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011	23
3.6	Means of adjusted yearling weight for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011	24
3.7	Means of scrotal circumference (SC) for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011	25

ABSTRACT

The first objective of these two studies was to evaluate genetic trends for bulls that have comprised the LSU AgCenter Dean Lee performance bull test for the past 55 years. Data included birth weight (BW), initial weight, 112-day weight, average daily gain (ADG), adjusted yearling weight, and scrotal circumference (SC), on 7,488 yearling bulls of 34 breeds on 112d of test for the last 55 years. The top 4 represented bull breeds with greater than 500 animals (Angus, Charolais, Hereford, and Simmental) were included in this analysis. Analyses revealed that growth traits for all bulls regardless of breed demonstrated a linear increase across the years with BW and SC being the lone exceptions. Birth weight demonstrated a decrease over the years. Hereford and Simmental breeds displayed the greatest decrease in birth weight. For start weight and 112-day weight, Simmental and Angus exhibited the greatest increase in weight over the years. Adjusted yearling weight had the greatest increase in the Simmental breed. Simmental breed exhibited the greatest decrease for SC over the years.

The second objective was to test the association of single nucleotide polymorphisms (SNPs) on three candidate genes calpastatin (CAST), somatotropin (GH1), and insulin-like growth factor 1 (IGF-1) with growth and performance traits in bulls participating in a forage based performance bull test. Of the 49 SNP genotyped, 20 were chosen for CAST, 9 for GH1, and 20 for IGF-1. These SNP were genotyped on 47 purebred Angus, Braford, and Brahman bulls against traits including average daily gain, birth weight, weaning weight, initial weight, final weight, hip height, backfat (BF), intramuscular fat %, ribeye area (REA), and scrotal circumference (SC). The mixed

model procedure of SAS was utilized to evaluate associations of the 49 SNPs and measured traits. Insulin-like growth factor 1 markers (rs133980322, rs137651874, rs132665612, rs132951819, rs110959643, rs109022910, rs110266103, rs109199979 and rs109327701) were determined to be associated with growth and performance traits, including weaning weight, initial weight, final weight, average daily gain, backfat, intramuscular fat %, hip height and scrotal circumference. GH1 marker rs10927590 was significantly associated with weaning weight, initial weight, and final weight.

CHAPTER I. INTRODUCTION

Selection for growth and production traits in beef cattle has been of great importance in the industry and significant improvements have been made towards more efficient and more productive cattle over the past few decades. Performance testing has been a way to enable producers to make knowledgeable selection decisions based on growth and efficiency data. This type of testing helps producers evaluate superior bulls and replacement heifers of multiple breeds in a uniform environment (Auchtung et al., 2001). Producers can incorporate these superior cattle into their breeding systems and significant improvement will be made. The research presented herein evaluates 54 years of performance bull test data from the Dean Lee Research Station to identify the change in bulls over the years. Growth traits were reported for birth weight (BW), start weight (SW), 112-day weight, average daily gain (ADG), adjusted yearling weight, and scrotal circumference (SC). *Bos indicus* influence has become prevalent in the cattle industry and researchers from the U.S. Meat Animal Research Center have presented studies that have reported *Bos indicus* and *Bos taurus* crosses to be more productive and efficient cows and perform extremely well in subtropical environments (Cundiff et al, US MARC).

Although traditional methods of selecting superior animals have been proven to be beneficial, genomic mapping has become a more effective method of selection in the livestock industry today. Specifically, single nucleotide polymorphisms (SNPs) are used to identify quantitative trait loci (QTL) in the genome. SNPs have been associated with a variety of phenotypes, including disease resistance (humans), milk production, fertility,

meat quality and composition, and vulnerability (Collins et al, 1997; Baeza et al, 2011; Mullen et al, 2011).

Previous reported SNPs located within three known candidate genes calpastatin (CAST) somatotropin (GH1), and insulin-like growth factor 1 (IGF-1) were utilized for possible associations with growth and performance traits in yearling bulls on a forage based performance test at LSU AgCenter's Central Research Station's Purebred Beef Unit.

CHAPTER II. REVIEW OF LITERATURE

Performance Testing

Centralized performance bull tests have allowed producers a method to evaluate growth and efficiency of young herd sires for many decades. Performance testing of beef cattle has proven a beneficial tool for producers that has allowed for the implementation of superior genetics into their beef cattle herds. This has been accomplished through the evaluation of superior bulls and replacement heifers of multiple breeds in a uniform environment (Auchtung et al., 2001). In order to collect uniform data, performance testing is conducted at a centralized location to evaluate cattle from different herds and breeds in one standardized environment. Centralized testing removes bias of feed and land resources, as well as management. The testing procedure measures a bull's ability to grow from weaning until approximately one year of age. Typically the traits evaluated in a performance test are average daily gain (ADG), feed to gain ratio, weight per day of age, and body weight in 28 day intervals (Simpson et al., 1986).

Historically, performance bull tests were conducted for a period of 140 days. However, current procedures dictate that the test be conducted for 112 days. Justification for reduced days of testing is that feeding bulls beyond 112 days had no advantageous effects because of the similarity of data at both 112 and 140 days. This has only been suggested for growth traits that are not dependent on maturity or growth patterns (Brown et al., 1991). In order to accurately evaluate growth curves, bulls are weighed every 28 days after a designated acclimation period until termination of testing

at 112 days. An acclimation period is a necessity in order to reduce the stress of animal when it is brought to a new facility and new farm. This acclimation period should be at least a 21-days as it allows animals to adjust to the test facilities and feeding practices. During this time, animals are given a transitional diet to aid in the adaption of the new test diet (BIF, 2010). Another reasoning behind the acclimation period is to allow those bulls that have been reared under inadequate nutritional levels time to adjust to the higher nutritional practices of the new facility and experience compensatory gain without that gain being included into its performance data (Sainz et al, 1995). Data can vary depending on the station performing the test due to diet, genetics, environment, feeding procedures, contemporary groups, and breed makeup. Performing tests under standard conditions is a method to identify genetically superior bulls for producers to incorporate into their mating systems (Liu et al., 1993). Knowledge of different production traits is important for selection and evaluation of a bull on a performance bull test. This is important due to multiple factors such as, no one breed is superior, no one breed fits into every production scheme and no one breed is superior in all performance traits (Wheeler et al., 1997). However, it must be noted that there are negative aspects to utilize a bull from a performance test. The first is the majority of bulls are not being maintained in a feedlot system during the breeding season. Producers are then utilizing bulls that do not perform as well as the data from the test had reported. This is due to change in diet and a change in rumen function. Another negative effect of using bulls from a performance bull test is the bulls decreasing in weight and body condition score (BCS) during breeding season and subsequent investments to increase BCS prior to the next breeding season.

Growth Hormone

Growth hormone (GH) is a protein hormone that is synthesized by the somatotroph cells of the anterior pituitary gland (Bauman, 1992). Growth Hormone's physiological function has been reported to be associated with initiating longitudinal bone growth, increase muscle growth, and improvement in ruminant lactation (Florini et al., 1996; Etherton and Bauman, 1998; Ohlsson et al., 1998). The primary target of GH is the liver where insulin-like growth factor 1 (IGF-1) is released to control nutrient utilization and partitioning (Bauman, 1992). Growth hormone also regulates postnatal growth and metabolism, which is important in controlling lactation, development of mammary glands, increased protein anabolism, reduced fat deposition, enhanced growth rate, and fertility in cattle (Jiang and Lucy, 2001; Renaville et al., 2002; Lucy, 2008).

Growth hormone releasing hormone (GHRH) stimulates synthesis and secretion of growth hormone in an episodic or periodic manner and is secreted by the hypothalamus (Trenkle and Topel, 1978; Kojima et al., 1999). During an animal's physiological development, increased growth has been observed which contributes to an animal's increase in size and weight from cellular hypertrophy, hyperplasia, and accretion. Growth hormone has been identified as the main hormone associated with both skeletal and body growth (Trenkle and Topel, 1978).

There are many factors that can influence the release and level of GH secretion. Age can play a role in the release of GH and as reported by Thomas and associates (2000) age increases the secretion of GH from the pituitary would decrease. Other

factors affecting GH release can be malnutrition with inadequate energy and amino acid levels and injury/illness (Thissen et al., 1999).

Genetic Markers

According to the National Human Genome Research Institute (NHGRI), a genetic marker is a DNA sequence that has an identifiable physical location on a chromosome, and can be inherited together, have no known function, or be a part of a gene. The NHGRI also state that because most genes have only an approximate location, these markers can be used to identify the inheritance pattern of a gene that is close by. The most commonly utilized genetic markers include restriction fragment length polymorphisms (RFLP's), single nucleotide polymorphisms, and microsatellites.

According to the National Center for Biotechnology Information (NCBI), a restriction fragment length polymorphism is a variation in homologous DNA sequences that is identified by fragments of different lengths after the digestion of the DNA. Restriction endonuclease cut the DNA sequences producing fragments of various defined lengths. The differences in fragment length are determined by genotypic variants. Differences in individual bases can result in the loss or addition of a cleavage site. Furthermore, an insertion or deletion of segments of DNA could modify size (Botstein et al. 1980). Single nucleotide polymorphisms occur when a gene has a single base-pair change (Crawford and Nickerson, 2005). These variations or changes have the potential to alter the amino acid to be produced. In order for a base change to be considered an SNP, the least frequent allele must have at least a frequency of 1% (Vignal et al., 2002). Microsatellites are considered to be short tandem repeats with repeats usually of 1-5 base pairs. The number of tandem repeats can determine the

variation in allele. Microsatellites are most commonly used in a situation that would require highly polymorphic and locus-specific genetic systems, example: paternity testing, linkage analysis, and population and evolutionary genetics (Ellegren et al., 1997).

SNP

A single nucleotide polymorphism (SNP) is a genetic marker defined by a change in a single nitrogenous base- cytosine, adenine, guanine, and thymine (Crawford and Nickerson, 2005). SNPs have been associated with a variety of phenotypes, including disease resistance (humans), milk production, fertility, meat quality and composition, and vulnerability (Collins et al, 1997; Mullen et al, 2011; Baeza, et al, 2011). The objective of SNP association studies is to evaluate SNPs as a probable source of variation. This variation may have an effect on whether an individual is pre-disposed to be superior or inferior for an economically important trait.

Reyna and associates (2010) reported an association of SNP IGF1/*SnaBI* in the Charolais breed. The AB and BB genotypes affected weaning weight, weaning weight adjusted to 210 days and preweaning weight gain significantly by exhibiting an increase when BB genotype was present. Their results were the same as previous studies where allele B showed a dominant effect over allele A. For carcass traits, researchers have looked towards SNPs to aide in the selection process for carcass qualities such as ribeye area, backfat thickness, and intramuscular fat %. The CAST gene is located on chromosome 7 and has been reported to express both additive and dominant affect on meat tenderness (Bishop et al, 1993; Pinto et al., 2010).

Bos taurus* vs *Bos indicus

Bos taurus and *Bos indicus* differ in many aspects and can be incorporated into a variety of beef production schemes. *Bos taurus* cattle are typically adapted for the cooler, wet climates while *Bos indicus* are generally more adapted to the hotter, dry climates and have been documented to have greater parasite resistance (Thrift and Thrift, 2003). The US Meat Animal Research Center (MARC) reported that *Bos indicus* are later maturing and have longer gestation lengths than *Bos taurus* breeds. *Bos indicus* crosses also had higher birth weight, but a detrimental effect of that is their survival of calves from birth to weaning was significantly lower. They also reported that offspring of Brahman influence were heaviest at birth, which contributed to them having the greatest calving difficulties. Brahman were also the heaviest at 200 days and grew the fastest (Casas et al., 2011). Previous studies have reported that meat from *Bos indicus* cattle has decreased tenderness than that from *Bos taurus* cattle (Crouse et al., 1987, 1989).

Previous researchers reported that *Bos indicus* X *Bos taurus* are remarkably productive and efficient cows and perform extremely well in subtropical environments (Cundiff et al, US MARC). Although these crosses have been proven to be valuable, the higher percentage of *Bos indicus* influence has been reported to have a detrimental effect in terms of producing heifer calves that are older at puberty (Casas et al, 2011). When crossing *Bos indicus* bulls to *Bos taurus* females, the offspring tend to be heavier at birth and have more calving difficulties (Reynolds et al., 1980 and Roberson et al., 1986). In order to study carcass and meat palatability between breeds, a study evaluating differences between Angus, Brahman, and Angus-Brahman cross was

performed by Elzo and associates. They reported that Brahman had higher dressing percent, lower marbling, smaller ribeye area, and less fat over ribeye than Angus. Their beef had more connective tissue and was less tender and less juicy. The Angus-Brahman cross showed heterosis by exhibiting an increase in hot carcass weight, dressing percent, ribeye area, fat over the ribeye and kidney, pelvic, and heart fat. This study reports that a *Bos taurus/Bos indicus* cross demonstrates heterosis on meat yield while showing negative effects on meat quality (Elzo et al., 2011).

QTL Associated with Growth

A quantitative trait is a phenotypic trait in which variation can be measured on a numerical scale. A quantitative trait loci (QTL) is the genetic location that may harbor the genes and mutations that may account for observed variation in an economically important trait. Mapping QTLs depends on the number of genes that affect it, its genetic nature (dominant, recessive, or additive), and the heritability of the trait being evaluated (Members of the Complex Trait Consortium, 2003). In order to identify QTLs for growth traits in cattle, researchers have concentrated research on commercial half-sib families. (Mizoshita et al., 2004; Mizoguchi et al., 2005) Previous research reported the most significant QTL was determined to be between markers DIK1054 and DIK082 on chromosome 6. This finding accounted for around 20% of the phenotypic variation for total bone proportion (Gutiérrez-Gil et al, 2009). Snelling and associates (2010) reported that the greatest concentration of SNP strongly associated with direct growth was between 25 and 53 Mbp on BTA 6. This region overlaps the QTL described by Gutierrez-Gil et al. (2009) for birth weight. They also found 6 or more SNP were on BTA 7, 11, 14, and 20 and BTA 10 and 23 had one SNP associated with direct growth.

Candidate Genes

According to the NHGRI, a candidate gene is a gene whose loci has an association with a particular trait. The candidate gene approach has been proven to be one of the more effective ways to find trait loci. The candidate gene approach is useful in locating loci with small effects however, can be more time-consuming due to the many candidate genes associated with a specific trait of interest (Andersson, 2001).

Leptin is a candidate gene that has been reported to be associated with regulation of feed intake, energy metabolism, growth and reproduction in cattle (Ramsay and Cranwell, 1999) as well as IGF-1 and CAST genes. Results from a study performed by DeAtley and associates (2011) reported that *STAT6* can be used as a candidate gene underlying cattle growth QTL on chromosome 5. The study reported that ETH10 (dinucleotide microsatellite within the promoter of *STAT6*) locus was associated with growth and carcass traits in the Angus and Brangus cattle represented in their study.

GH (Growth Hormone) Gene

Hediger and associates (1990) mapped the growth hormone (GH) gene to *Bos taurus* autosome (BTA) 19 in the region of bands q26-qter. There have been reports on the GH gene being associated with milk production, fertility, growth regulation, and carcass quality (Thomas et al, 2007; Mullen et al, 2010). Previous studies have reported that there is an association between increased pituitary secretion of GH and selection for increased growth and body leanness (Bunger and Hill, 1999. te Pas et al., 2001,2004).

Zhang and coworkers (1993) searched for polymorphisms in the bovine GH gene. A segment of the GH gene consisting of 891 bp (base pairs) was amplified then digested with the restriction enzyme Msp-I. From the digestion of the PCR product with Msp-I, 2 alleles (C and D) were identified. Lagzeil and associates (2000) used the previous described Msp-I RFLP to evaluate gene distribution and frequency across the hemispheres. It was reported that the Msp-I (-) originated in *Bos indicus* and the Msp-I (+) from *Bos Taurus*. Indicating that the further from the Indian subcontinent the less frequent of Msp-I (-) allele.

Schlee and associates (1994) observed that the GH1 gene is associated with plasma levels of GH. This association indicated that mutations in GH gene have the potential to produce variable levels of GH. With this association, GH1 can be considered a favorable candidate gene marker in cattle for the improvement of growth, fertility, and meat and milk production (Mullen et al., 2010).

IGF-1 Gene

Previous studies (Grosse et al., 1999) have mapped the Insulin-like growth factor 1 (IGF-1) gene to BTA 5 of the bovine genome. Insulin-like growth factor 1 is stimulated by growth hormone to be released from the liver (Bauman, 1992). The IGF-1 gene has been reported to be associated with growth production and meat quality in animals (Machado et al., 2003; Andrade et al., 2008). A study performed by Ge and associates (2001) evaluated a biallelic marker in the first promoter region of IGF-1 gene in Angus cattle. The mutation was a T-to-C substitution. The marker genotypes were determined for the Angus population that was selected based on high or low serum IGF-I concentrations (allele A: 63.9%, B: 36.1%). They reported that analysis of both IGF-I

concentrations (high/low) discovered that BB genotype was associated with higher weight gain during the first 20 days after weaning and had a dominant effect on post weaning gain. The low IGF-I was significantly associated with BB genotype for higher weight gain during first 20 days after weaning and with on-test weight. On the other hand, IGF-I concentrations had no significant associations.

CAST Gene

The calpastatin (CAST) gene is located on BTA 7 (Bishop et al., 1993). Calpastatin and calpain act together within a system to regulate physiological change in muscle structure in a postmortem tenderization process (Koochmaraie, 1994). Increase CAST was determined to be correlated with a decrease in meat tenderness (Pringle et al., 1997). It is considered a candidate gene for tenderness (Schenkel et al., 2006) and used by private companies including IGENITY and GeneSTAR.

Ultrasound Technology for Carcass Traits

Ultrasound technology although traditionally utilized as an instrument for reproductive management in cattle has also been utilized to evaluate live carcass traits. The use of ultrasound technology to evaluate carcass traits in live cattle has been used for over 40 years to determine carcass composition in live animals (Stouffer et al., 1959). Prior to the utilization of live animal ultrasound, visual appraisal and raw phenotypic data was collected for a limited number of traits such as hip height, scrotal circumference, and weights (birth weight, weaning weight, and yearling weight). As for carcass traits, animals could only be measured at harvest. Collection of carcass data at harvest is a long and expensive process compared to the information that can be produced via live animal ultrasound evaluation. Thus, the use of ultrasound technology

has been implemented into the prediction of carcass composition traits. The utilization of ultrasound technology is a method that has been implemented to improve genetic progress for certain carcass traits such as fat deposition and eye muscle depth. (Gutiérrez-Gil, 2009). According to Koots and associates (1994a) carcass traits are considered to be moderate to highly heritable traits, through the use of ultrasound technology a producer can improve the accuracy of selection for specific carcass quality or composition traits.

Marker Assisted Selection

Marker Assisted Selection (MAS) is the use of molecular markers as a means to improve the accuracy of selection in livestock species through the identification of superior breeding animals early in the production process. This is a method for producers to decrease costs associated with performance testing by only testing superior animals. Marker assisted selection has the potential to rapidly improve lowly heritable traits. The rate of genetic improvement achieved by MAS may be greater than by selection based upon Expected Progeny Differences (EPDs) (Davis & DeNise 1998). Genetic markers can be used as a tool to test animals in the early stages of production rather than waiting for animals to reach a specific production stage. The identification of genetic markers that are closely linked to QTL could positively influence animal selection programs (Soller and Beckmann, 1983). Different types of genetic markers used for MAS include restriction fragment length polymorphisms (RFLPs), microsatellites, amplified fragment length polymorphisms (AFLPs), and single nucleotide polymorphisms (SNPs).

The success of MAS depends highly on the amount of variation for the trait that is being controlled by that marker. Producers should be careful when using genetic markers solely as a means of selection. Although some markers are associated with positive traits, they might be linked with detrimental traits.

Whole Genome Selection

Whole genome selection has been described as a variation of MAS that uses genetic markers covering the whole genome so that all QTL are in linkage disequilibrium (LD) with at least one marker (Goddard and Hayes, 2007). Being that the markers are in LD with the QTL, this keeps the number of effects per QTL at a small quantity (Meuwissen et al., 2001). WGS has been implemented into the cattle industry for management and breeding decisions in order to supplement the large amount of data sets with genomic data that predicts genetic merit values (Matukumalli et al, 2009).

CHAPTER III.

EVALUATION OF 54 YEARS OF LOUISIANA BULL TESTING

Introduction

The LSU AgCenter Dean Lee Research Station located in Alexandria, Louisiana has been conducting performance bull tests for over 50 years for interested breeders in the state of Louisiana. Performance tests are an excellent way for a producer to evaluate their young herd sires for growth and efficiency. Performing tests under standard conditions is a method to identify genetically superior bulls for producers to incorporate into their mating systems (Liu et al., 1993). Dean Lee states that their primary objective is to evaluate and compare the capability of weanling bull calves after being tested under uniform or common environmental conditions for the capacity to gain rapidly and efficiently by the time they are a year old. The performance bull test was conducted for 140 days from 1958 to 1990; however, starting in 1991, the test has been shortened to 112 days. For each year, there are 2 tests conducted in the summer and in the winter.

The research herein utilizes 54 years of performance bull test data to evaluate the variation for growth traits throughout the years that Dean Lee has offered their performance bull test. The growth traits were individually graphed to visualize the improvement and quality of bulls on test from beginning years to present. The data will assist producers in Louisiana by giving insight on the changes bulls have experienced and the direction in which they are improving. Not only will the producers gain insight on overall performance changes in bulls; they will become knowledgeable of what breeds have excelled over the years for Dean Lee's performance bull test. The

objective of this study was to evaluate 54 years of performance data to observe genetic trends from a performance bull test conducted in Central Louisiana.

Experimental Animals

Performance data was evaluated from 54 years of bull test data provided by the LSU AgCenter Dean Lee Research Station. By the winter of 2011 and 2012 performance bull test, 7,488 bulls from 34 different breeds had been tested. After the initial weight was determined, each bull was measured every 28 days until the completion of the test at 112 days. At the completion of the test, growth traits were measured including average daily gain (ADG) and weight per day of age as well as final weight, total gain, adjusted 365 weight (not until 1974), and scrotal circumference (SC; not until 1987) were recorded. All performance tests since Test 81 included carcass traits such as ribeye area (REA), backfat (BF) thickness, and intramuscular (IM) fat %.

Statistical Analysis

Utilizing the Mixed Model procedures of SAS (version 9.2, SAS Institute, Cary, NC) changes in performance data for bulls participating in the Dean Lee Research Station Performance Bull Test from 1958 to winter 2011/2012 were evaluated. Birth weight (BW), initial weight, 112day weight, average daily gain (ADG), adjusted yearling weight, and scrotal circumference (SC) were fit as random variables in the model and year and breed fit as fixed variables. Initial analysis evaluated the number of bulls within each breed participating in performance bull tests over a 54-year period. Following evaluation, breeds with greater than 500 bulls tested were included in further analysis, which were Angus, Charolais, Hereford and Simmental. Interval regression analyses as described by Steele et al. (1997) were conducted to determine if

improvement between breeds was significantly different. Traits evaluated included birth weight, initial weight, 112day weight, ADG, adjusted yearling weight, and SC.

Results

All breeds and number of bulls within each breed are portrayed in Table 3.1.

Table 3.1: Breeds evaluated, number of bulls tested per breed in the Dean Lee Bull Research Station Bull Test from 1958-2011.

Breed of Bulls	No. of Bulls
Angus	2638
Angus +	2
Beefmaster	235
Black Maximizer	14
Black Simmental	5
Blonde d'Aquitaine	2
Braford	66
Brahman	143
Brangus	297
Braunvieh	7
Brown-Swiss	5
Char-Angus	4
Charbray	6
Charolais	1274
Char-Swiss	5
Chi-Angus	1
Chianina	3
Chimaine	1
Devon	11
Gelbray	55
Gelbvieh	325
Hereford	1211
Limousin	33
Maine-Anjou	10
Red Angus	49
Red Brahman	24
Red Brangus	36
Red Poll	42
Santa Gertrudis	262
Senepol	4
Shorthorn	20
Simbrah	79
Simmental	596
Texas Longhorn	23
Total	7488

There were a total of 7,488 bulls that have participated in the Dean Lee Research Station Performance Bull Test from 1958 to winter 2011/2012. The breeds that were most represented in the tests containing greater than 500 were Angus, Charolais, Hereford, and Simmental breeds (Figure 3.1). Independent variables of breed and

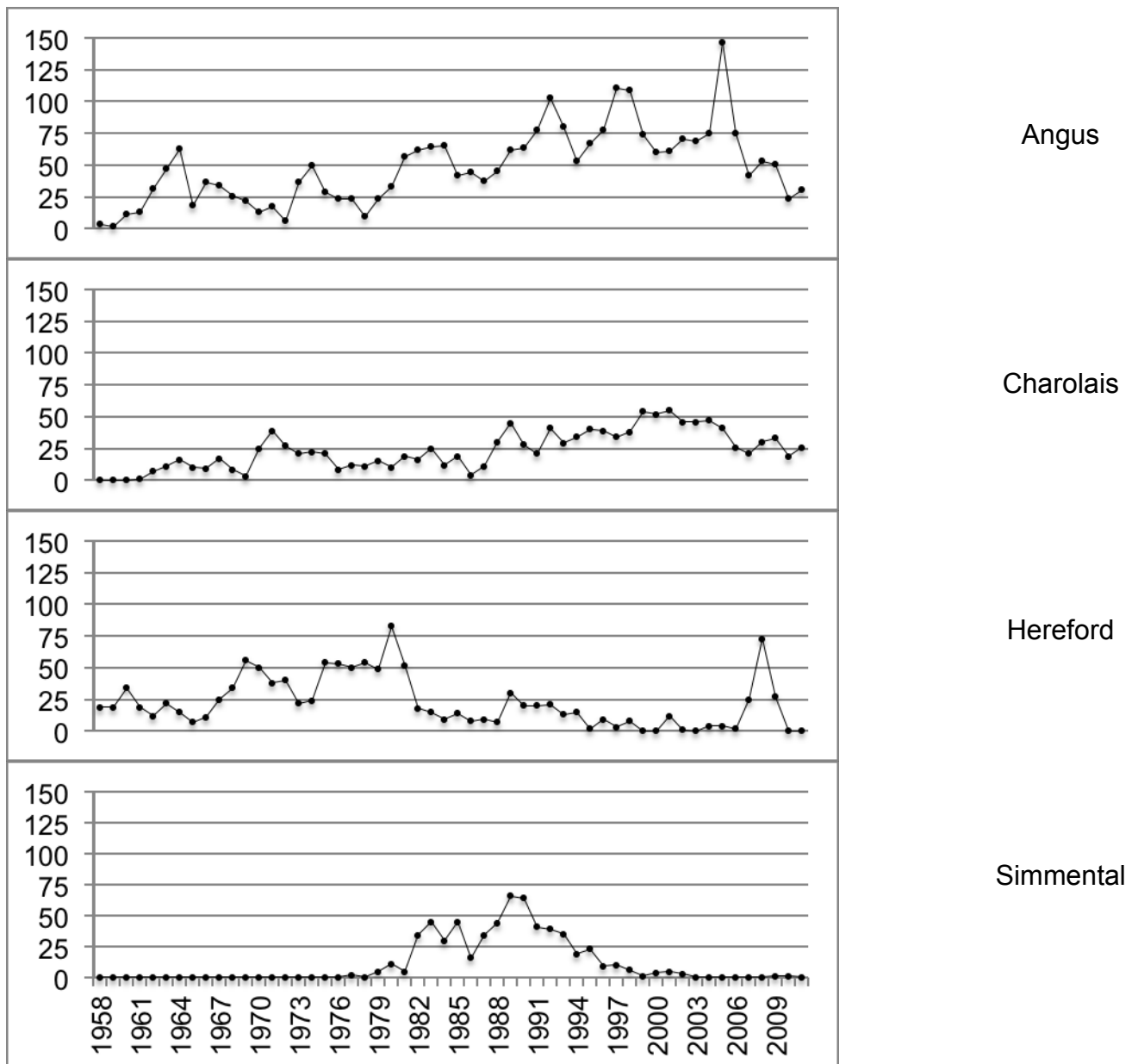


Figure 3.1: Number of bulls tested in breeds with greater than 500 bulls evaluated in the Dean Lee Research Station Performance bull test from 1958 to 2011.

interaction of breed and year were significant ($P < .05$) sources of variation in prediction of growth traits. Analysis was performed on breeds with greater than 500 bulls.

In 1958, initial weights averaged 249.90 kg and 112-day weights averaged 362.95 kg. Initial weights and 112-day weights in 2011 averaged 335.49 kg and 511.56 kg, respectively. Analyses revealed that all growth traits for all bulls regardless of breed demonstrated a linear increase across the years with BW and SC being the lone exceptions (Figures 3.2 – 3.7). Birth weight demonstrated a decrease over the years with Angus and Charolais breeds being the same ($P > .05$). Hereford and Simmental breeds were significantly different ($P < .05$) than Angus and Charolais and exhibited a greater decrease in birth weight. For initial weight, no two breeds were the same ($P < .05$) with Simmental and Angus exhibiting the greatest increase in weight over the years. Angus and Simmental also displayed the greatest increase in final 112-day weight and ADG over Charolais and Hereford of which they were significantly different ($P < .05$). Adjusted yearling weight had the greatest increase in the Simmental breed with no two breeds being the same ($P < .05$). Overall, there was a decrease in scrotal circumference over the years with the Simmental breed having the greatest decrease. Angus and Charolais were statistically different ($P < .05$) from the Hereford breed with the Hereford breed being significantly different ($P < .05$) than the Simmental.

Discussion

Over the years of Dean Lee performance bull testing, breed representation of has changed due to the fact that preference to specific breeds is different today as compared to 50 years ago. Angus, Charolais, and Simmental exhibited an increase in representation while the popular Hereford breed becoming uncommon. Breed analysis

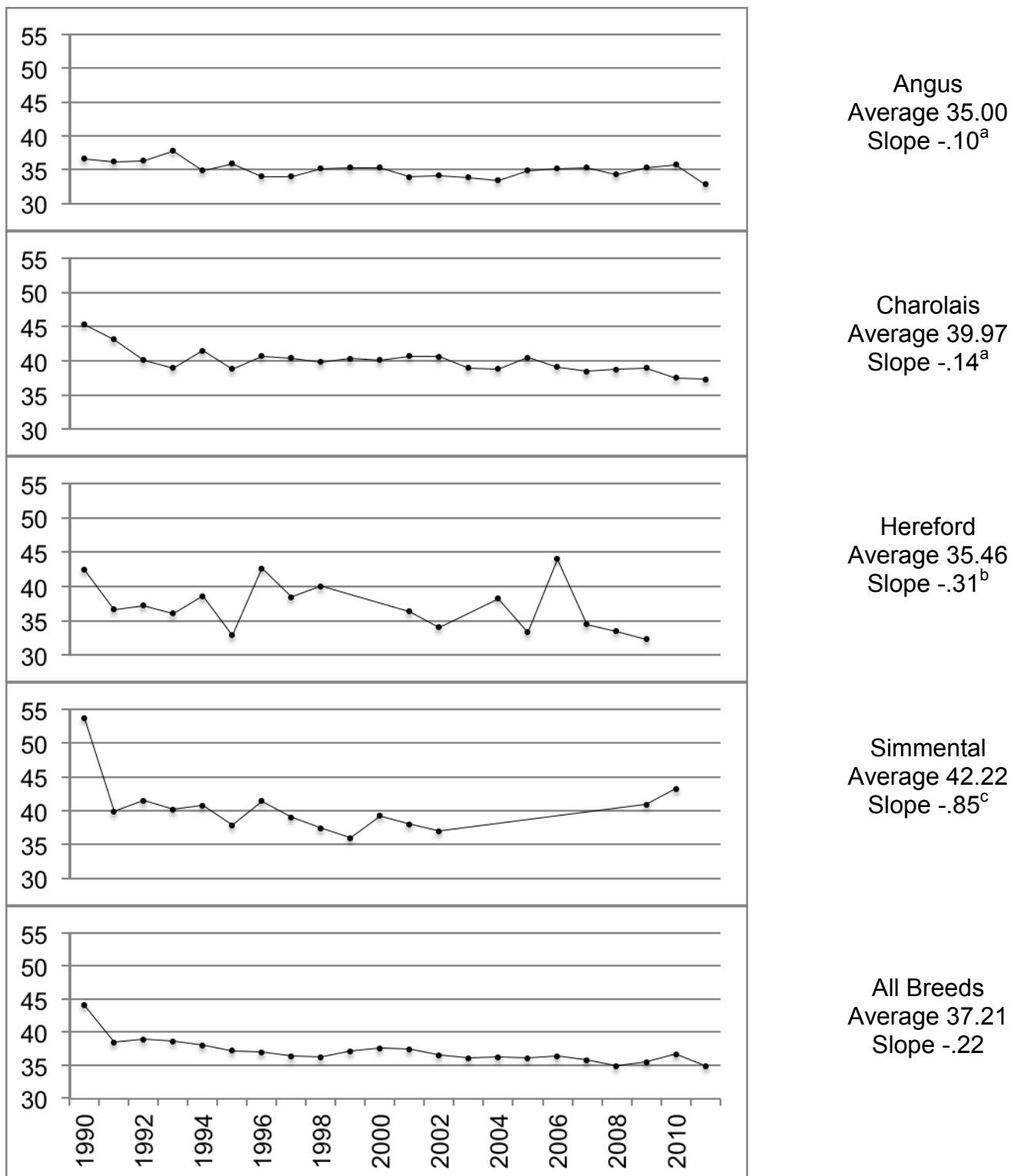


Figure 3.2: Means of birth weight, kg, for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011.

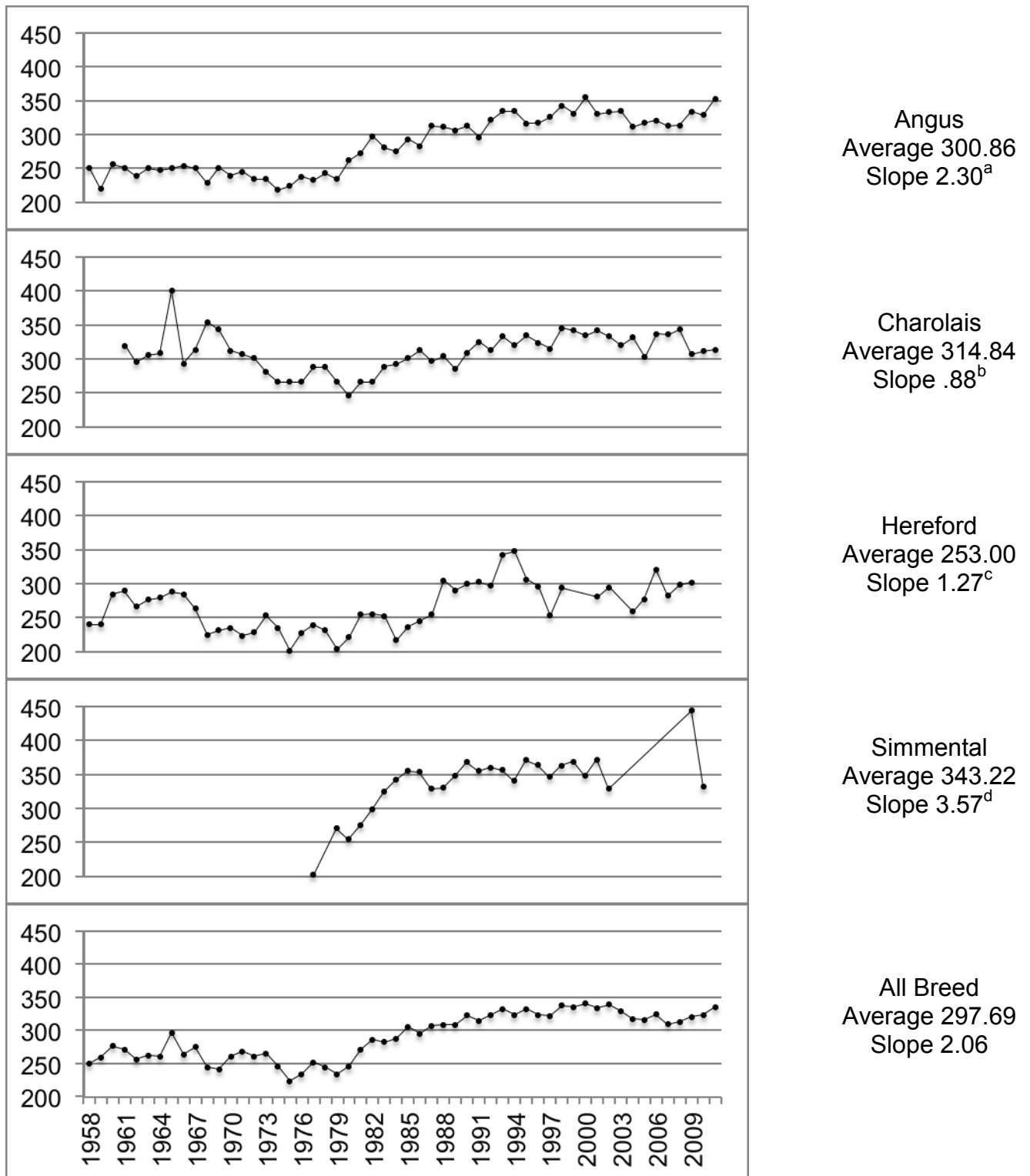


Figure 3.3: Means of initial weight, kg, for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011.

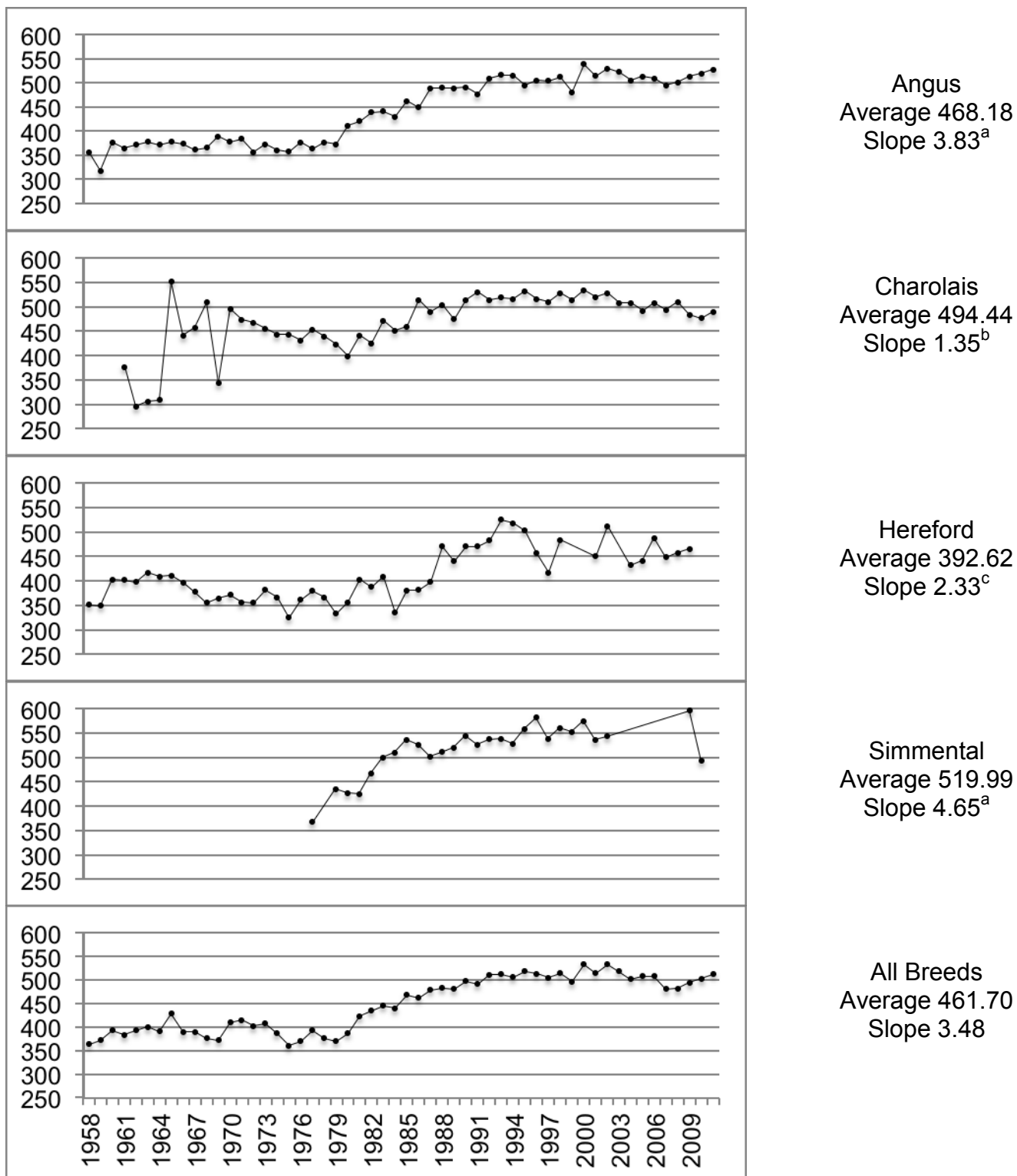


Figure 3.4: Means of 112 day weight, kg, for all breeds (bottom panel) and the top representing breed (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011.

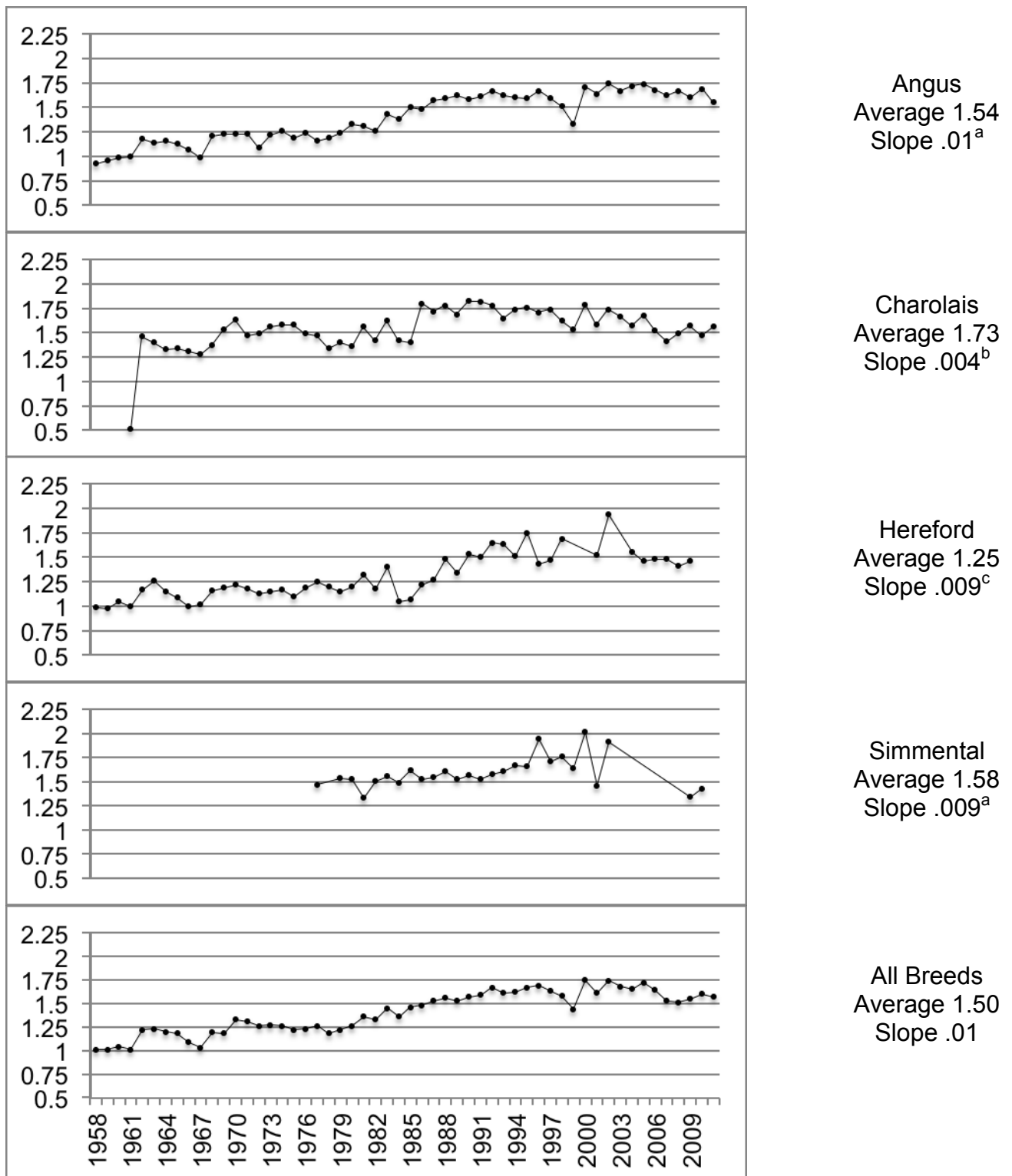


Figure 3.5: Means of average daily gain (ADG), kg, for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011.

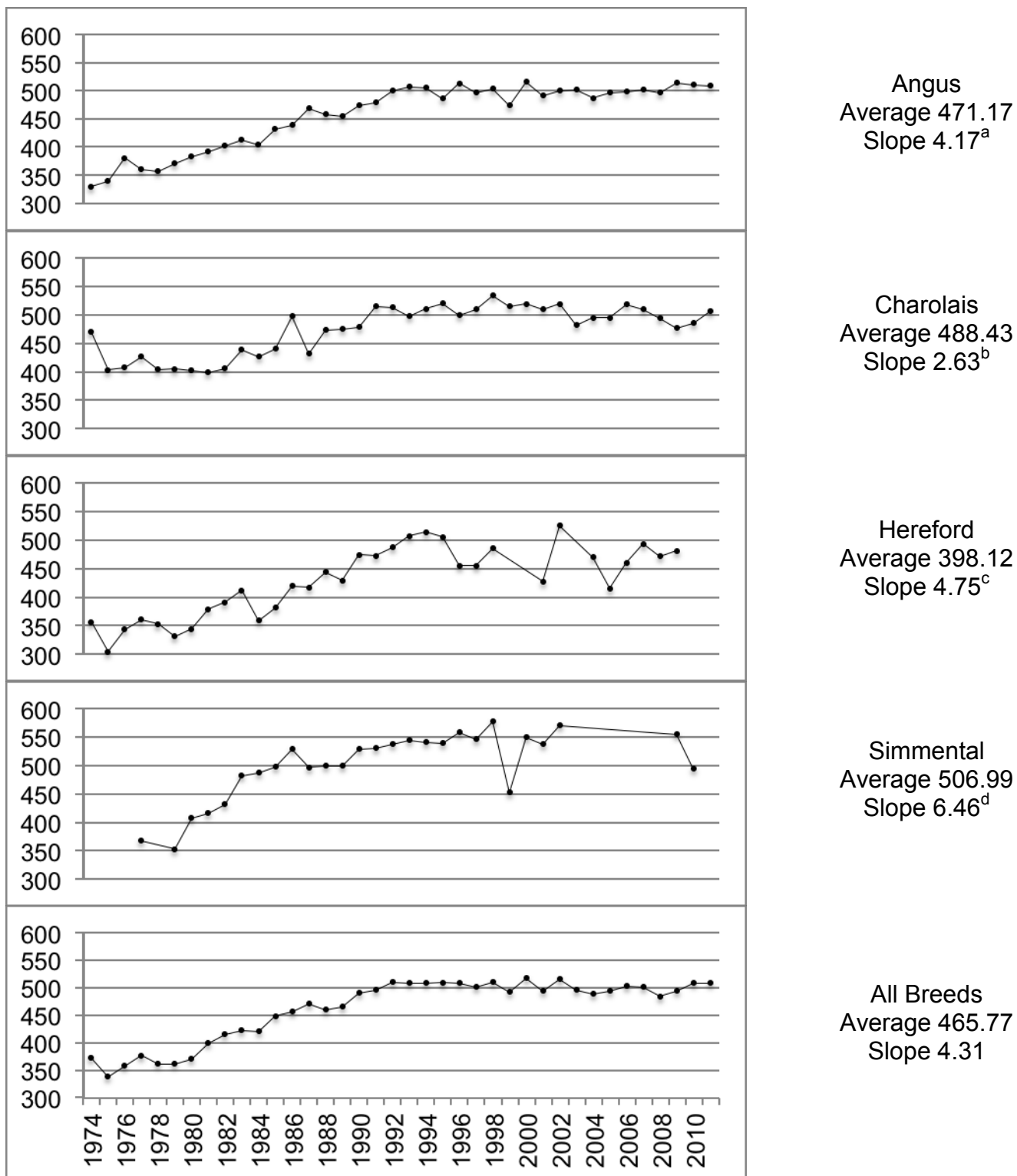


Figure 3.6: Means of adjusted yearling weight, kg, for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011.

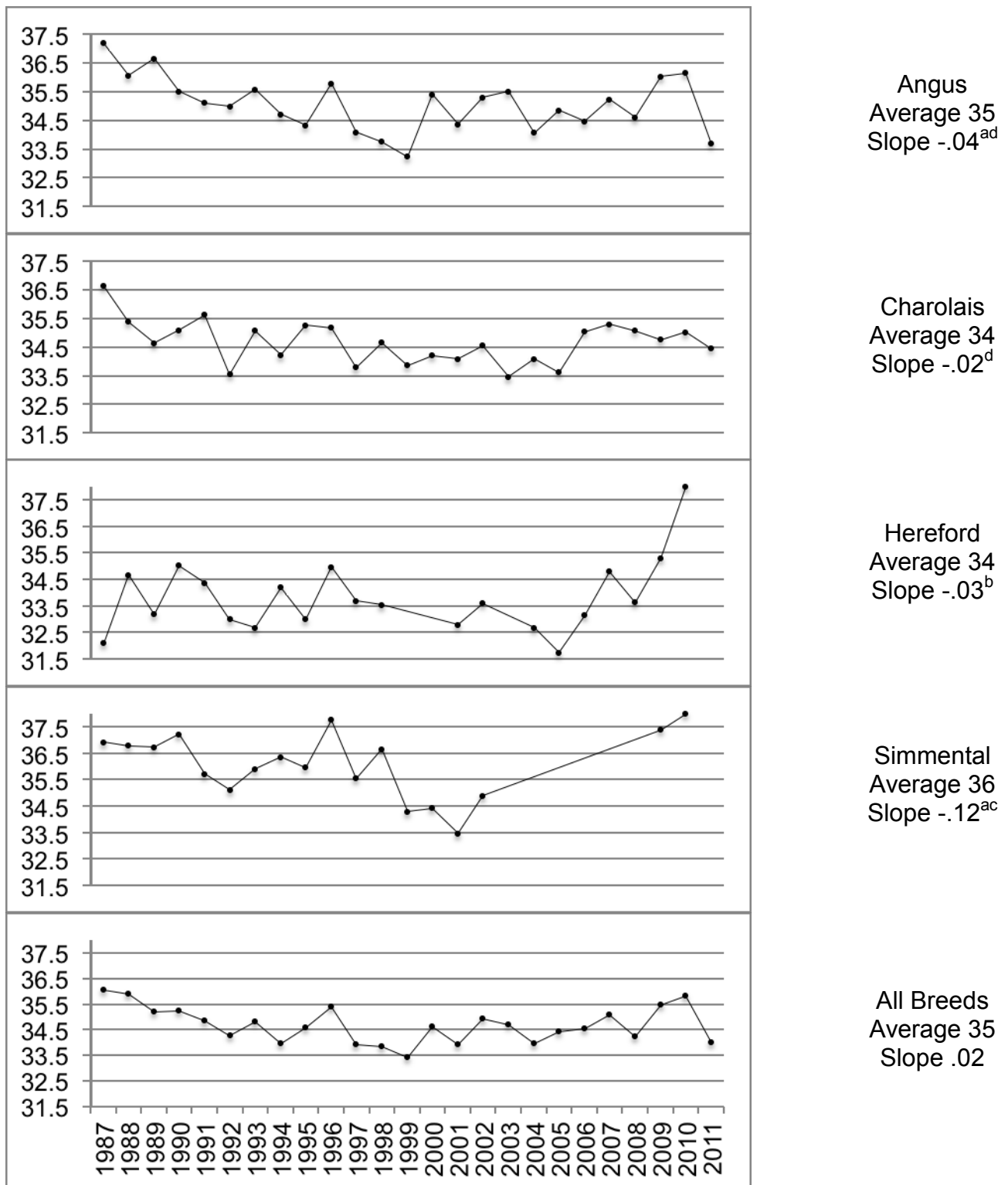


Figure 3.7: Means of scrotal circumference (SC), cm, for all breeds (bottom panel) and the top representing breeds (top 4 panels) participating in the Dean Lee Research Station Bull Test from 1958-2011.

is an important tool to implement hybrid vigor into a production scheme through crossbreeding. Crossbreeding is a way to match the genetic potential of breeds through climates, feed resources, and diverse markets (Cundiff et al, 1993). Breed representation is not only due to the fact of breed preference but the producer's willingness to include their bull in the test.

Growth traits for all bulls regardless of breed demonstrated a linear increase across the years with BW and SC being the lone exceptions. The results were similar to the findings of Garcia and associates (2004) as far as growth performance rates of Angus, Charolais, and Hereford breeds. However, the study did not include the Simmental breed, which was included in this study. Over the years of testing, Simmental was the largest and exhibited the greatest rate of change as compared to the other three breeds. Also, the Hereford breed tended to be the lowest performing breed for each trait evaluated which is most likely due to the high representation at the beginning and the low representation after a few decades. These findings are similar to the findings of Schenkel and associates (2003) with the Simmental breed exhibiting faster growth and larger size while Hereford displayed the least gain.

Birth weight and scrotal circumference were the only two traits that displayed a decrease over the years with Simmental exhibiting the greatest rate of change. The findings of a decrease in scrotal circumference over the years is contradictory to the findings of Simpson and associates (1986) who reported as growth traits increased scrotal circumference increased as well. Angus and Simmental showed the greatest rate of change over the years for initial weight and final weight as well as ADG. For

adjusted yearling weight, Simmental by far had the greatest rate of change for this growth trait.

As mentioned previously, performance testing of beef cattle has proven a beneficial tool for producers that has allowed for the implementation of superior genetics into their beef cattle herds. This has been accomplished through the evaluation of superior bulls and replacement heifers of multiple breeds in a uniform environment (Auchtung et al., 2001). By evaluating performance bull test data, producers are able to select an elite bull(s) to incorporate into the production scheme. Elite bull(s) will in return increase profit and sustainability in their herds.

CHAPTER IV.

SNP AFFECTING GROWTH AND PERFORMANCE OF YEARLING BULLS ON A FORAGE PERFORMANCE BULL TEST

Introduction

Multiple tools have been developed in order to increase the accuracy of selection in the beef industry. Tools such as Expected Progeny Differences (EPDs) and performance testing have aided in the improvement of beef traits over the past few decades. However, Collins and associates (1997) have reported that SNPs are responsible for a variety of phenotypes. The rate of genetic improvement achieved by marker assisted selection may be greater than by selection based upon EPDs (Davis & DeNise, 1998). SNPs have been associated with a variety of phenotypes, including disease resistance (humans), milk production, fertility, meat quality and composition, and vulnerability (Collins et al, 1997; Mullen et al, 2011; Baeza, et al, 2011). Associations can be tested between an SNP and a specific trait of interest in order to potentially identify significant sources of variation for economically important traits in the genome.

Three known candidate genes calpastatin (CAST), growth hormone (GH1), and insulin-like growth factor 1 (IGF-1) were chosen for SNP analysis. GH1 was included in the association study because of previous reports of the gene being associated with milk production, fertility, growth regulation and carcass quality (Thomas et al, 2007; Mullen et al, 2010). Similar to GH1, IGF-1 has been reported to exhibit an association with growth production as well as meat quality in animals (Yap et al, 1996; Machado et al, 2003; Andrade et al., 2008). Pringle and associates (1997) reported that CAST demonstrates an association with meat tenderness. The objective of this study was to

evaluate the associations between growth and production traits and the chosen SNPs for each candidate gene.

Experimental Animals

A total of 47 bulls from the Angus (18), Braford (27), and Brahman (2) breeds were evaluated for 112 days on a forage based performance bull test. The test was conducted at the LSU AgCenter Central Station's Purebred Beef Unit and bulls were managed on native forage and ryegrass by Mr. Mike Canal, Research Associate for the Beef Units at Central Stations. Post weaning, bulls were turned out in pasture for 2-3 months before the start of the forage based performance bull test. After initial weights were determined, weights were taken on each bull every 28 days until the 112th day was reached. At the completion of the performance test, final weight and average daily gain (ADG) were measured. Also, carcass data, including REA and backfat, were determined using the ultrasound method along with hip height and scrotal circumference. Performance bull test data from the 3 tests were evaluated for associations between SNP and growth and performance of yearling bulls.

Blood Collection and DNA Extraction

Blood was collected from all bulls on the performance bull test at the LSU AgCenter Central Research Station's Purebred Beef Unit. The blood was collected via jugular venipuncture. After collection, blood was transferred into 15 ml tubes and centrifuged at 4000 rpm at 4°C for 20 minutes. Following centrifugation, white blood cell buffy coats were removed and transferred to 250 µL micro centrifuge tubes. DNA was then extracted from buffy coats using a saturated salt procedure previously described by Miller et al., 1988 (Appendix A). Two hundred microliter DNA working solutions were

prepared with a combination of DNA and rehydration buffer. Unused buffy coat, extracted DNA, and working solutions were all stored at -4°C.

SNP and Genotyping

Previously reported SNPS on candidate genes CAST, GH1, and IGF-1 were collected from the dbSNP website (<http://www.ncbi.nlm.nih.gov/projects/SNP/>). Single nucleotide polymorphisms were selected that were evenly distributed across the entire candidate genes genomic sequence. Single nucleotide polymorphisms, allele substitutions, and forward and reverse primer sequences are reported in Table 4.1-4.3. Single nucleotide polymorphism genotyping was performed utilizing sequenome technology (Sequenome, San Diego, CA) by GeneSeek, Inc. (Lincoln, Nebraska).

Statistical Analysis

The mixed model procedure of SAS (version 9.2, SAS Institute, Cary, NC) was utilized for statistical analysis of SNP associations. Random variables of average daily gain, birth weight, weaning weight, initial weight, final weight, hip height, backfat, ribeye area, and scrotal circumference were fit into the model and variables of sire and individual genotype were fit in the model as fixed variables to evaluate potential SNP associations. Single nucleotide polymorphisms that exhibited more than one genotype were incorporated into the analysis. A SNP with only one genotype was excluded from the analysis because of the lack of marker effects. Statistical significance was assessed at $P < .05$ and a statistical trend at $P < .10$. Due to the small sample size, P-values of $< .2$ were considered relevant for use in a larger population study in order to evaluate their statistical significance. This idea is due to the fact that there could be Type 2

Table 4.1: Single nucleotide polymorphisms ID, allele substitution, and forward and reverse primer sequences utilized for amplification and visualization of genotypes for CAST

SNP ID	Allele Substitution	Forward Sequence	Reverse Sequence
rs137780582	G/T	ATAAGAAAATAAAAAAAAAAAAAAGAAC	CTTAACCCACGATCAGAAAATAAC
rs137777861	G/T	CTGGTGAATGAATAAACTAATATATG	TGAATTGAGCCATCACGTAATACTC
rs137726884	A/G	AAACTTACCATTAAATGTTCCCCTG	AAGTTGCAAGTCTTTGATAGACTCC
rs137722600	C/T	CCAAGCAGAAGACGTGGGTTCTATCT	GGGGTTGGAAAGATCCCCTGGAGAA
rs137711215	A/G	TAAAATGTTAGAGAAAAGCAAAGGGA	TTCAGGGAAACATGAGGATTTTCTAGA
rs137662301	C/T	CATGGGGTCACAAAGAGTCAGACATG	CTCAGCAGTCAGACAAACAGCAAGG
rs137601357	C/T	CAGAACTCAGGCTGGTGAAAAAGCCC	GGTCCCCAAGGTCAGTCATTTTCTG
rs137561617	A/T	ATTGAATTTAACTTTTACATGCTGAT	TTCAGTATCTAAAGGATATTTATTG
rs137374423	C/G	TCATTTTCCTTTCTGTTCTCAGACT	TATAATTTTCTGTTGCTCCTATTTTTG
rs137330201	A/G	CTCATCTGCTCACCCCTTTATCATTTT	TTGATTCTTTGCTAGCAGTATTGGC
rs137265200	C/T	ACAAAGAGTCAGACATGTCTCAGCAG	CAGACAAACAGCAAGGGTGTTAATG
rs137211570	A/C	CCAGGCCTCCCTGTCCATCACCAACT	CCGGAGTTTACTCAAACATCATGTCC
rs137151719	G/T	AGTTCAAGTGTAAGTGTATTCTTCCA	AAGGAAAAGCATTTTCTTATCTCTC
rs137140434	G/T	TTCAGTTATTATATGTCTCCACTCTA	AATTTTTTTTTTGGTTTCTTTTTAGA
rs137104571	C/G	AGTGGTTCTGCTTCTGGGCCAAAGAG	GCTGAAAAGTGAATTCTCTCAGTCG
rs136982429	C/T	CCAGGCAAGAATACTGGAGTGGGTTG	CATTTCTCCTCCAGGAGATCTTCC
rs136939207	G/T	TAAACATTCATTATTACCTATATTGT	TTTTGCTTTTTTGAAGTCAGAATACC
rs136882857	C/T	CAGATCTCCTGCCTGGGAAGGGCCTT	ATTCATTTTATTCAATCAAACCTCTT
rs136875549	C/T	ATAACTTCCACCTTTTGTGGCTTTTT	CCTAAGCGTTTGGGGTGCTCCTGTG
rs136873074	C/T	CTCCCGAACTACAGGCGGATTCTTTA	GAACTGAGCTAGGAGGGAAGCCCAG

Table 4.2: Single nucleotide polymorphisms ID, allele substitution, and forward and reverse primer sequences utilized for amplification and visualization of genotypes for GH1

SNP ID	Allele Substitution	Forward Sequence	Reverse Sequence
rs133438805	C/T	TCCATGCTGGGGGCCATGCCCCGCCCT	TCCTGGCTTAGCCAGKAGAATGCAC
rs109275907	G/T	CTTAGCCAGKAGAATGCACGTGGGCT	GGGGAGACAGATCCCTGCTCTCTCC
rs134389836	C/T	ACAGATCCCTGCTCTCTCCCTCTTTC	AGCAGTCCAGCCTTGACCCAGGGGA
rs133403174	A/G	CAGGGGAAACCTTTTCCCYTTTTGAA	CCTCCTTCCTCGCCCTTCTCCAAGC
rs137651874	C/T	CCTTGACCCAGGGGAAACCTTTTCCC	TTTTGAARCCTCCTTCCTCGCCCTT
rs137252133	A/G	CTTCCTCGCCCTTCTCCAAGCCTGTA	GGGAGGGTGGAAAATGGAGCGGGCA
rs135322669	G/-	GGGGGTATGAGAAGCTGAAGGACCTG	CAGGAGCTGGAAGATGGCACGACAC
rs136132855	C/T	AACATGCGCAGTGACGACGCGCTGCT	AAGAACTACGGTCTGCTCTCCTGCT
rs134687399	A/G	ACTTCATGACCCTCAGGTACGTCTCC	TCTTATGCAGGTCCTTCCGGAAGCA

Table 4.3: Single nucleotide polymorphisms ID, allele substitution, and forward and reverse primer sequences utilized for amplification and visualization of genotypes for IGF-1

SNP ID	Allele Substitution	Forward Sequence	Reverse Sequence
rs137605212	A/G	CCACTCCCCTGGCAAGGACCCAGGAG	AAGATGACCCTCCTTCTGCTTTTTC
rs137250028	C/T	GGACAGAGCACATGACTAGCCAATGA	GCTATAATGGAATTGATTAGTTAGT
rs136493168	A/G	AACCACTTCCTGCTCCAAGTACAGGA	AAAGCAACAACCTTATGGCTAGCTAG
rs135968955	G/T	AGATAAAGGAGTCTAAAATGTTCTTT	GTCACTATTTGAATCCAAGATTCTC
rs135711837	G/T	GCGTACTTTTGATGGATTAAATATTA	AAAATATTAAGGAAATTCAAATCTA
rs135230510	A/G	TGAAACACTAGGCTCGCATTAAAGGTG	GGAATCTCGGAGGCTGAGGACGGCT
rs134494935	C/T	TTCCATCTTTGATTCTGTGTTAAGAA	CCCAGCCACTAAGCACCCCATCTA
rs133980322	G/T	GCATTATTACTGTATCCATTTACAGA	GAGGAAATGGAGATTTAGCAAGGGT
rs133253110	C/T	GGCTTAGAGAATTCCATGGACCATAC	CATGGGGTTGCAAAGAGTCGGACAT
rs132951819	G/T	CTTTGCAATAATATATTACCAACAAT	TCCCTTTGTTGAATGCTTTCTATTA
rs132665612	A/G	CAGTGAGTCAAGTGGACTGGAATAAA	TAGGGGAGAATTATTCCTGTCTGAG
rs110959643	A/G	TCCCACACAAGATGGAGAGCAGACCC	TCCCAGTATTTGGGGAGGCCCATCA
rs110266103	A/G	AGCAGTGAAACAATGCAAAGGTGATC	TTAAGTTTTTCCACATTGCTACTTG
rs109327701	A/G	AAGAATCGCAGTGTACTGGGTGAGAT	TGAACACCCAGCCATGCCTTAAACT
rs109227434	C/T	TCCATTTYCCTTTGGCCTGTCAAGCC	GTAGTRGTTGTGTGTACCCATAAGA
rs109199979	C/T	CAGCCTTTCTAGGACCTCAGCTAGAC	ACAGGTGAAAGAAGAAAAATCTGAA
rs109074329	C/T	TAAGAGGAAGAAAGGRGGAGCATACC	GCCCAGCTAGCCCTGTTGACCAACT
rs109022910	A/G	TGCGAGCCTAGTGTTTCAGCGGGGCC	TGGCACGTTTTGCAGATTTTGGATG
rs43434843	A/T	AAACAATAAAGAACTTGCTTAGGAAT	AAAAAGTTTGAAATGAGTGGCCCCA
rs43434842	A/G	ATATGTGGGGGGCATATGTAAACTCA	ATGCCTATCAGAGCCACACAAGTCA

errors. By including the specific SNP, those that are borderline trending will not be ignored in future studies.

Results

Three SNP were significantly associated with growth and performance trait of which two were associated with final weight and one with hip height and scrotal circumference. Also, 6 SNP exhibited a trend with traits including final weight, ADG, and backfat.

No SNP were statistically associated with birth weight however 3 SNP located on the IGF-1 (rs109327701) and CAST (rs136939207 and rs13714034) genes have the potential to be associated (Table 4.4). These SNP should be reevaluated in future analysis with a larger population.

Table 4.4: Level of significance and number of animals from each genotype associated with birth weight

Trait	Gene	SNP ID	Allele ²	Minor Genotype Frequency ³	Het Genotype Frequency ³	Major Genotype Frequency ³	P-value
BW ¹	IGF-1	rs109327701	A/G	2	19	25	.1987
BW	CAST	rs136939207	G/T	8	17	10	.1667
BW	CAST	rs137140434	G/T	8	17	16	.1694

¹Birth Weight

²Representation of the minor allele is located on the left

³Number of animals inheriting each genotype

Table 4.5: Single nucleotide polymorphisms associated with birth weight and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
BW ¹	IGF1	rs109327701	A/G	28.87 ± 6.36 ^a	39.63 ± 1.49 ^a	37.29 ± 1.85 ^a
BW	CAST	rs136939207	G/T	32.40 ± 2.45 ^a	35.21 ± 1.49 ^a	40.45 ± 2.76 ^a
BW	CAST	rs137140434	G/T	45.22 ± 4.47 ^a	35.64 ± 2.54 ^a	37.39 ± 2.45 ^a

¹Birth Weight

²Representation of the minor allele is located on the left

^{a,b} Superscripts indicate significant difference within row (P<.05)

Three SNP (rs109275907, rs109327701, and rs132951819) were associated with weaning weight and located on the GH1 and CAST genes (Table 4.6). Along with the 3 associated markers, 6 other SNP (rs136875549, rs136882857, rs137374423, rs137561617, rs137601357, and rs137726884) were included in Table 4.6 for use in future association analysis of a larger population. Markers rs109275907 and rs132951819 were statistically associated with weaning weight. Animals inheriting the heterozygous GT genotype displayed a larger weaning weight than those with the homozygous TT genotype for marker rs109275907 (Table 4.7). For marker rs132951819, animals inheriting the homozygous GG genotype revealed a larger weaning weight than those inheriting the homozygous TT genotype (Table 4.7).

Table 4.6: Level of significance and number of animals from each genotype associated with weaning weight

Trait	Gene	SNP ID	Allele ²	Minor Genotype Frequency ³	Het Genotype Frequency ³	Major Genotype Frequency ³	P-value
WW ¹	GH1	rs109275907	G/T	5	17	26	.0422
WW	IGF1	rs109327701	A/G	2	19	25	.0869
WW	IGF1	rs132951819	G/T	2	18	28	.0218
WW	CAST	rs136875549	T/C	9	16	23	.1471
WW	CAST	rs136882857	C/T	8	23	17	.1978
WW	CAST	rs137374423	C/G	8	23	17	.1978
WW	CAST	rs137561617	T/A	8	23	17	.1978
WW	CAST	rs137601357	C/T	10	22	16	.1471
WW	CAST	rs137726884	A/G	8	24	16	.1280

¹Weaning Weight

²Representation of the minor allele is located on the left

³Number of animals inheriting each genotype

Two SNP were statistically associated with initial weight however 1 SNP located on the IGF-1 (rs132951819) and 1 on GH1 (rs109275907) genes (Table 4.8). Markers rs109275907 and rs132951819 exhibited a trend for initial weight with p-values of .05

Table 4.7: Single nucleotide polymorphisms associated with weaning weight and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
WW ¹	GH1	rs109275907	G/T	264.24 ± 12.03 ^{ab}	276.70 ± 8.34 ^b	245.83 ± 5.31 ^a
WW	IGF1	rs109327701	A/G	280.86 ± 25.79 ^{ab}	269.20 ± 7.51 ^b	243.47 ± 6.05 ^a
WW	IGF1	rs132951819	G/T	286.16 ± 25.08 ^{ab}	274.50 ± 7.28 ^b	244.62 ± 5.21 ^a
WW	CAST	rs136875549	T/C	265.18 ± 14.38 ^a	245.95 ± 6.43 ^a	266.88 ± 8.16 ^a
WW	CAST	rs136882857	C/T	265.18 ± 13.85 ^a	246.77 ± 6.89 ^a	265.77 ± 13.85 ^a
WW	CAST	rs137374423	C/G	265.18 ± 13.85 ^a	246.77 ± 6.89 ^a	265.77 ± 13.85 ^a
WW	CAST	rs137561617	T/A	265.18 ± 13.85 ^a	246.77 ± 6.89 ^a	265.77 ± 13.85 ^a
WW	CAST	rs137601357	C/T	264.44 ± 13.86 ^a	245.21 ± 6.64 ^a	266.14 ± 8.23 ^a
WW	CAST	rs137726884	A/G	265.20 ± 13.42 ^a	246.36 ± 6.25 ^a	267.26 ± 8.08 ^a

¹Initial Weight

²Representation of the minor allele is located on the left

^{a,b} Superscripts indicate significant difference within row (P<.05)

Table 4.8: Level of significance and number of animals from each genotype associated with initial weight

Trait	Gene	SNP ID	Allele ²	Minor Genotype Frequency ³	Het Genotype Frequency ³	Major Genotype Frequency ³	P-value
InWt ¹	GH1	rs109275907	G/T	5	17	26	.0524
InWt	IGF1	rs109327701	A/G	2	19	25	.1609
InWt	IGF1	rs132951819	G/T	2	18	28	.0696
InWt	CAST	rs136875549	T/C	9	23	16	.1971
InWt	CAST	rs137601357	C/T	10	22	16	.1971
InWt	GH1	rs137651874	T/C	5	10	33	.1582

¹Initial Weight

²Representation of the minor allele is located on the left

³Number of animals inheriting each genotype

and .07 respectively. Animals inheriting the heterozygous GT genotype exhibited a larger initial weight than those inheriting the homozygous TT genotype for marker rs109275907 (Table 4.9). For marker rs132951819, animals inheriting the heterozygous AG genotype exhibited a larger initial weight than the homozygous (Table 4.9). Four other markers (rs109327701, rs136875549, rs137601357, and rs137651874) with p-values between .1 and .2 are included in Table 4.8. These SNP should be reevaluated in future analysis with a larger population.

Table 4.9: Single nucleotide polymorphisms associated with initial weight and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
InWt ¹	GH1	rs109275907	G/T	277.00 ± 11.79 ^{ab}	301.42 ± 8.18 ^b	276.22 ± 5.21 ^a
InWt	IGF1	rs109327701	A/G	265.53 ± 26.87 ^a	295.58 ± 7.82 ^a	276.21 ± 6.30 ^a
InWt	IGF1	rs132951819	G/T	269.31 ± 25.77 ^{ab}	299.36 ± 7.48 ^b	277.13 ± 5.35 ^a
InWt	CAST	rs136875549	T/C	296.64 ± 14.15 ^a	275.23 ± 6.33 ^a	291.26 ± 8.02 ^a
InWt	CAST	rs137601357	C/T	295.82 ± 13.63 ^a	274.40 ± 6.53 ^a	290.43 ± 8.09 ^a
InWt	GH1	rs137651874	T/C	325.42 ± 22.08 ^a	281.93 ± 12.17 ^a	273.52 ± 9.56 ^a

¹Initial Weight

²Representation of the minor allele is located on the left

^{a,b} Superscripts indicate significant difference within row (P<.05)

Five SNP located on the IGF-1 (rs109327701, rs110959643, rs132951819, and rs133980322) and GH1 (rs109275907) genes were associated with final weight (Table 4.10). Although not statistically associated with final weight, 4 SNP (rs109022910, rs109199979, rs110266103, and rs132665612) were included in Table 4.10 for consideration in future SNP analysis of a larger population. Markers rs109275907 and rs132951819 (P = .03 and .02 respectively) were significantly associated with final weight (Table 4.10). Animal inheriting the heterozygous GT genotype for marker rs109275907 had a larger final weight thought those inheriting the homozygous genotypes (Table 4.11). The animals inheriting the homozygous GG genotype for marker rs132951819 had a larger final weight (Table 4.11). Markers rs109327701, rs110959643, and rs133980322 exhibited a trend for final weight with p-values of .09, .05, and .07 respectively (Table 4.10). Animals inheriting the homozygous AA genotype for marker rs109327701 had a larger final weight than those inheriting the heterozygous GA genotype (Table 4.11). For marker rs110959643, animals inheriting homozygous AA genotype had a larger final weight than animals inheriting the heterozygous AG genotype (Table 4.11). Animals inheriting the homozygous GG genotype for marker

rs133980322 had a larger final weight than those inheriting the heterozygous GT genotype (Table 4.11).

Table 4.10: Level of significance and number of animals from each genotype associated with final weight

Trait	Gene	SNP ID	Allele ²	Minor Genotype Frequency ³	Het Genotype Frequency ³	Major Genotype Frequency ³	P-value
FW ¹	IGF1	rs109022910	A/G	7	16	25	.1268
FW	IGF1	rs109199979	T/C	7	16	25	.1268
FW	GH1	rs109275907	G/T	5	17	26	.0285
FW	IGF1	rs109327701	A/G	2	19	25	.0922
FW	IGF1	rs110266103	G/A	7	16	25	.1268
FW	IGF1	rs110959643	A/G	6	15	27	.0528
FW	IGF1	rs132665612	G/A	8	15	21	.1405
FW	IGF1	rs132951819	G/T	2	18	25	.0173
FW	IGF1	rs133980322	T/G	2	18	1	.0672

¹Final Weight

²Representation of the minor allele is located on the left

³Number of animals inheriting each genotype

Table 4.11: Single nucleotide polymorphisms associated with final weight and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
FW ¹	IGF1	rs109022910	A/G	452.87 ± 32.87 ^a	416.04 ± 28.49 ^a	438.23 ± 15.13 ^a
FW	IGF1	rs109199979	T/C	452.87 ± 32.87 ^a	416.04 ± 28.49 ^a	438.23 ± 15.13 ^a
FW	GH1	rs109275907	G/T	422.22 ± 17.82 ^a	463.36 ± 12.36 ^b	420.76 ± 7.87 ^a
FW	IGF1	rs109327701	A/G	458.21 ± 37.08 ^a	452.16 ± 10.79 ^{ab}	415.11 ± 8.69 ^a
FW	IGF1	rs110266103	G/A	452.87 ± 32.87 ^a	416.04 ± 28.49 ^a	438.23 ± 15.13 ^a
FW	IGF1	rs110959643	A/G	459.98 ± 34.62 ^a	414.02 ± 30.29 ^b	436.21 ± 11.71 ^{ab}
FW	IGF1	rs132665612	G/A	457.73 ± 31.72 ^a	420.91 ± 27.54 ^a	443.10 ± 17.47 ^a
FW	IGF1	rs132951819	G/T	468.81 ± 37.47 ^{ab}	462.75 ± 10.87 ^a	416.02 ± 7.78 ^b
FW	IGF1	rs133980322	T/G	392.96 ± 15.37 ^{ab}	330.40 ± 22.16 ^b	404.84 ± 3.91 ^a

¹Final Weight

²Representation of the minor allele is located on the left

^{a,b} Superscripts indicate significant difference within row (P<.05)

Two SNP (rs132665612 and rs132951819) were associated with average daily gain (ADG) and were located on the IGF-1 gene (Table 4.12). Along with the 2 associated markers, 5 other SNP (rs109022910, rs109199979, rs109327701,

rs110266103, and rs110959643) were included in Table 4.12 for use in future association analysis of a larger population. No SNP had a significant association with ADG; however, a trend was observed for all previous mentioned markers (.09 and .05 respectively) (Table 4.12). Animals inheriting the homozygous GG genotype for marker rs132665612 had a higher ADG than those inheriting the heterozygous GA genotype (Table 4.13). The animals inheriting the homozygous GG genotype for marker rs132951819 had a higher ADG (Table 4.13).

Table 4.12: Level of significance and number of animals from each genotype associated with average daily gain

Trait	Gene	SNP ID	Allele ²	Minor Genotype Frequency ³	Het Genotype Frequency ³	Major Genotype Frequency ³	P-value
ADG ¹	IGF1	rs109022910	A/G	7	16	25	.1008
ADG	IGF1	rs109199979	T/C	7	16	25	.1008
ADG	IGF1	rs109327701	A/G	2	19	25	.1656
ADG	IGF1	rs110266103	G/A	7	16	25	.1008
ADG	IGF1	rs110959643	A/G	6	15	27	.1366
ADG	IGF1	rs132665612	G/A	8	15	25	.0856
ADG	IGF1	rs132951819	G/T	2	18	28	.0546

¹Average Daily Gain

²Representation of the minor allele is located on the left

³Number of animals inheriting each genotype

Table 4.13: Single nucleotide polymorphisms associated with average daily gain and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
ADG ¹	IGF1	rs109022910	A/G	1.51 ± .21 ^a	1.26 ± .18 ^b	1.43 ± .10 ^{ab}
ADG	IGF1	rs109199979	T/C	1.51 ± .21 ^a	1.26 ± .18 ^b	1.43 ± .10 ^{ab}
ADG	IGF1	rs109327701	A/G	1.79 ± .26 ^a	1.46 ± .08 ^a	1.29 ± .06 ^a
ADG	IGF1	rs110266103	G/A	1.51 ± .21 ^a	1.26 ± .18 ^b	1.43 ± .10 ^{ab}
ADG	IGF1	rs110959643	A/G	1.50 ± .24 ^a	1.25 ± .21 ^a	1.42 ± .08 ^a
ADG	IGF1	rs132665612	G/A	1.50 ± .19 ^a	1.24 ± .17 ^b	1.41 ± .11 ^{ab}
ADG	IGF1	rs132951819	G/T	1.85 ± .26 ^{ab}	1.52 ± .08 ^a	1.29 ± .05 ^b

¹Average Daily Gain

²Representation of the minor allele is located on the left

^{a,b} Superscripts indicate statistical difference within row (P<.05)

One SNP (rs137651874) located on the IGF-1 gene was associated with backfat (Table 4.14). Two SNP (rs132951819 and rs133980322) had an observed p-value of .15 and .12 respectively, which is small enough to be considered in future association analysis in a larger population size (Table 4.14). Marker rs137651874 exhibited a trend (p=.06) for association with backfat (Table 4.14). Animals inheriting the heterozygous CT genotype for marker rs137651874 had significantly greater backfat than animals inheriting the homozygous TT genotype (Table 4.15).

Table 4.14: Level of significance and number of animals from each genotype associated with backfat

Trait	Gene	SNP ID	Allele ²	Minor Genotype Frequency ³	Het Genotype Frequency ³	Major Genotype Frequency ³	P-value
BF ¹	IGF1	rs132951819	G/T	2	18	28	.1499
BF	IGF1	rs133980322	T/G	2	1	18	.1186
BF	IGF1	rs137651874	T/C	5	10	33	.0583

¹Backfat

²Representation of the minor allele is located on the left

³Number of animals inheriting each genotype

Table 4.15: Single nucleotide polymorphisms associated with backfat and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
BF ¹	IGF1	rs132951819	G/T	.08 ± .03 ^a	.08 ± .01 ^a	.10 ± .01 ^a
BF	IGF1	rs133980322	T/G	.16 ± .02 ^a	.07 ± .03 ^a	.09 ± .01 ^a
BF	IGF1	rs137651874	T/C	.05 ± .03 ^a	.11 ± .01 ^b	.10 ± .01 ^{ab}

¹Backfat

²Representation of the minor allele is located on the left

^{a,b} Superscripts indicate statistical difference within row (P<.05)

One SNP (rs133980322) located on the IGF-1 gene was associated with intramuscular fat %. The SNP was significantly associated and had a p-value of .0149 (Table 4.16). The animals that inherited the homozygous TT genotype for marker

rs133980322 had a significantly higher intramuscular fat % than those inheriting the heterozygous GT genotype and homozygous GG genotype (Table 4.17).

Table 4.16: Level of significance and number of animals from each genotype associated with intramuscular fat %

Trait	Gene	SNP ID	Allele ²	Minor Genotype Frequency ³	Het Genotype Frequency ³	Major Genotype Frequency ³	P-value
IMF	IGF1	rs133980322	T/G	2	1	18	.0149

¹Intramuscular Fat %

²Representation of the minor allele is located on the left

³Number of animals inheriting each genotype

Table 4.17: Single nucleotide polymorphisms associated with intramuscular fat % and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
IMF	IGF1	rs133980322	T/G	4.37 ± .37 ^a	2.32 ± .53 ^b	2.33 ± .09 ^b

¹Intramuscular Fat %

²Representation of the minor allele is located on the left

^{a,b} Superscripts indicate statistical difference within row (P<.05)

For ribeye area, there were no SNP associated; however, there were 6 SNP that need to be reconsidered in future association analysis in a larger population (Table 4.18). Of the 6 SNP, 5 were located on the IGF-1 gene (rs109022910, rs109199979, rs110266103, rs110959643, and rs132665612) and 1 on the GH1 gene (rs137651874), and are included in Table 4.18.

Lastly, one SNP (rs133980322) was associated with both hip height and scrotal circumference, and was located on the IGF-1 gene. The SNP was significantly associated and had a p-value of <.0001 (Table 4.20). The animals that inherited the homozygous GG genotype for marker rs133980322 had a significantly larger hip height and scrotal circumference than those inheriting the heterozygous GT genotype (Table 4.21).

Table 4.18: Level of significance and number of animals from each genotype associated with ribeye area

Trait	Gene	SNP ID	Allele ²	Minor Genotype Frequency ³	Het Genotype Frequency ³	Major Genotype Frequency ³	P-value
REA ¹	IGF1	rs109022910	A/G	7	16	25	.1580
REA	IGF1	rs109199979	T/C	7	16	25	.1580
REA	IGF1	rs110266103	G/A	7	16	25	.1580
REA	IGF1	rs110959643	A/G	6	15	27	.1801
REA	IGF1	rs132665612	G/A	8	15	21	.1727
REA	GH1	rs137651874	T/C	5	10	33	.1267

¹Ribeye Area

²Representation of the minor allele is located on the left

³Number of animals inheriting each genotype

Table 4.19: Single nucleotide polymorphisms associated with ribeye area and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean	Het Genotype Mean	Major Genotype Mean
REA ¹	IGF1	rs109022910	A/G	21.44 ± 5.88 ^a	16.16 ± 5.09 ^a	24.60 ± 2.71 ^a
REA	IGF1	rs109199979	T/C	21.44 ± 5.88 ^a	16.16 ± 5.09 ^a	24.60 ± 2.71 ^a
REA	IGF1	rs110266103	G/A	21.44 ± 5.88 ^a	16.16 ± 5.09 ^a	24.60 ± 2.71 ^a
REA	IGF1	rs110959643	A/G	20.87 ± 6.51 ^a	15.55 ± 5.69 ^a	23.99 ± 2.20 ^a
REA	IGF1	rs132665612	G/A	22.54 ± 5.67 ^a	17.25 ± 4.92 ^a	25.70 ± 3.12 ^a
REA	GH1	rs137651874	T/C	14.96 ± 6.02 ^a	26.69 ± 3.32 ^a	21.99 ± 2.61 ^a

¹Ribeye Area

²Representation of the minor allele is located on the left

^{a,b} Superscripts indicate significant difference within row (P<.05)

Table 4.20: Level of significance and number of animals from each genotype associated with hip height and scrotal circumference

Trait	Gene	SNP ID	Allele ³	Minor Genotype Frequency ⁴	Het Genotype Frequency ⁴	Major Genotype Frequency ⁴	P-value
HH ¹	IGF1	rs133980322	T/G	2	1	18	<.0001
SC ²	IGF1	rs133980322	T/G	2	1	18	<.0001

¹Hip Height

²Scrotal Circumference

³Representation of the minor allele is located on the left

⁴Number of animals inheriting each genotype

Table 4.21: Single nucleotide polymorphisms associated with hip height and scrotal circumference and least square means estimate comparisons between reported genotypes

Trait	Gene	SNP	Allele ²	Minor Genotype Mean ³	Het Genotype Mean ³	Major Genotype Mean ³
HH ¹	IGF1	rs133980322	T/G	63.97 ± 1.06 ^a	-66.33 ± 1.53 ^b	65.24 ± .27 ^a
SC ¹	IGF1	rs133980322	T/G	16.90 ± 1.03 ^a	-13.85 ± 1.48 ^b	17.15 ± .26 ^a

¹Hip Height

²Scrotal Circumference

³Representation of the minor allele is located on the left

^{a,b} Superscripts indicate statistical difference within row (P<.05)

Discussion

Insulin-like growth factor 1 markers (rs133980322, rs137651874, rs132665612, rs132951819, rs110959643, rs109022910, rs110266103, rs109199979 and rs109327701) were determined to be associated with growth and performance traits, including weaning weight, initial weight, final weight, average daily gain, backfat, intramuscular fat %, hip height and scrotal circumference. After evaluation of association analysis, notable markers were considered that were not statistically significant. These markers should be taken into consideration when performing an association analysis on a much larger population of performance test bulls. CAST markers showed no significant association; however, they should be reconsidered in a larger population. Previous findings report that increase CAST correlated with a decrease in meat tenderness (Pringle et al., 1997). For this reason Schenkel and associates (2006) stated that CAST is a good candidate gene for meat tenderness. GH1 marker rs109275907 was associated with weaning weight, initial weight, and final weight. GH1 has been previously reported as a favorable candidate gene marker in cattle for the improvement of growth, fertility, and meat and milk production (Mullen et al., 2010).

Insulin-like growth factor 1 marker rs133980322 was associated with intramuscular fat %, hip height, scrotal circumference, and final weight, demonstrating that a single marker can be associated with multiple traits. Effects of IGF-1 on growth production and meat quality have previously been reported (Machado et al., 2003; Andrade et al., 2008).

Proper identification of markers significantly associated with economically important growth and performance traits will enable a producer to increase the accuracy of their selection process. Increase accuracy will result in increase profits and sustainability within their production scheme. This study aimed to identify markers that were significantly associated with growth and performance traits. The markers, once validated, can be used in other marker assisted selection programs. Within the current study, two IGF-1 and one GH1 markers were significantly associated with weaning weight, final weight, intramuscular fat %, hip height, and scrotal circumference. Other markers within this study should be reconsidered within a larger population to determine significant associations.

Before utilization of this study's marker association, further analysis must be completed in order to validate these associations. Analysis should be reconsidered in a much larger population with other breeds and environments contributing. Also, more SNP need to be evaluated along with more candidate genes in order to identify significant associations between markers and economically important traits.

CHAPTER V. SUMMARY

Performance bull testing held at the Dean Lee Agricultural Research Station over the past 54 years has produced data to be evaluated in order to determine rate of change for growth performance traits. Performing tests under standard conditions is a method to identify genetically superior bulls for producers to incorporate into their mating systems (Liu et al., 1993). After interpretation of data, Simmental bulls displayed exhibited the greatest rate of change as compared to the other three breeds and were the largest. Of the 4 top representing breeds, Hereford bulls tended to be the lowest performing breed for each trait evaluated. This data is valuable because it allows producers a method to visualize how cattle have changed and how their selection strategies have impacted the industry.

Traditional methods of performance testing include bulls fed a diet of concentrate rather than the forage based performance testing. The majority of performance test are performed by utilizing the traditional method of testing. However, forage based performance testing has been reported to be similar with its end results. Although an all concentrate corn based diet exhibited superior feedlot performance and carcass quality, Oltjen and associates (1971) reported that steers being fed a pelleted all forage alfalfa based diet, an all concentrate diet followed by all forage diet, and an all forage diet followed by all concentrate diet all displayed a similar response in feedlot performance and carcass quality. The method of an all forage based performance test can be a cheaper approach to analyze a bull's performance in a more realistic setting. This can give a producer insight on a bull's future performance once turned out on pasture.

Utilization of candidate genes for SNP association analyses on bulls being evaluated on a forage performance bull test have been identified to affect traits such as weaning weight, initial weight, final weight, average daily gain, backfat, intramuscular fat %, hip height, and scrotal circumference. Within the current study, two IGF-1 and one GH1 markers were significantly associated with weaning weight, intramuscular fat %, hip height, scrotal circumference, and final weight. Other markers within this study should be reconsidered within a larger population to determine significant associations. In order for SNP to be incorporated into MAS programs for selection, more SNP and more candidate regions need to be evaluated. Furthermore, many more animals will need to be evaluated to identify if significant SNP are in fact population, species, and breed specific.

LITERATURE CITED

- Andersson, L. 2001. Genetic dissection of phenotypic diversity in farm animals. *Nature Rev. Genet.* 2:130-138.
- Andrade, P.C., D.A. Grossi, C.C. Paz, M.M. Alencar, et al. 2008. Association of an insulin-like growth factor 1 gene microsatellite with phenotypic variation and estimated breeding values of growth traits in Canchim cattle. *Anim. Genet.* 39:480-485.
- Auchtung, T.L., S.M. Barao, and G.E. Dahl. 2001. Relation of growth hormone response to growth hormone-releasing hormone before weaning and postweaning growth performance in beef calves. *J. Anim. Sci.* 79:2217-2223.
- Baeza, M.C., P.M. Corva, L.A. Soria, G. Rincon, J.F. Medrano, E. Pavan, E.L. Villarreal, A. Schor, L. Melucci, C. Mezzadra, and M.C. Miquel. 2011. Genetic markers of body composition and carcass quality in grazing Brangus steers. *Genet. Mol. Res.* 10(4):3146-56.
- Barendse, W., A. Reverter, R.J. Bunch, B.E. Harrison, W. Barris, and M.B. Thomas. 2007. A validated whole-genome association study of efficient food conversion in cattle. *Genetics.* 176:1893-905.
- Bauman, D.E. 1992. Bovine somatotropin: Review of an emerging animal technology. *J. Dairy Sci.* 75:3432-3451.
- BIF. 2010. Guidelines for Uniform Beef Improvement Programs. 9th ed. Beef Improvement Federation, North Carolina State University, Raleigh, NC.
- Bishop, M. D., M. Koohmaraie, J. Killefer, and S. Kappes. 1993. Rapid communication: Restriction fragment length polymorphisms in the bovine calpastatin gene. *J. Anim. Sci.* 71:2277.
- Bostein D., R.L. White, M. Skolnick, and R.W. Davis. 1980. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *Am. J. Hum. Genet.* 32(3):314-331.
- Brown, A.H. Jr., J.J. Chewning, Z.B. Johnson, W.C. Loe, C.J. Brown. 1991. Effects of 84-, 112-, and 140-day postweaning feedlot performance test for beef bulls. *J. Anim. Sci.* 69(2):451-61.
- Buchanan, F.C., C.J. Fitzsimmons, A.G. Van Kessel, T.D. Thue, D.C. Winkleman-Sim, S.M. Schmutz. 2002. Association of a missense mutation in the bovine leptin gene with carcass fat content and leptin mRNA levels. *Genet. Sel. Evol.* 34:105-116.

- Bunger, L and W.G. Hill. 1999. Role of growth hormone in the genetic change of mice divergently selected for body weight and fatness. *Genet. Res.* 74: 351-360.
- Casas, E., R.M. Thallman, and L.V. Cundiff. 2011. Birth and weaning traits in crossbred Cattle from Hereford, Angus, Brahman, Boran, Tuli, and Belgian Blue sires. *J. Anim. Sci.* 89:979-987.
- Collins, F. S., M.S. Guyer, and A. Chakravarti. 1997. Variations on a Theme: Cataloging Human DNA Sequence Variation. *Science.* 278:1580-1581.
- Crawford, D.C., and D.A. Nickerson. 2005. Definition and Clinical Importance of Haplotypes. *Annu. Rev. Med.* 56:303-20.
- Crouse, J. D., L.V. Cundiff, R.M. Koch, M. Koohmaraie, and S.C. Siedeman. 1989. Comparison of *Bos indicus* and *Bos Taurus* inheritance for carcass beef characteristics and meat palatability. *J. Anim. Sci.* 67:2661.
- Crouse, J.D., S.C. Seideman, and L.V. Cundiff. 1987. The effect of carcass electrical stimulation on meat obtained from *Bos indicus* and *Bos Taurus* cattle. *J. Food Quality.* 10:407.
- Cundiff, L.V., R.M. Thallman, and L.A. Kuehn. Impact of *Bos indicus* Genetics on the Global Beef Industry. U.S. Meat Animal Research Center.
- Davis, G.P., S.K. DeNise. 1998. The impact of genetic markers on selection. *J. Anim. Sci.* 76:2331-9.
- DeAtley, K.L., G. Rincon, C.R. Farber, J.F. Medrano, P. Luna-Nevarez, R.M. Enns, D. M. Vanleeuwen, G.A. Silver and M.G. Thomas. 2011. Genetic analyses involving microsatellite ETH10 genotypes on bovine chromosome 5 and performance trait measures in Angus- and Brahman-influenced cattle. *J. Anim. Sci.* 89:2031-2041.
- De la Rosa Reyna, X.F., H.M. Montoya, V.V. Castrellón, A.M.S. Rincón, M.P. Bracamonte, and W.A. Vera. 2010. Polymorphisms in the IGF1 gene and their effect on growth traits in Mexican beef cattle. *Genet. Mol. Res.* 9(2):875-883.
- Ellegren, H., S. Moore, N. Robinson, K. Byrne, W. Ward, and B.C. Sheldon. 1997. Microsatellite Evolution – A Reciprocal Study of Repeat Lengths at Homologous Loci in Cattle and Sheep. *Mol. Biol. Evol.* 14(8):854-860.
- Elzo, M.A., D.D. Johnson, J.G. Wasdin, and J.D. Driver. 2011. Carcass and meat palatability breed differences and heterosis effects in an Angus-Brahman multibreed population. *J. Meat Sci.* 90:87-92.

- Etherton, T.D. and D.E. Bauman. 1998. Biology of somatotropin in growth and lactation of domestic animals. *Physiol. Rev.* 78:745-761.
- Florini, J.R., D.Z. Ewton, and S.A. Coolican. 1996. Growth hormone and insulin-like growth factor system in myogenesis. *Endocr. Rev.* 17(5):481-517.
- Garcia, M.D., M.G. Thomas, W.R. Parker, V.R. Beauchemin, and R.M. Enns. 2004. Evaluation of Performance Trends in the Tucumcari Bull Test 1961 and 2000. New Mexico State University Agriculture Experiment Station: Research Report 754.
- Goddard, M.E. and B.J. Hayes. 2007. Genomic Selection. *J. Anim. Breed. Genet.* 124:323-330.
- Grosse, W.M., S.M. Kappes, W.W. Laegreid, J.W. Keele, C.G. Chitko-McKown, and M.P. Heaton. 1999. Single nucleotide polymorphism (SNP) discovery and linkage mapping of bovine cytokine genes. *Mamm. Genome.* 10:1062-1069.
- Ge, W., M.E. Davis, H.C. Hines, K.M. Irvin, R.C.M. Simmen. 2003. Association of single nucleotide polymorphisms in the growth hormone and growth hormone receptor genes with serum insulin-like growth factor I concentration and growth traits in Angus cattle. *J. Anim. Sci.* 81: 641-648.
- Ge, W., M.E. Davis, H.C. Hines, K.M. Irvin and R.C. Simmen. 2001. Association of a genetic marker with blood serum insulin-like growth factor-I concentration and growth traits in Angus cattle. *J. Anim. Sci.* 79(7):1757-62.
- Gutiérrez-Gil, B., J.L. Williams, D. Homer, D. Burton, C.S. Haley, and P. Wiener. 2009. Search for quantitative trait loci affecting growth and carcass traits in a cross population of beef and dairy cattle. *J. Anim. Sci.* 87:24-36.
- Hediger, R., S.E. Johnson, W. Barendse, R.D. Drinkwater, S.S. Moore, and J. Hetzel. 1990. Assignment of the growth hormone gene locus to 19q26-qter in cattle and to 11q25-qter in sheep by in situ hybridization. *Genomics* 8(1): 171-174.
- Jiang, H., and M.C. Lucy. 2001. Variants of the 5'-untranslated region of the bovine growth hormone receptor mRNA: Isolation, expression and effects on translational efficiency. *Gene* 265:45-53.
- Kirkpatrick, B. W. 1992. Identification of a conserved microsatellite site in the porcine and bovine insulin-like growth factor-I gene 5' flank. *Anim. Genet.* 23:543-548.
- Koohmaraie, M. 1994. Muscle proteinases and meat aging. *Meat Sci.* 36:93-104.

- Kojima M, Hosoda H, Date Y, Nakazato M, Matsuo H, Kangawa K. 1999. Ghrelin is a growth hormone-releasing hormone acylated peptide from stomach. *Nature*. 402:656-660.
- Koots, K. R., J. P. Gibson, C. Smith, and J. W. Wilton. 1994a. Analyses of published genetic parameter estimates for beef production traits. 1. Heritability. *Anim. Breed. Abstr.* 63:309–338.
- Lagonigro, R., P. Wiener, F. Pilla, J.A. Woolliams, J.L. Williams. 2003. A new mutation in the coding region of the bovine leptin gene associated with feed intake. *Anim. Genet.* 34:371-374.
- Lagziel A, S. Denise, O. Hanotte, S. Dhara, V. Glazko, A. Broadhead, R. Davoli, V. Russo, M. Soller. 2000. Geographic and breed distribution of an MspI PCR-RFLP in the bovine growth hormone (bGH) gene. *Anim. Genet.* 31: 210-213.
- Liu, M.F. and M. Markarechian. 1993. Factors influencing growth performance of beef bulls in a test station. *J. Anim. Sci.* 71:1123-1127.
- Lucy, M. C. 2008. Functional differences in the growth hormone and insulin-like growth factor axis in cattle and pigs: Implications for post-partum nutrition and reproduction. *Reprod. Domest. Anim.* 43(Suppl. 2):31–39.
- Machado M.B.B., M.M. Alencar, A.P. Pereira, H.N. Oliveira, et al. (2003). QTL affecting body weight in a candidate region of cattle chromosome 5. *Genet. Mol. Biol.* 26: 259-265.
- Matukumalli, L.K., C.T. Lawley, R.D. Schnabel, J.F. Taylor, M.F. Allan, M.P. Heaton, J. O'Connell, S.S. Moore, T.P.L. Smith, T.S. Sonstegard and C.P. Van Tassell. 2009. Development and characterization of a high density SNP genotyping assay for cattle. *Plos One*. 4: 1-13.
- Members of the Complex Trait Consortium. 2003. The nature and identification of Quantitative trait loci: a community's view. *Nature Rev. Genet.* 4, 911-916.
- Meuwissen, T.H.E., B.J. Hayes and M.E. Goddard. 2001. Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps. *Genet.* 157: 1819-1829.
- Mizoguchi, Y., T. Watanabe, K. Fujinaka, E. Iwamoto, and Y. Sugimoto. 2005. Mapping of quantitative trait loci for carcass traits in a Japanese Black (Wagyu) cattle population. *Anim. Genet.* 37:51-54.
- Mizoshita, K, T. Watanabe, H. Hayashi, C. Kubota, H. Yamakuchi, J. Todoroki, and Y. Sugimoto. 2004. Quantitative trait loci analysis for growth and carcass traits in a half-sib family of purebred Japanese Black (Wagyu). *J. Anim. Sci.* 82:3415-3420.

- Moody, D.E., D. Pomp, S. Newman, and M.D. MacNeil. 1994. Characterization of DNA polymorphisms and their associations with growth and maternal traits in line 1 Hereford cattle." In: Proc. 5th World Cong. Genet. Appl. Livest. Prod., Guelph, Ontario, Canada. 21:221–224.
- Moody, D.E., D. Pomp, S. Newman, and M.D. MacNeil. 1996. Characterization of DNA polymorphisms in three populations of Hereford cattle and their associations with growth and maternal EPD in Line 1 Herefords. *J. Anim. Sci.* 74:1784–1793.
- Mullen, M.P., C.O. Lynch, S.M. Waters, D.J. Howard, P. O'Boyle, D.A. Kenny, F. Buckley, B. Horan, and M.G. Diskin. 2011. Single nucleotide polymorphisms in the growth hormone and insulin-like growth factor-1 genes are associated with milk production, body condition score and fertility traits in dairy cows. *Genet. Mol. Res.* 10(3):1819-30.
- Mullen, M.P., D.P. Berry, D.J. Howard, M.G. Diskin, C.O. Lynch, E.W. Berkowicz, D.A. Magee, D.E. MacHugh, and S.M. Waters. 2010. Associations between novel single nucleotide polymorphisms in the *Bos taurus* growth hormone gene and performance traits in Holstein-Friesian dairy cattle. *J. Dairy Sci.* 94:5959-5969.
- Pinto, L.F.B., J.B.S. Ferraz, F.V. Meirelles, J.P. Eler, F.M. Rezende, M.E. Carvalho, H.B. Almeida and R.C.G. Silva. 2010. Association of SNPs on CAPN1 and CAST genes with tenderness in Nellore cattle. *Genet. Mol. Res.* 9(3):1431-1442.
- Ohlsson, C., B.A. Bengtsson, O.G. Isaksson, T.T. Andreassen, et al. 1998. Growth hormone and bone. *Endocr. Rev.* 19:55-79.
- Oltjen, R.R., T.S. Rumsey, and P.A. Putnam. 1971. All-Forage Diets for Finishing Beef Cattle. *J. Anim. Sci.* 32:327-333.
- Ramsay, T.G. and P.D. Cranwell. 1999. A review - Leptin: A regulator of feed intake and physiology in swine. Proceeding of the Seventh Biennial Conference of the Australasian Pig Science Association (APSA), 28 November - 1 December, Adelaide, Australia, pp 157-170.
- Renaville, R., M. Hammadi, and D. Portetelle. 2002. Role of the somatotrophic axis in the mammalian metabolism. *Domest. Anim. Endocrinol.* 23:351–360.
- Reynolds, W.L., T.M. DeRouen, S. Moin and K.L. Koonce. 1980. Factors influencing gestation length, birthweight and calf survival of Angus, Zebu, and Zebu cross beef cattle. *J. Anim. Sci.* 51:860.
- Roberson, R.L., J.O. Sanders and T.C. Cartwright. 1986. Direct and maternal genetic effects on preweaning characters of Brahman, Hereford and Brahman-Hereford crossbred cattle." *J. Anim. Sci.* 63:438.

- Saiki, R.K., S.J. Scharf, F. Faloona, K.B. Mullis, G.T. Horn, H.A. Erlich, and N. Amheim. 1985. Enzymatic amplification of beta- globin genomic sequences and restriction site analysis of sickle cell anemia. *Science* (Washington DC) 230:1350.
- Sainz, R.D., F. De la Torre, and J.W. Oltjen. 1995. Compensatory growth and carcass quality in growth-restricted and refed beef steers. *J. Anim. Sci.* 73:2971-2979.
- Schenkel, F.S., S.P. Miller, and J.W. Wilton. 2003. Genetic parameters and breed differences for feed efficiency, growth, and body composition traits of young beef bulls. *Can. J. Anim. Sci.* 177-185.
- Schenkel, F.S., S.P. Miller, Z. Jiang, I.B. Mandell, X. Ye, H. Li and J.W. Wilton. 2006. Association of a single nucleotide polymorphism in the calpastatin gene with carcass and meat quality traits of beef cattle. *J. Anim. Sci.* 84:291-299.
- Schlee, P., R. Graml, E. Schallenberger, D. Schams, O. Rottmann, A. Olbrich-Bludau, and F. Pirchner. 1994. Growth hormone and insulin-like growth factor I concentrations in bulls of various growth hormone genotypes. *Theor. Appl. Genet.* 88:497–500.
- Simpson, J.D., A.H. Brown and C.J. Brown. 1986. Trends of performance in Arkansas cooperative beef-bull performance tests from 1962-1982. *Growth.* 50(1):77-83.
- Snelling, W.M., M.F. Allan, J.W. Keele, L.A. Kuehn, T. McDanel, T.P.L. Smith, T.S. Sonstegard, R.M. Thallman, and G.L. Bennett. Genome-wide association study of growth in crossbred beef cattle. 2010. *J. Anim. Sci.* 88:837-848
- Soller, M. and J.S. Beckmann. 1983. Genetic polymorphism in varietal identification and genetic improvement. *Theor. Appl. Genet.* 67:25.
- Steele, R., J. Torrie, and D. Dickey. 1997. Analysis of covariance. Principles and procedures of statistics: A Biometrical Approach. 3rd edition, McGraw Hill, Inc. New York, NY. 447-449.
- te Pas MF, Freriksen JW, van Bijnen AJ, Gerritsen CL, et al. 2001. Selection for growth rate or against back fat thickness in pigs is associated with changes in growth hormone axis plasma protein concentration and mRNA level. *Domest. Anim. Endocrinol.* 20: 165-184.
- te Pas MF, Visscher AH and de Greef KH. 2004. Molecular genetic and physiologic background of the growth hormone-IGF-I axis in relation to breeding for growth rate and leanness in pigs. *Domest. Anim. Endocrinol.* 27: 287-301.
- Thissen, J.P., L.E. Underwood, J.M. Ketelslegers. 1999. Regulation of Insulin-like Growth Factor-I in Starvation and Injury. *Nutr. Rev.* 57(6):167-76.

- Thrift, F. A. and T. A. Thrift. 2003. Review: Longevity attributes of Bos indicus × Bos taurus crossbred cows. Prof. Anim. Sci. 19:329–341.
- Thomas, M.G., J.A. Carroll, S.R. Raymond, R.L. Matteri and D.H. Keisler. 2000. Transcriptional regulation of pituitary synthesis and secretion of growth hormone in growing wethers and the influence of zeranol on these mechanisms. Dom. Anim. Endocrinol. 18:309-324.
- Trenkle, Allen and David G. Topel. 1978. Relationships of some endocrine measurements to growth and carcass composition of cattle. J. Anim. Sci. 46(6):1604
- Vignal, A., D. Milan, M. SanCristobal and A. Eggen. 2002. A review on SNP and other types of molecular markers and their use in animal genetics. Genet. Sel. Evol. 34: 275-305.
- Wheeler, T. L., L. V. Cundiff, R. M. Koch, M. E. Dikeman, and J. D. Crouse. 1997. Characterization of different biological types of steers (cycle IV): wholesale, subprimal, and retail product yields. J. Anim. Sci. 75:2389-2403.
- Yao J., S.E. Aggrey, D. Zadworny , J.F. Hayes , U. Kuhnlein. 1996. Sequence variations in the bovine growth hormone gene characterized by single-strand conformation polymorphisms (SSCP) analysis and their association with milk production traits in holsteins. Genet. 144: 1809-1816.
- Zhang, H.M., D.R. Brown, S.K. DeNise, R.L. Ax. 1993. Rapid Communication: Polymerase Chain Reaction-Restriction Fragment Length Polymorphism Analysis of the Bovine Somatotropin Gene. J. Anim. Sci. 71:2276.

APPENDIX A: DNA EXTRACTION – SATURATED SALT PROCEDURE

Based on extraction procedures described in Miller et al., 1988. Nucl. Acids Res. 16: 1215

Day 1: in 15 ml centrifuge tube

Add: 10-12 ml Lysis buffer (Appendix B) to 250 L white blood cell buffy coat; invert to mix

Spin: 7000rpm for 10 minutes at 4°C; aspirate supernatant from pellet

Add: 3 mls Digestion Buffer (Appendix B); shake vigorously to resuspend pellet

Add: 200 µl 10% SDS and 60 µl RNase A (10 mg/ml); invert to mix; incubate for 1 hr at 37°C with gentle shaking

Add: 25 µl Proteinase K (20 mg/ml); invert to mix; incubate overnight at 37°C with gentle shaking

Day2:

Add: 1 ml Saturated NaCl; shake vigorously by hand for 15 seconds

Spin: 2800 rpm for 30 mins at 4°C; transfer supernatant to new 15 ml tube

Add: 2 volumes of 100% Ethanol (stored in freezer); invert gently to mix

Remove: DNA with soft pipette; transfer DNA into 1.5 ml snap-cap tube

Spin: at 10 setting for 10 min. in refrigerated bench-top centrifuge; aspirate off most of ethanol

Add: 1 ml of 80% cold ethanol (keep on ice); vortex for 20 seconds; spin 5 minutes in refrigerated bench-top centrifuge; aspirate off most of ethanol

Add: 500 µl of 80% cold ethanol; vortex 20 seconds; spin 5 minutes in refrigerated bench-top centrifuge; aspirate off most of ethanol

Leave tubes uncovered to allow pellet to dry overnight

Add: 350 µl Rehydration Buffer (Appendix B) to resuspend DNA

Read: on spectrophotometer

APPENDIX B: BUFFER SOLUTION LABORATORY PROTOCOL

LYSIS BUFFER (1L):

7.49g NH_4Cl

2.059g Tris-HCl

pH to 7.4

DIGESTION BUFFER (1L):

1.211g Tris-HCl

23.376g NaCl

0.744g EDTA

pH to 8.0

REHYDRATION BUFFER (1L):

1.21g Tris-HCl

0.37g EDTA

VITA

Tabitha Renea Howard was born in 1988 to Max Howard and Renea Keahey in West Monroe, Louisiana. Tabitha attended Tensas Academy in Saint Joseph, Louisiana where she graduated in May of 2006. She received her Bachelor of Science degree in Animal, Dairy, and Poultry Sciences at Louisiana State University in December of 2010.

Tabitha began her Master of Science degree at Louisiana State University under the direction of Dr. Matthew D. Garcia in Spring 2011. Upon completion of her Master of Science degree, she plans on continuing to work in the cattle industry.