EFFECTS OF SELECTION ON HIGHLY HERITABLE TRAITS IN GELBVIEH AND GELBVIEH HYBRID CATTLE

by

Leopoldo Arturo Pacheco IV, B.S.

A THESIS

IN

ANIMAL SCIENCE

Submittted to the Graduate Faculty
of Texas Tech University in
Partial Fulfillment of
the Requirements for
the Degree of

MASTER OF SCIENCE

Jay W. Johnson
Chairperson of the Committee

Samuel P. Jackson

Samuel D. Prien

Accepted

John Borrelli
Dean of the Graduate School

August, 2007

ACKNOWLEDGEMENTS

The time I have spent in West Texas has been a life changing experience. I do not believe you could find better people anywhere else. I have learned a lot from my professors and friends at Texas Tech University. The knowledge which I have gained during my master's program has opened many doors for me and will continue to lead me to many great opportunities. My time here has also helped me define what I want to do with my life as a professional.

I would like to first thank my committee members, Dr. Jay W. Johnson, Dr. Samuel P. Jackson and Dr. Samuel D. Prien. I am truly honored you all supported me and allowed me to experience a master's program under such great direction.

I would also like to thank the American Gelbvieh Association for providing me the data on which my research project is based, and especially Susan Willmon, the Director of Breed Improvement for the Gelbvieh Association. She always answered questions in a timely manner and provided me with extra information needed to complete the study.

Another group of people who have made my time at Texas Tech a truly memorable experience would be my fellow graduate students. These individuals are: Kory Evenson, Amanda Burns and Carrie Phipps. I would especially like to thank Kory and Zeke McCarty, an undergraduate assistant, for helping me at the farm in the absence of Lonnie Hughes.

Lonnie is an individual who has impacted my life, by showing me many tricks of the trade. Lonnie is one of the most honest and humble men you will ever meet, and I wish Lonnie and his family the best.

Finally and most importantly I would like to thank Wrenn Harris for supporting me and allowing me to follow my dreams. I truly appreciate her patience and willingness to allow me to continue my education. I cannot wait to start the next chapter of our lives. To my family, who probably still does not truly understand what I have been doing at Texas Tech for the last few years, but has supported me unconditionally. These individuals are: Juana and Ross and Arturo and Janet.

Lastly, I would like to dedicate this thesis to my late step-father Ross, who now truly understands what this is all about, because he has been able to look down on me the last couple of months.

TABLE OF CONTENTS

ABSTRACT

Cattle breed associations have realized the usefulness of real time ultrasound (RTU) measures of body composition from yearling bulls and heifers in combination with live weights to conduct national cattle genetic evaluations for carcass merit. The data collected in these evaluations are used to adjust carcass data collected on the progeny of sires. Including live animal data allows evaluation of a larger, more random sample of the population while increasing the accuracy with which replacements are evaluated. Research has reported genetic parameter estimates among live animal measurements of yearling replacements and carcass traits of market progeny in the Simmental breed.

The objective of this study is to determine how accurate sire expected progeny differences (EPDs), ultrasound data and progeny carcass data is at predicting phenotype of offspring, and the level of selection at which the most rapid genetic advancements be made. The bull's EPD percentile ranks for intramuscular fat (IMF), longissimimus muscle area (LMA) and rib fat (RF) were compared against a sire's progeny's ultrasound or carcass measurements. The number of sires included 1376 Gelbvieh, 78 Red Angus and 287 Angus bulls. Comparing Angus sire IMF rank to progeny ultrasound IMF scores was significant in yr 01 ($P < 0.05$). Gelbvieh group sire EPD ranked IMF were compared to progeny carcass IMF (CIMF). Sire IMF rank correlated to progeny CIMF scores in yrs 89, 90, 94, 95 96, 98, 99, 00, and 01 ($P < 0.05$). Gelbvieh sire LMA rank compared to progeny carcass LMA correlated in yrs 94, 96, and 98 ($P < 0.05$). Angus sire RF rank correlated to progeny ultrasound RF (URF) in yrs 99 and 00 ($P < 0.05$). Comparing Red

Angus sire RF rank to progeny URF in cm was significant in yrs 02 and 03 ($P < 0.05$). Comparing Gelbvieh sire RF rank to progeny URF in cm was significant in yrs 99 and 01 ($P < 0.05$). Comparing Gelbvieh sire RF rank to progeny carcass RF in cm was significant in yrs 82, 92, 95, 96, and 02 ($P < 0.05$). However, results did not yield findings to allow producers to make mating selections at a specific selection pressure and more research should be conducted to determine at what level of selection the most rapid genetic improvement will be made.

LIST OF TABLES

CHAPTER I

INTRODUCTION

Seedstock producers have widely used expected progeny differences (EPDs) as a valuable tool in making mating selections, and with great success as published by Arnold et al. (1990). However, there are concerns that by making corrective matings using EPDs there could be an increase in phenotypic variation of subsequent generations. Additionally, one must remember that a sire's EPDs have the potential to change, particularly if he is a widely used sire within a breed, as found in a study by Bullock et al. (2000). Selection plays an important role in the progress that animal breeders can make from generation to generation. Therefore, the more informed decisions that breeders can make the more progressive they can be. By using EPDs as a tool to make mating selections, one would expect to make more rapid genetic improvement. However, it is unknown at what level of selection the most rapid genetic improvement can be made, or if greater selection pressure is applied can more rapid genetic improvement be made.

The objective of the present study was to determine at what level of selection the most rapid genetic improvement could be made with regards to carcass traits such as intramuscular fat, longissimus muscle area, and rib fat, using the EPD model.

CHAPTER II

REVIEW OF LITERATURE

Genetic Trends

The beef cattle industry has undergone many changes over the years in management practices and the breed type of cattle used in today's commercial operations. Today's feedlot managers prefer the cattle they feed to be at least 1/2 English breeding. However, what drives the industry and cattlemen most is the consumer. Consumers are becoming more health conscious and are demanding meat products that are lean, without sacrificing a favorable eating experience. Therefore beef is required to be lean, yet tender and flavorful, two aspects of palatability that can be hindered by the leanness of meat. Further, the recent occurrence of Bovine Spongiform Encephalitis (BSE) in beef has caused ever closer inspection of the beef supply, provoking more thought from the public at the retail counter, therefore producers must be even more aware of the public's concerns.

The National Beef Market Basket Survey (Savell et al., 1991) and the National Beef Tenderness Survey (Morgan et al., 1991) noted great variation in beef composition and palatability traits at the retail level in the United States. Additionally, Savell et al. (1991) found that consumers consider retail cuts with excessive external fat wasteful, low in taste, and unhealthful (Lorenzen et al., 1993). In 1973-1974, the last USDA Market Consist Report was conducted. Since that time the beef industry has undergone many changes. Continental breeds of cattle have become widely used and even more influential in the diet and health concerns of consumers in the US and abroad. The

primary question is whether beef has changed significantly during that time (Lorenzen et al., 1993). Therefore it is up to beef producers to meet the concerns of the consumer; they must fulfill their requirements in order for beef to retain its wholesome status in the consumer's mind. To make the most rapid and efficient changes in production the beef industry must utilize all the tools available to it.

Ultrasound

Carcass quality grade in beef is determined almost entirely by marbling score, a phenotypic trait that is difficult to estimate in live animals. Estimating marbling with ultrasound has significantly improved carcass estimations of quality grade and aids in targeting carcasses to more exact packer and consumer specifications. Ultrasound has been used for years to estimate backfat thickness (Hazel and Kline, 1959) and rib eye area (Stouffer, 1959). Currently, ultrasound is accurately used to predict marbling in commercial feedlots. Furthermore, the data gathered from ultrasound can be a valuable tool for the beef industry.

Ultrasound and its Impact on Seedstock Production

Ultrasound has become a widely used tool in seedstock production, commercial operations and in the feedyard, to predict carcass merit. It has also been used to assess the value of individuals as parents. Ultrasound has many advantages including the fact that it is relatively inexpensive, produces results more rapidly when compared to progeny testing programs, and the data obtained with ultrasound should experience less selection bias than carcass data collected via sire progeny testing programs. Studies have shown

that ultrasound measures of fat thickness (FT) and ribeye area (RE), (Perkins et al., 1992; Herring et al., 1994; Bergen et al., 1996), and intramuscular fat percentage (IMF), (Reverter et al., 2000; Hassen et al., 2001) are accurate predictors of their corresponding carcass traits in fed slaughter cattle. Thus average heritability estimates of seedstock cattle ultrasound measures of FT, RE, and IMF could be expected to be moderate-to-high. This moderate-to-high heritability gives confidence that selecting seedstock animals based on their ultrasound measures should improve the carcass characteristics of their progeny.

An important issue affecting the ultimate usefulness of live-animal ultrasound (US) information as a tool for carcass genetic improvement is the genetic relationship between the live-animal measurements of seedstock cattle and the corresponding carcass measurements of their progeny (Baud et al., 1998). Research conducted by Moser et al. (1998); Devitt and Wilton, (2001); and Reverter et al. (2000) show that there is a positive genetic correlation between US measurements of seedstock cattle and the corresponding carcass measurements of fed cattle; however, some variability exists. Sapp et al. (2002) conducted a study to determine the impact of selecting sires based on phenotypic yearling ultrasound intramuscular fat percentage (UIMF), or UIMF EPD, on marbling score of steer progeny. Prior to this research, little information was available in the literature focusing on the consequences of actual sire selection, based on US measures, and their impact on carcass measures of their progeny.

In the study by Sapp et al. yearling Angus bulls were selected for high-phenotypic ultrasound intramuscular fat percentage or phenotypic ultrasound intramuscular fat percentage EPDs. It was found that these sires could be expected to produce steers with

significantly higher amounts of marbling and quality grade. They determined marbling can be increased without increasing the external fat thickness and yield grade, implying that producers can and should use UIMF to aid in genetic evaluation and sire selection at a younger age that can impact the genetic progress in future generations of slaughter progeny and seedstock progeny alike.

Research by Devitt et al. (2001) drew much the same conclusion, that genetic evaluations for carcass traits based on US measurements of yearling cattle have the potential to increase the rate of genetic progress and reduce the expense involved in progeny testing. The research evaluated genetic correlation estimates between US measurements on yearling bulls and carcass measurements on finished steers, and found that age constant heritability measurements for longissimus muscle area, UIMF ultrasound backfat, and average daily postweaning gain were 0.48, 0.23, 0.52, and 0.46, respectively. Similar estimates were found for backfat and weight-constant traits in the same study. Further, there was also an age-constant genetic correlation estimates between steer carcass longissimus muscle area and bull ultrasound longissimus muscle area, steer carcass backfat and bull US backfat, steer carcass marbling and bull ultrasound intramuscular fat, and steer average daily gain and bull average daily gain measured as 0.66, 0.88, 0.80, and 0.72, respectively. Devitt et al. concluded there was a strong, positive genetic correlation estimates between bull US measurements and corresponding steer carcass measurements suggest that genetic improvement for steer carcass traits can be achieved by using yearling bull US measurements as selection criteria. They believe yearling US measurements of carcass traits could be used under the assumption that genetic differences detected with US at yearling will be reflected in carcasses of finished

progeny. This data suggests the importance of reliable heritability ($\mathbf{h_2}$) and genetic correlation ($\mathbf{r_g}$) estimates between carcass measurements on finished steers and US measurements on yearling bulls. The importance of reliable $\mathbf{h_2}$ and $\mathbf{r_g}$ is compounded by the fact that in previous studies the results have been contradictory. They concluded there are high additive genetic correlation estimates between the steer and bull traits indicating that genetic progress can be made in actual carcass traits with US based selection. It was also concluded that by using a yearling bull's US measurements to aid in mating selections can affect the rate of genetic change, by influencing the generation interval, accuracy of selection, and selection intensity. In another study by Moser et al. (1998) there was a positive $\mathbf{r_g}$ between carcass and US measured traits in a population of Brangus cattle. However, the findings of these studies were in contrast to the earlier findings of Arnold et al. (1991) in a study of carcass and US measurements in Hereford cattle.

Another application for real-time ultrasound (RTU) is its use in national cattle evaluation programs, where yearling ultrasound-predicted percentage of intramuscular fat (UPFAT) and other ultrasound-measured traits are used to compute animal EPDs. Hassen et al. (2003) felt that these evaluation programs could benefit from additional research on genetic and residual (co)variances for UPFAT and other ultrasound-measured composition traits. Hassen et al. also noted the importance of accuracy of the yearling ultrasound measurements compared with those taken on animals at younger or older ages. Such data would be beneficial in terms of practical application of ultrasound scanning.

As the beef industry depends more on a value-based marketing system, accurate selection of parent animals and evaluation of genetic responses to selection become more crucial to producers (Hassen et al., 2003). The genetic and residual variance components for UPFAT and other ultrasound measures in young beef breeding cattle need to be determined for a wide range of ages and production conditions (Hassen et al., 2003).

In a study, conducted by Hassen et al. (2003), estimated variance components, heritability, and repeatability of serially measured UPFAT data in purebred Angus bulls and heifers, it was found that heritability and repeatability of ultrasound-predicted percentage of intramuscular fat in young Angus cattle are optimally collected at approximately 52 wk through at least 63 wk of age. This study set the standard practice of collecting US measures of yearling bulls and 13- to 14-mo-old heifers and using acceptable images to evaluate the compositional genetic potential of future generations of Angus seedstock. The study suggests a large proportion of the phenotypic variance at earlier ages is not genetic; selection at these ages may slow genetic progress. Additionally, the standard age set for collection of US measures in British breeds is assumed to be correct for continental cattle as well. The optimum age for collection of US measures in continental cattle is currently being analyzed by Burns et al. (2006). It is generally agree that more information on the correct age for US measures in continental influenced cattle needs to be obtained if US is to gain widespread acceptance for genetic improvement.

Evaluation of Carcass EPDs Using Live and Carcass Data

Cattle breed associations are realizing the usefulness of RTU measures of body composition from yearling bulls and heifers in combination with live weights to conduct national cattle genetic evaluations for carcass merit. The data collected in these evaluations are used to adjust carcass data collected on progeny of sires. Including live animal data allows evaluation of a larger, more random sample of the population while increasing the accuracy with which replacements can be evaluated.

Crews et al. (2003) reported genetic parameter estimates among live animal measurements of yearling replacements and carcass traits of market progeny in the Simmental breed. In multivariate carcass merit evaluations, carcass and live animal measures were considered separate but correlated. Through this additive relationship and genetic correlation, such an evaluation results in EPDs for both live and carcass traits (Crews et al., 2003). Crews and Kemp (2002) found including live animal data with carcass data resulted in the most significant accuracy increases for EPDs of young non-parent replacements without progeny carcass data.

Literature based on the relationship between sire carcass EPDs and progeny phenotype is lacking, but obvious differences in sire carcass EPDs are related to differences in progeny phenotypes at or near theoretical expectation in Charolais were described by Crews in 2002. However, the relationship between parent carcass EPDs based on combinations of progeny live and/or carcass data has been only minimally investigated. Genetic (co)variance estimates in the report by Crews et al. (2003) and other recent studies (Reverter et al., 2000; Crews and Kemp, 2001; Devitt and Wilton,

2001) indicate that mean and variance differences between carcass traits and their live animal indicators suggest that EPDs based on combinations of carcass and/or live animal data should be compared.

This information lead to a study by Crews et al. (2003) where carcass EPDs estimated using either live or carcass data alone and in combination were compared and used to estimate the EPDs influences on differences in progeny phenotypes. They found that beef carcass EPDs derived from a combination of live animal and carcass data had a larger range and were more reliable for a larger sample of animals than carcass EPDs based on live or carcass data alone. Sire EPDs based on only yearling live animal data differed from those derived only on carcass data and from those derived on both types of data due to: differences in age at data collection, gender, and variance components. Results of this study demonstrated carcass phenotypes of progeny exhibited a close linear relationship with sire EPD based on both carcass data alone and a combination of live animal and carcass data. The linear association between carcass phenotype of progeny and sire EPD based on live animal data tended to be improved by scaling the live data EPD to a carcass trait basis. The study also determined that, due to the increased mean accuracy, EPDs based on both live animal and carcass data are optimal for genetic evaluation of beef carcass merit.

EPDs and Carcass Manipulation

The United States cattle feeding industry has developed the method of feeding beef cattle to a level of external fat that provides a reasonable chance for adequate marbling

and a desirable dressing percentage. It is also becoming more apparent that consumers desire lean beef without sacrificing palatability. One approach is to trim excess fat from carcasses, but as found in the 1991 National Beef Quality Audit (Griffin, 1992; Savell, 1992) excessive fat was reducing the value of beef carcasses up to $190.00 each. Therefore, it seems to be more realistic to reduce fatness through genetic manipulation. However, as the beef industry moves toward producing more efficient cattle with higher red meat yield, care must be taken to avoid compromising palatability, an important trait to consumers.

Several investigators have observed genetic differences in partitioning of fat among the major carcass depots in cattle (Charles and Johnson, 1976; Kempster et al., 1976; Tatum et al., 1986). Lamb et al. (1990); and Arnold et al. (1991) suggested low genetic correlations between marbling (M) and fat deposition rate in the various depots. Thus it was theorized by Gwartney et al. (1996) that selection of sires with a high EPD for M could result in progeny with lower amounts of subcutaneous and seam fat at a constant M score or more M at a constant fat thickness or carcass weight. The object of the study was to determine the effect of sire M EPD on M score, palatability and carcass fatness of progeny. The data suggests that it is possible to reduce carcass fatness (subcutaneous and intramuscular) while maintaining M and eating quality of beef by using M EPD when selecting sires. Producers who want to increase the percentage of cattle grading choice or to minimize the amount of subcutaneous fat present when sufficient marbling for the choice grade is achieved could benefit from selecting sires with high M EPD.

Many U.S. beef breed associations have carcass EPDs available for producers to use as a selection tool. However, care needs to be taken to avoid single trait selection in regards to carcass traits as single trait selection could possibly affect other production traits negatively; specifically, the relationship of marbling to growth and other carcass traits. Previous literature indicates that the genetic correlation of marbling score and fat thickness or live growth traits is low (Koch et al., 1982; Benyshek et al., 1988; Shimada and Willham, 1992; Wilson et al., 1993). In a study by May et al. (1992), M score was the highest correlated trait with the palatability attributes amongst carcass grade traits, and M score was moderately related to taste panel tenderness (r=.51) and shear force (r=-.61) in Angus x Hereford steers. Furthermore, intramuscular marbling, which aids in determining USDA quality grade, is important to the pricing of beef. Vieselmeyer et al. (1996) evaluated the impact of the EPD for marbling on progeny production and carcass (USDA grade) traits. In that study, Vieselmeyer et al. demonstrated Angus sires can be selected to produce progeny that have increased ability to marble without increasing subcutaneous fat. These data would suggest it is possible to enable cattle to have higher efficiencies, more specifically grade Choice with fewer days on feed and potentially reduce the amount of external fat produced and subsequently trimmed from the carcass or retail cuts. The current beef producer-packer marketing system is primarily based on weight, encouraging the production of heavier, fatter carcasses (Vieselmeyer et al., 1996). A value-based marketing system focusing on quality and yield would allow the genetic potential of carcass merit to be reflected in economic terms through all areas of the beef industry.

The Importance of Crossbreeding

Heterosis achieved through continuous crossbreeding can be used to increase weight of calf weaned per cow exposed to breeding by 20% (Gregory and Cundiff, 1980). When focusing on breed type one would expect to see some differences among breeds for most bioeconomic traits, or traits that are of economic importance to the beef industry such as marbling, longissimus muscle area and rib fat. So when implementing a rotational crossbreed system there will be a fluctuation in breed composition between generations which can result in considerable variation among both cows and calves in level of performance for major bioeconomic traits. This variability can be reduced if breeds with similar performance characteristics are used in the rotation. However, use of breeds with similar performance characteristics would reduce the amount of breed complementarity that will be observed possibly slowing the progress of specific production objectives and hindering marketing situations. Retention of initial (F1) heterozygosity after crossing and subsequent tandem (*inter se*) mating within the crosses is proportional to $(n - 1)/n$, where n breeds contribute equally to the foundation (Wright, 1922; Dickerson, 1969, 1973). When breeds used in the foundation of a composite breed do not contribute equally, percentage of mean F1 heterozygosity retained is proportional to $1 -$ sum P^2 where Pi is to the fraction of each of n contributing breeds to the foundation of a composite breed (Dickerson, 1973). This loss of heterozygosity occurs between the F1 and F2 generations, and if inbreeding is avoided, further loss of heterozygosity in inter se-mated populations does not occur (Wright, 1922; Dickerson, 1969, 1973).

Gregory et al., (1994) conducted a study to: 1) evaluate differences among parental breeds in growth, carcass and meat traits of castrated males finished on two levels of dietary energy density, and 2) estimate retention of combined individual and maternal heterosis in the F3 generation for growth, carcass, and meat traits in inter se-mated composite populations of beef cattle. They found large differences among breeds of cattle in lean tissue growth rate and in carcass composition. These differences provide an opportunity to use breed complementarities to meet a wide range of production and market requirements. The study also found variations in dietary energy density may be used to alter lean tissue growth rate and deposition of carcass fat in a wide range of biological types of cattle. The effects of dietary energy density varying from 2.82 to 3.07 Mcal of ME/kg of dry matter did not differ greatly among breeds that vary from 21.1 to 31.8 carcass fat and from 53.8 to 64.6% carcass lean. This supports the theory that different breed types response in performance can vary significantly on comparable diets. Therefore, breed complementarity can be a useful tool in providing an opportunity to use breed differences to achieve and maintain optimum additive genetic (breed) composition for carcass composition traits and to use heterosis to increase lean tissue growth rate and or to increase rate of fat deposition.

Conclusion and Objectives

The use of crossbreeding is an invaluable tool to today's beef industry. Crossbreeding allows producers to utilize breed differences to exploit breed

complementarity and heterosis. Heritability estimates for carcass traits can be expected to be moderate to high. Thus, selection based on accurate carcass traits can be expected to be rather reliable. The level of heterosis expressed for a given trait is inversely related to heritability for that trait, so lowly heritable traits such as female fertility and longevity experience more benefits from heterosis, and highly heritable traits like those that affect carcass composition experience fewer benefits from heterosis. So the question can be asked, if carcass composition can only minimally be affected through cross breeding and heterosis, at what level of selection will the most rapid genetic progress be made to improve carcass composition? More specifically, how can it affect marbling and ribeye area in Gelbvieh and Gelbvieh hybrid cattle? Thus the objective of this study is to determine how accurately sire EPDs, ultrasound data and progeny carcass data predict phenotype of offspring of these breeds, and at what level of selection will the most rapid genetic advancements be made.

CHAPTER III

MATERIALS AND METHODS

Sampling Methods

The goal of this project was to establish whether or not a bull's carcass expected progeny difference (EPD) accurately depict his breeding value for the carcass traits he will pass on to his offspring. Bull's EPD percentile ranks were compared against his progeny's ultrasound or carcass measurements. This study was designed to answer the following questions: 1) at what percentile rank level of selection can changes be made to ultrasound intramuscular fat (UIMF), ultrasound longissimus muscle area (ULMA), and ultrasound rib fat (URF) or carcass intramuscular fat (CIMF), carcass longissimus muscle area (CLMA) and carcass rib fat (CRF) scores in offspring, and 2) Does intense selection pressure make more rapid genetic progress in subsequent generations? Progeny ultrasound or carcass data (intramuscular fat, longissimus muscle area and rib fat) of yearling bulls, heifers and steers was provided from the American Gelbvieh Association (AGA). All data from 1973 to 2003 were included. Gelbvieh, Red Angus Balancers™ (Red Angus/Gelbvieh cross) and Angus Balancers™ were included in the study. All offspring used have known sires and breed percentages. Number of sires included 1376 Gelbvieh, 78 Red Angus and 287 Angus bulls. Ultrasound images were generated using an Aloka 500V with a 17.5 cm probe scanning between the 12^{th} and 13^{th} rib. One technician generated measurements for IMF, LMA and RF on an

individual animal, multiple technicians were used across the country. Multiple technicians was not considered a significant source of variation as all technicians were trained by The National CUP (Centralized Ultrasound Processing) Lab and Technology Center. The CUP Lab is also responsible for the unbiased interpretation of the ultrasound data. Carcass measurement for IMF, LMA and RF were taken in commercial plants by trained personnel. The EPD information was provided by the AGA. Red Angus and Angus EPDs were converted to a Gelbvieh EPD base by the AGA. Records included all EPD measures taken according to AGA requirements.

Because a sire's EPDs can change over time, the most current spring 2007 EPDs were used in the study. Sires were then ranked for carcass traits from highest to lowest and his EPDs for IMF, LMA and RF were compared to trait specific percentile rankings. Once bulls were ranked, they were placed into 12 categories based on their IMF, LMA and RF EPDs. That rank was then compared to it's progeny's ultrasound or carcass IMF score, LMA and RF thickness in cm. Groups were sorted by the year the sire produced the progeny, but also analyzed without a variable for year. Embryo transfer calves were treated equally among contemporaries within a year.

Grouping for bull rank (IMF, LMA and RF EPDs) was determined from the breed association's percentile rankings chart. Twelve groups were chosen arbitrarily from 23 total groups provided by the AGA. Groups included the top 1, 2, 3, 4, 5, 10, 20, 30, 40, 50, 60, and 75 percentile ranks for all three carcass EPDs. These 12 groups were used for all three sire groups in the study.

Data Analyses

The data were analyzed as a completely randomized design (CRD) with a sampling error. Once data were obtained and studied, it was realized that treatments were assigned to experimental units completely at random. Sire group rank was the treatment. Experimental units were the progeny of a given sire. Treatments or sires were also randomly assigned to cows to produce a calf that was the experimental unit. This experimental design also partitions the total variation of the dependent variable into two independent and additive components corresponding to "between treatment" variation and "within treatment" variation. Thus if there is more variation between treatments than within treatments, treatment means differ from each other. Several samples were recorded for each experimental unit. The variation in progeny phenotype from the same sire group was not treated as experimental error. Therefore, the variation between specific measurements (i.e. UIMF, ULMA, URF, CIMF, CLMA and CRF) within each experimental unit was not experimental error but rather an estimate of sampling error. All data were subject to ANOVA using SAS rank comparisons using Proc Mixed procedures.

CHAPTER IV

RESULTS AND DISCUSSION

Intramuscular Fat

Ultrasound. The Angus group sire EPD ranked IMF compared to progeny UIMF are shown in table 1.1. Comparing sire IMF rank to progeny, UIMF scores were significant in yr 01 ($P < 0.05$). The red Angus group sire EPD ranked IMF compared to progeny UIMF are shown in table 1.2. Comparing sire IMF rank to progeny, UIMF scores were not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$). The Gelbvieh group sire EPD ranked IMF compared to progeny UIMF are shown in table 1.3. Sire IMF rank compared to progeny, UIMF scores were also not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$).

Carcass. The Angus group sire EPD ranked IMF compared to progeny CIMF are shown in table 1.4. Comparing sire IMF rank to progeny, CIMF scores were not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$). The Red Angus group sire EPD ranked IMF compared to progeny CIMF are shown in table 1.5. Comparing sire IMF rank to progeny, CIMF scores were not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$). The Gelbvieh group sire EPD ranked IMF compared to progeny CIMF are shown in table 1.6. Comparing sire IMF rank to progeny, CIMF scores were significant in yrs 89, 90, 94, 95 96, 98, 99, 00, 01, and when not blocked by year ($P < 0.05$).

Longissimus Muscle

Ultrasound. The Angus group sire EPD ranked LMA compared to progeny ULMA are shown in table 1.7. Comparing sire LMA rank to progeny, ULMA in cm, was not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$). The Red Angus group sire EPD ranked LMA compared to progeny ULMA are shown in table 1.8. Comparing sire LMA rank to progeny, ULMA in cm, was not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$). The Gelbvieh group sire EPD ranked LMA compared to progeny ULMA are shown in table 1.9. Comparing sire LMA rank to progeny, ULMA in cm, was not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$).

Carcass. The Angus group sire EPD ranked LMA compared to progeny CLMA are shown in table 1.10. Comparing sire LMA rank to progeny, CLMA in cm, was not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$). The Red Angus group sire EPD ranked LMA compared to progeny CLMA are shown in table 1.11. Comparing sire LMA rank to progeny, CLMA in cm, was not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$). The Gelbvieh group sire EPD ranked LMA compared to progeny CLMA are shown in table 1.12. Comparing sire LMA rank to progeny, CLMA in cm, was significant in yrs 94, 96, and 98 and when not blocked by year ($P < 0.05$).

Rib Fat

Ultrasound. The Angus group sire EPD ranked RF compared to progeny URF are shown in table 1.13. Comparing sire RF rank to progeny, URF in cm, was significant in yrs 99 and 00 ($P < 0.05$). Red Angus group sire EPD ranked RF compared to progeny URF are shown in table 1.14. Comparing sire RF rank to progeny, URF in cm, was significant in yrs 02, 03 and when not blocked by year ($P < 0.05$). The Gelbvieh group sire EPD ranked RF compared to progeny URF are shown in table 1.15. Comparing sire RF rank to progeny, URF in cm, was significant in yrs 99, 01 and when not blocked by year ($P < 0.05$).

Carcass. The Angus group sire EPD ranked RF compared to progeny CRF are shown in table 1.16. Comparing sire RF rank to progeny, CRF in cm, was not significant across all 12 groups when blocked by year and when not blocked by year ($P > 0.05$). The Red Angus group sire EPD ranked RF compared to progeny CRF are shown in table 1.17. Comparing sire RF rank to progeny, CRF in cm, was significant when not blocked by year ($P > 0.05$). The Gelbvieh group sire EPD ranked RF compared to progeny CRF are shown in table 1.18. Comparing sire RF rank to progeny, CRF in cm, was significant in yrs 82, 92, 95, 96, 02 and when not blocked by year ($P < 0.05$).

The results of the current study are similar to a study performed by Crews et al. (2004) which also dealt with sire EPDs and the effect they had on selection. In that study carcass traits of 824 steers and heifers were evaluated to determine the impact that a sire's carcass EPD had on progeny phenotype examined. Comparisons indicate that among the data used to compute EPDs, carcasses tend to have lower marbling scores

(5.04 vs. 5.24) compared to data added after the study of Crews et al. (2003); although these differences may be considered minor (Crews et al., 2004). The study used three models to quantify the association between progeny carcass phenotype and sire EPD, including: a live data model (L) containing scan weight, ultrasound fat thickness, longissimus muscle area, and percentage intramuscular fat from yearling Simmental bulls and heifers. The carcass data model (C) contained hot carcass weight, fat thickness, longissimus muscle area, and a marbling score from Simmental sired steers and heifers. The combined model (F) contained live animal and carcass data as separate but correlated traits. The study found that including carcass data along with live data in the calculation of sire EPDs resulted in a more reliable and accurate EPD.

In the past the American Gelbvieh Association has used progeny carcass data to adjust sire EPDs. This current study can aid the AGA in the development of ultrasound EPDs. Additionally, by including live and carcass data in the model for an EPD there will be an increase in the reliability and accuracy of EPDs. This will speed up genetic progress of future generations in the Gelbvieh breed.

CHAPTER V

IMPLICATIONS

Intramuscular Fat

This study indicates a significant difference between EPD IMF group sire ranks to actual progeny UIMF scores in yr 01 of the Angus data set shown in table 1.1. Interestingly the Angus data in table 1.1 implies that by selecting sires with marbling EPDs closer to breed average, rather then extreme outliers, had a more significant effect on increasing marbling scores of ultrasounded progeny. However the Red Angus data in table 1.2 and the Gelbvieh data in table 1.3 did not yield any information suitable to make any similar conclusions.

There was no significant difference between EPD IMF group sire ranks to actual progeny CIMF scores of Angus and Red Angus sired calves shown in tables 1.4 and 1.5. This may probably be attributed to the fact that the two sire groups have only recently been heavily used in the production of Balancers™. It will be interesting to see the impact Angus and Red Angus have on marbling in the Gelbvieh breed in future generations particularly as carcass merit has become a large priority in all three breeds included in the study. The study indicates that there were significant differences between EPD IMF group sire ranks to actual progeny CIMF scores in yrs 89, 90, 94, 95, 96, 98, 99, 00, 01, and when not blocked by year of the Gelbvieh data set shown in table 1.6. From these data, one would expect increases in marbling scores of fed progeny when choosing sires that ranked in the upper quartile. Equally intriguing, no sire group

appeared to have a large advantage over another in regards to fed progeny marbling scores.

Longissimus Muscle Area

This study indicates there is was a significant difference between EPD LMA group sire rank to actual progeny, ULMA in cm, for the Angus (data set shown in table 1.7) when the data is not blocked by year. These data suggest that, over time progeny ULMA has been increased if using sires from group 8. There is no significant difference between EPD LMA group sire ranks to actual progeny, ULMA in cm, for the Red Angus and Gelbvieh (data sets shown in table 1.8 and 1.9), suggesting no useful correlation between sire EPD and progeny ULMA.

The data also suggests that there is no significant difference between EPD LMA group sire ranks to actual progeny, CLMA in cm, for Angus and Red Angus (data sets shown in tables 1.10 and 1.11). Interestingly, the two English sire groups when converted to a Gelbvieh base EPD, did not have any data points in the upper ten percent for LMA EPD. Further, data from this study indicates there is a significant difference between EPD LMA group sire ranks to actual progeny, CLMA in cm, for the Gelbvieh sire group in yrs 94, 96, 98 and when not blocked by year (shown in table 1. 12). The three years of data that showed significant results suggests one could make expected increases in CLMA of fed progeny if sires were selected from the upper fifty percent, and over time selecting sires from the upper fifty percent increases CLMA.

Rib Fat

Data from this study indicates there is significant differences between EPD RF group sire ranks to actual progeny URF in the Angus, Red Angus and Gelbvieh data sets shown in tables 1.13, 1.14 and 1.15. Interestingly all the sires present in the study either fell in the top 1% or bottom 75% for rib fat thickness in both ultrasound and carcass data sets. The Angus data set demonstrated significant differences in yrs 99 and 00 where one could accurately increase RF by selecting sires from Gp1 and sires from Gp12 produced lower RF. The Red Angus data set showed significant differences in yrs 02, 03, and when not blocked by year, where one could accurately increase RF by selecting sires from Gp1 and sires from Gp12 produced lower RF. The Gelbvieh data set showed significant differences in yrs 99, 01 and when not blocked by year, where one could accurately increase RF by selecting sires from Gp1 and sires from Gp12 produced lower RF.

This study indicates there are no significant differences between EPD RF group sire ranks to actual progeny CRF in the Angus (data sets shown in tables 1.16). The Red Angus data set indicates there are was significant differences between EPD RF group sire rank to actual progeny CRF when not blocked by year (shown in table 1.17), suggesting that, over time, CRF can be increased in progeny by selecting sires from group 1 rather than Group 12. This study indicates there is a significant difference between EPD RF group sire ranks to actual progeny CRF in the Gelbvieh data (shown in table 1.18). The Gelbvieh data set demonstated significant differences in yrs 82, 92, 95, 96, 02, and when not blocked by year, where one could accurately increase RF by selecting sires from Gp1 and sires from Gp12 produced lower RF.

The data suggests that selecting for carcass traits in sires does allow genetic progress. Unfortunately these results could not be translated to mating selections with expected precise results in progeny. This can be explained by the findings of Bullock et al. (2000) which states that an individual expresses genetic variation in its progeny by passing a different sample of genetics to each offspring. So the large variation in genetics of the cattle included in this study is potentially responsible for the large variation seen in this research.

This study interestingly demonstrated that most sires either fell into the top 1% or lower 75% for RF. The economical importance of RF should not be over looked. Rib fat which has been widely used as an external indicator of market readiness, and has also been shown to have an impact on yield grade. Thus, it would be interesting to see if these predictable changes that can be made by selecting sires to increase rib fat could impact the economic values of carcasses and whether the increase in RF resulted in a subsequent increase or decrease of IMF. This theory is supported by similar research conducted by Vieselmeyer et al. (1996), where Angus sires could be selected to produce progeny that have increased ability to marble without increasing subcutaneous fat

This study also suggests an impact that progeny testing can have on sire EPDs, and proves that progeny testing yields valuable information which can greatly impact the change and accuracies of proven and unproven sire EPDs alike. While ultrasound did not show significant impact upon selection opportunities within this study ultrasound is a less expensive replacement for progeny testing. Progeny testing is more expensive and time consuming then ultrasound but the two combined can allow for the most accurate and complete evaluation of potential elite sires. More research should be conducted to

determine at what level of selection the most rapid genetic improvement can be made, and whether a sires EPD accuracies my play a role in the number of head needed to achieve significant results and if these accuracies yield more significant results.

LITERATURE CITED

Arnold, J. W., J. K. Bertrand, L. L. Benyshek, and C. Ludwig. 1991. Estimates of genetic parameters for live animal ultrasound, actual carcass data, and growth traits in beef cattle. J. Anim. Sci. 69:985-992.

Arnold, J. W., J. K. Bertrand, L. L., Benyshek, J. W. Comerford, and T.E. Kiser. 1990. selection for low birth weight and high yearling weight in Angus beef cattle. Livest. Prod. Sci. 25:31-41.

Baud, S., C. M. Wade, and M. E. Goddard. 1998. An evaluation of the use of ultrasound scanning to predict carcass traits in steers grain fed for the Japanese market. Aust. J. Agric. Res. 49:147-152.

Bergen, R. D., J. J. McKinnon, D. A. Christensen, and N. Kohle. 1996. Prediction of lean yield in yearling bulls using real-time ultrasound. Can. J. Anim. Sci. 76:305-311.

Brethour, J. R., 1990. Relationship of ultrasound speckle to marbling score in cattle. J. Anim. Sci. 68:2603-2613.

Bullock, K. D., F. A. Thrift, D. K. Aaron, and J. K. Bertrand. 2000. Relationship between a bull's parental genetic merit difference and subsequent progeny trait variability in Angus, Gelbvieh, and Limousin cattle. J. Anim. Sci. 78:2540-2546.

Crews, D. H., E. J. Pollak, and R. L. Quaas. 2004. Evaluation of Simmental carcass EPD estimated using live and carcass data. J. Anim. Sci. 82:661-667.

Crews, D. H., Jr. 2002. The relationship between beef sire carcass EPD and progeny phenotype. Can. J. Anim. Sci. 82:503–506.

Crews, D. H., Jr., E. J. Pollak, R. L. Weaber, R. L. Quaas, and R. J. Lipsey. 2003. Genetic parameters for carcass traits and their live animal indicators in Simmental cattle. J. Anim. Sci. 81:1427-1433.

Crews, D. H., Jr. and R. A. Kemp. 2002. Genetic evaluation of carcass yield using ultrasound measures on young replacement beef cattle. J. Anim. Sci. 80:1809-1818.

Crews, D. H., Jr. and R. A. Kemp. 2001. Genetic parameters for ultrasound and carcass measures of yield and quality among replacement and slaughter beef cattle. J. Anim. Sci. 79:3008-3020.

Devitt, C. J. B., and J. W. Wilton. 2001. Genetic correlation estimates between ultrasound measurements on yearling bulls and carcass measurements on finished steers. J. Anim. Sci. 79:2790-2797.

Gregory, K.E., L.V. Cundiff, R.M. Koch, M.E. Dikeman, M. Koohmaraie. 1994. Breed effects and retained heterosis for growth, carcass, and meat traits in advanced generations of composite populations of beef cattle. J. Anim. Sci. 72:833-850.

Gregory, K.E., L.V. Cundiff, R.M. Koch. 1995. Genetic and phenotypic (co)variances for growth and carcass traits of purebred and composite populations of beef cattle. J. Anim. Sci. 73:1920-1926.

Gwartney, B.L., C.R. Calkins, R.J. Rasby, R.A. Stock, B.A. Vieselmeyer, J.A. Gosey. 1996. Use of expected progeny differences for marbling in beef: II. Carcass and palatability traits. J. Anim. Sci. 74:1014-1022.

Hassen, A., D. E. Wilson, V. R. Amin, G. H. Rouse, and C. L. Hays. 2001. Predicting percentage of intramuscular fat using two types of real-time ultrasound equipment. J. Anim. Sci. 79:11-18.

Hassen, A., D. E. Wilson, and G. H. Rouse. 1998. Evaluation of carcass, live, and real-time ultrasound measures in feedlot cattle: I. assessment of sex and breed effects. J. Anim. Sci. 76:273-282.

Hassen, A., D. E. Wilson and G. H. Rouse. 2003. Estimation of genetic parameters for ultrasound-predicted percentage of intramuscular fat in Angus cattle using random regression models. J. Anim. Sci. 81:35-45.

Herring, W. O., D. C. Miller, J. K. Bertrand, and L. L. Benyshek. 1994. Evaluation of machine, technician, and interpreter effects on ultrasonic measures of backfat and longissimus muscle area in beef cattle. J. Anim. Sci. 72:2216-2226.

Lamb, M. A., O. W. Robison, and M. W. Tess. 1990. Genetic Parameters for Carcass Traits in Hereford Bulls. J. Anim. Sci. 68:64-69.

Lorenzen, C. L., D. S. Hale, D. B. Griffin, J. W. Savell, K. E. Belk, T. L. Frederick, M. F. Miller, T. H. Montgomery, and G. C. Smith. 1993. National beef quality audit: survey of producer-related defects and carcass quality and quantity attributes. J. Anim. Sci. 71:1495-1502.

Morgan, J. B., J. W. Savell, D. S. Hale, R. K. Miller, D. B. Griffin, H. R. Cross, and S. D. Shackelford. 1991. National beef tenderness survey. J. Anim. Sci. 69:3274-3283.

Moser, D. W., J. K. Bertrand, I. Misztal, L. A. Kriese, and L. L. Benyshek. 1998. Genetic parameter estimates for carcass and yearling ultrasound measurements in Brangus cattle. J. Anim. Sci. 76:2542-2548.

Perkins, T. L., R. D. Green, and K. E. Hamlin. 1992. Evaluation of ultrasonic estimates of carcass fat thickness and longissimus muscle area in beef cattle. J. Anim. Sci. 70:1002-1010.

Reverter, A., D. J. Johnston, H. U. Graser, M. L. Wolcott, and W. H. Upton. 2000. Genetic analyses of live-animal ultrasound and abattoir carcass traits in Australian Angus and Hereford cattle. J. Anim. Sci. 78:1786-1795.

Sapp, R. L., J. K. Bertrand, T. D. Pringle and D. E. Wilson. 2002. Effects of selection for ultrasound intramuscular fat percentage in Angus bulls on carcass traits of progeny. J. Anim. Sci. 80:2017-2022.

Savell, J. W., J. J. Harris, H. R. Cross, D. S. Hale, and L. C. Beasley. 1991. National Beef Market Basket Study. J. Anim. Sci. 69:2883-2893.

Vieselmeyer, B.A., R.J. Rasby, B.L. Gwartney, C.R. Calkins, R.A. Stock, J.A. Gosey. 1996. Use of expected progeny differences for marbling in beef: I. production traits. J. Anim. Sci. 74:1009-1013.

Wilson, D. E., R. L. Willham, S. L. Northcutt, and G. H. Rouse. 1993. Genetic parameters for carcass traits estimated from Angus field records. J. Anim. Sci. 71:2365-2370.

APPENDIX

TABLES

Table 1.1 Progeny ultrasound intramuscular fat % by Angus bull EPD grouping

AN RIMF_S TO IMF_P						
Yr	99	00	01	02	03	all yrs
Gp 1	2.22	.	2.08[a]	2.67	3.21	2.50
Gp 2	2.62	3.71	3.22[b]	2.73	3.68	3.11
Gp 3	2.60	4.56	2.97[a,b]	2.90	3.15	3.04
Gp 4	4.56	2.38	3.30[b,c]	2.89	3.04	3.10
Gp 5	.	.	3.67[b,c]	2.81	2.65	3.12
Gp 6	2.78	3.25	3.10[b]	2.89	3.12	3.01
Gp 7	2.92	3.39	3.94[c]	2.82	2.86	3.08
Gp 8	2.62	.	2.89[a,b]	3.29	2.78	2.98
Gp 9	.	3.48	2.17[a,b]	3.10	.	3.12
Gp 10	2.74	3.81	.	3.74	.	3.50
Gp 11	2.26	2.84	.	2.34	3.04	2.66
Gp 12	2.67	3.34	.	3.08	3.45	3.19

[a,b,c] IMF means within a column without common superscripts differ P > 0.05
Gp=Group; Yr=Year; AN=Angus Breed; RIMF_S=Rank Intramuscular Fat Sire; IMF_P=Intramuscular Fat Progeny

Table 1.2 Progeny ultrasound intramuscular fat % by Red Angus bull EPD grouping

RA RIMF_S TO IMF_P						
Yr	99	00	01	02	03	all yrs
Gp 1	2.97	3.22	.	3.23	2.97	3.13
Gp 2	3.02	3.05	2.89	2.46	2.59	2.82
Gp 3	3.31	.	3.44	3.47	3.10	3.32
Gp 4	.	.	2.72	2.68	.	2.71
Gp 5	.	.	2.80	3.05	1.92	2.72
Gp 6	2.37	3.18	3.18	2.82	2.89	2.95
Gp 7	3.17	3.28	3.49	2.63	3.11	3.02
Gp 8	.	2.96	.	2.85	3.84	3.04
Gp 9	.	.	.	.	.	.
Gp 10	.	.	.	2.99	.	2.99
Gp 11	2.44	3.27	.	.	2.21	2.66
Gp 12	2.99	2.66	.	.	.	2.70

P = 0.05
Gp=Group; Yr=Year; RA=Red Angus Breed; RIMF_S=Rank Intramuscular Fat Sire; IMF_P=Intramuscular Fat Progeny

Table 1.3 Progeny ultrasound intramuscular fat % by Gelbvieh bull EPD grouping

G RIMF_S TO IMF_P						
Yr	99	00	01	02	03	all yrs
Gp 1	2.68	2.58	2.83	2.48	2.85	2.77
Gp 2	2.65	2.77	2.50	2.60	3.02	2.70
Gp 3	2.45	2.74	2.40	2.16	2.38	2.33
Gp 4	.	3.41	2.04	2.16	2.53	2.55
Gp 5	2.20	2.08	2.61	2.64	2.54	2.62
Gp 6	2.52	2.71	2.80	2.59	2.77	2.66
Gp 7	2.56	2.69	2.65	2.47	2.64	2.62
Gp 8	2.52	2.75	2.73	2.44	2.81	2.68
Gp 9	2.76	2.63	2.70	2.78	2.96	2.74
Gp 10	2.54	2.91	2.56	2.26	2.40	2.57
Gp 11	2.51	2.67	2.65	2.42	2.43	2.53
Gp 12	2.52	2.64	2.62	2.42	2.55	2.54

P = 0.05
Gp=Group; Yr=Year; G=Gelbvieh Breed; RIMF_S=Rank Intramuscular Fat Sire; IMF_P=Intramuscular Fat Progeny

Table 1.4 Progeny carcass intramuscular fat % by Angus bull EPD grouping

AN RIMF_S TO IMF_P							
Yr	96	97	98	99	00	01	all yrs
Gp 1	5.12	6.60	5.33	4.10	4.45	5.27	5.27
Gp 2	5.38	6.23	4.87	5.50	5.30	5.57	5.52
Gp 3	4.90	5.42	5.63	.	4.60	7.30	5.57
Gp 4	5.50	5.90	5.50	6.10	5.30	6.53	5.79
Gp 5	5.03	6.50	5.10	.	5.20	6.10	5.47
Gp 6	5.12	5.33	5.45	5.51	5.56	6.51	5.59
Gp 7	5.77	5.85	5.31	6.19	4.90	6.17	5.78
Gp 8	5.55	6.48	4.78	4.71	.	5.37	5.42
Gp 9	5.80	6.00	5.08	.	.	.	5.32
Gp 10	5.20	.	5.00	.	.	6.50	5.56
Gp 11	.	5.63	5.60	.	.	7.00	5.99
Gp 12	.	5.60	5.38	.	.	.	5.48

P = 0.05
Gp=Group; Yr=Year; AN=Angus Breed; RIMF_S=Rank Intramuscular Fat Sire; IMF_P=Intramuscular Fat Progeny

Table 1.5 Progeny carcass intramuscular fat % by Red Angus bull EPD grouping

RA RIMF_S TO IMF_P				
Yr	96	97	02	all yrs
Gp 1	.	.	.	.
Gp 2	.	.	5.64	5.63
Gp 3	.	6.23	.	6.22
Gp 4	6.10	.	.	6.10
Gp 5	.	.	.	.
Gp 6	.	.	.	.
Gp 7	.	5.37	.	5.38
Gp 8	4.70	.	.	4.70
Gp 9	.	.	.	.
Gp 10	.	.	.	.
Gp 11	.	5.75	.	5.75
Gp 12	.	.	5.47	5.46

P = 0.05
Gp=Group; Yr=Year; RA=Red Angus Breed; RIMF_S=Rank Intramuscular Fat Sire; IMF_P=Intramuscular Fat Progeny

Table 1.6 Progeny carcass intramuscular fat % by Gelbvieh bull EPD grouping

G RIMF_S TO IMF_P									
Yr	73	74	81	82	84	85	86	87	88
Gp 1	.	6.42	.	5.35	5.18	.	.	.	.
Gp 2	.	.	.	.	5.00	.	.	.	.
Gp 3	.	5.30	5.75	.	.	.	.	.	4.89
Gp 4	5.40	4.82	.	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.	.	.	.
Gp 6	5.24	5.39	.	4.91	.	.	.	.	.
Gp 7	.	.	.	5.07	5.00	.	.	.	4.91
Gp 8	.	.	.	.	.	4.38	4.75	.	4.90
Gp 9	.	5.22	.	.	.	.	5.18	6.10	.
Gp 10	5.25	4.67	.	.	.	.	.	.	.
Gp 11	.	.	.	4.80	4.70	.	.	4.77	4.80
Gp 12	4.86	4.88	.	4.43	4.38	5.25	4.33	4.83	4.86

[a,b,c] IMF means within a column without common superscripts differ P > 0.05
Gp=Group; Yr=Year; G=Gelbvieh Breed; RIMF_S=Rank Intramuscular Fat Sire
IMF_P=Intramuscular Fat Progeny

Table 1.6 continued

Yr	89	90	91	92	93	94	95	96
Gp 1	5.50[a,b,c]	.	.	5.15	5.11	5.18[a]	5.65[a]	4.94[a,b,c,d,e,f,g]
Gp 2	.	.	.	4.85	5.21	4.66[a,b]	5.02[a,b,c,d,e,f]	5.37[a]
Gp 3	.	.	5.50	4.98	5.13	4.98[a,b]	4.57[b,c,e,f]	5.25[a,b]
Gp 4	.	.	.	.	4.80	5.28[a]	4.00[a,b,c,d,e,f]	4.47[c,d,e,f,g]
Gp 5	.	.	.	4.81	.	5.13[a,b]	5.03[b,c,d,e,f]	4.88[a,b,c,d,e,f,g]
Gp 6	4.90[a,b,c]	5.15[a,c]	4.45	4.58	4.30	5.22[a]	5.12[c,d,e]	4.90[a,b,c,d,e,f]
Gp 7	4.84[a,c]	4.73[a,d]	4.46	4.66	5.34	4.86[a,b]	4.95[b,c,d,e,f]	4.92[a,d,e,f]
Gp 8	.	6.00[c]	.	.	.	5.06[a,b]	5.06[a,b,c,d,e,f]	4.79[a,b,c,d,e,f,g]
Gp 9	4.82[c]	4.86[a,e]	.	4.17	4.83	4.97[a,b]	5.07[b,c,d,e,f]	4.86[a,b,c,d,e,f,g]
Gp 10	5.50[b]	.	4.70	.	5.42	4.99[a,b]	5.34[a,d]	4.74[e,f,g]
Gp 11	5.06[a,b,c]	4.40[b,d,e]	4.01	4.91	5.22	4.68[b]	4.85[e,f]	4.73[e,f,g]
Gp 12	4.67[a,c]	4.47[b,d,e]	4.57	4.61	4.87	4.66[b]	4.73[f]	4.60[e,f,g]

Table 1.6 continued

Yr	97	98	99	00	01	02	all yrs
Gp 1	5.06	4.83^{a,b,c,d}	.	5.24^{a,e}	6.08^{a}	.	5.38^{a}
Gp 2	4.97	5.12^{c,d}	5.84^{a,d}	5.64^{a}	.	.	5.28^{a,b}
Gp 3	4.32	3.80^{a}	5.15^{a,b,c,d,e,f,g}	.	.	4.64	4.99^{b,c,d}
Gp 4	4.61	.	4.68^{e,f,g}	.	.	.	4.86^{c,d,e}
Gp 5	4.72	4.80^{a,b,c,d}	4.84^{b,e,f,g}	3.76^{c}	.	.	4.84^{c,d,e}
Gp 6	4.82	5.17^{d}	5.42^{d,e}	4.65^{c,d,e}	5.22^{a,b,c}	5.67	5.03^{b,d}
Gp 7	4.76	4.82^{a,b,c,d}	4.88^{b,e,f,g}	.	5.96^{a,b}	5.28	4.93^{c,d}
Gp 8	4.43	5.36^{d}	5.25^{a,b,c,d,e,f,g}	4.80^{a,d}	5.11^{a,b,c}	4.38	5.00b^{c,d}
Gp 9	4.73	5.00^{a,b,c,d}	4.91^{a,b,c,d,e,f,g}	4.97^{a,d}	4.77^{b,d}	4.97	4.94^{c,d}
Gp 10	4.72	4.73^{a,b,c,d}	4.67^{f,g}	4.37^{b,c,d}	5.45^{a,d}	4.65	4.92^{c,d}
Gp 11	4.72	5.31^{d}	5.26^{a,b,c,d,e,f,g}	5.10^{a,d}	4.37^{c,d}	.	4.82^{c}
Gp 12	4.49	4.74^{a,b}	4.89^{g}	4.81^{b,d,e}	4.58^{c,d}	4.92	4.67^{e}

Table 1.7 Progeny ultrasound longissimus muscle area in cm by Angus bull EPD grouping

AN RLMA_S TO LMA_P						
Yr	99	00	01	02	03	all yrs
Gp 1	.	.	.	.	.	.
Gp 2	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.
Gp 7	.	.	.	22.61	.	22.61[b]
Gp 8	.	.	.	.	43.69	43.69[a]
Gp 9	32.77	39.12	24.38	24.38	.	29.40[b,c,d]
Gp 10	.	.	22.61	22.10	27.69	24.13[b,d]
Gp 11	32.24	30.73	.	32.89	33.94	32.27[c]
Gp 12	33.55	31.44	30.31	30.16	31.19	31.07[b,c]

P = 0.05
Gp=Group; Yr=Year; AN=Angus Breed;
RLMA_S=Rank Longissimus Muscle Area Sire;
LMA_P=Longissimus Muscle Area Progeny

Table 1.8 Progeny ultrasound longissimus muscle area in cm by Red Angus bull EPD grouping

RA RLMA_S TO LMA_P						
Yr	99	00	01	02	03	all yrs
Gp 1	.	.	.	.	.	.
Gp 2	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.
Gp 7	.	.	.	.	.	.
Gp 8	.	.	.	34.76	35.05	34.93
Gp 9	.	.	.	.	.	.
Gp 10	.	.	.	.	.	.
Gp 11	32.01	29.51	.	31.45	30.80	30.62
Gp 12	30.80	29.85	28.62	30.34	30.30	29.97

P = 0.05
Gp=Group; Yr=Year; RA=Red Angus Breed;
RLMA_S=Rank Longissimus Muscle Area Sire;
LMA_P=Longissimus Muscle Area Progeny

Table 1.9 Progeny ultrasound longissimus muscle area in cm by Gelbvieh bull EPD grouping

G RLMA_S TO LMA_P						
Yr	99	00	01	02	03	all yrs
Gp 1	31.62	29.77	30.11	29.76	35.13	32.17
Gp 2	31.46	30.97	29.81	32.65	31.93	31.53
Gp 3	31.50	30.94	31.75	32.24	31.68	31.35
Gp 4	31.06	34.76	32..05	31.29	33.50	32.90
Gp 5	33.32	31.27	31.77	33.65	32.78	31.80
Gp 6	34.18	30.46	32.16	31.76	32.40	31.96
Gp 7	31.94	30.73	31.44	31.65	33.34	31.48
Gp 8	34.08	30.99	30.83	31.00	30.96	30.93
Gp 9	31.17	29.89	30.17	30.87	32.15	30.91
Gp 10	34.03	30.00	31.41	31.27	30.82	30.91
Gp 11	32.50	31.16	30.96	30.74	32.65	31.30
Gp 12	31.73	30.82	30.74	30.76	31.33	30.80

P = 0.05
Gp=Group; Yr=Year; G=Gelbvieh Breed;
RLMA_S=Rank Longissimus Muscle Area Sire;
LMA_P=Longissimus Muscle Area Progeny

Table 1.10 Progeny carcass longissimus muscle area in cm by Angus bull EPD grouping

AN RLMA_S TO LMA_P							
Yr	96	97	98	99	00	01	all yrs
Gp 1	.	.	.	.	.	.	.
Gp 2	.	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.	.
Gp 7	36.32	.	.	.	.	.	36.32
Gp 8	.	.	28.45	.	.	.	28.44
Gp 9	29.97	31.37	24.13	.	.	.	28.97
Gp 10	.	.	28.38	.	.	.	28.42
Gp 11	.	30.23	33.63	.	.	32.15	32.16
Gp 12	32.34	32.33	34.75	36.23	34.96	32.35	33.00

P = 0.05
Gp=Group; Yr=Year; AN=Angus Breed;
RLMA_S=Rank Longissimus Muscle Area Sire;
LMA_P=Longissimus Muscle Area Progeny

Table 1.11 Progeny carcass longissimus muscle area in cm by Red Angus bull EPD grouping

RA RLMA_S TO LMA_P				
Yr	96	97	02	all yrs
Gp 1	.	.	.	.
Gp 2	.	.	.	.
Gp 3	.	.	.	.
Gp 4	.	.	.	.
Gp 5	.	.	.	.
Gp 6	.	.	.	.
Gp 7	.	.	.	.
Gp 8	.	.	.	.
Gp 9	.	.	.	.
Gp 10	.	.	.	.
Gp 11	.	.	33.98	33.97
Gp 12	33.00	34.16	32.57	33.39

P = 0.05
Gp=Group; Yr=Year; RA=Red Angus Breed;
RLMA_S=Rank Longissimus Muscle Area Sire;
LMA_P=Longissimus Muscle Area Progeny

Table 1.12 Progeny carcass longissimus muscle area in cm by Gelbvieh bull EPD grouping

G RLMA_S TO LMA_P									
Yr	73	74	81	82	84	85	86	87	88
Gp 1	.	30.45	.	38.25	35.92	.	.	34.75	.
Gp 2	.	.	.	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.	35.62	38.40	37.59
Gp 4	.	30.77	.	.	34.74	.	.	.	.
Gp 5	.	.	.	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.	.	.	39.12
Gp 7	.	.	.	.	.	.	.	.	32.02
Gp 8	32.55	29.21	.	.	.	.	.	.	36.98
Gp 9	.	.	.	35.91	.	.	36.70	.	32.95
Gp 10	30.63	32.00	.	.	.	34.67	.	.	.
Gp 11	.	.	.	.	.	.	.	32.85	.
Gp 12	29.41	28.57	37.02	35.20	34.34	33.96	27.69	32.91	31.41

[a,b,c,d,e,f,g] LMA means within a column without common superscripts differ P > 0.05
Gp=Group; Yr=Year; G=Gelbvieh Breed; RLMA_S=Rank Longissimus Muscle Area Sire
LMA_P=Longissimus Muscle Area Progeny

Table 1.12 continued

Yr	89	90	91	92	93	94	95	96
Gp 1	.	.	.	36.18	34.54	39.67[a]	35.30	36.40[a,b,c,d,f,g]
Gp 2	.	.	.	34.58	34.26	.	39.01	36.68[a,b,c,d,f,g]
Gp 3	.	36.41	.	37.48	41.15	40.73[a,b]	35.82	40.46[a]
Gp 4	.	.	35.97	32.21	44.29	35.76[a,b]	34.69	37.90[a,b,c,d,e,f,g]
Gp 5	.	.	.	31.62	38.86	40.3[a]	37.81	35.46[c,d,e,f,g]
Gp 6	37.08	35.23	33.25	38.54	.	37.98[a,b]	35.27	34.47[c,d,e]
Gp 7	36.12	.	.	35.38	35.76	39.53[a]	35.75	36.50[a,f]
Gp 8	34.29	.	.	36.06	35.96	36.84[a,b]	36.65	38.31[a,g]
Gp 9	.	32.26	.	38.10	35.31	35.66[a,b]	34.53	34.29[d,e,f]
Gp 10	35.73	34.50	34.44	33.53	33.46	34.17[b]	34.98	34.05[d,e]
Gp 11	.	.	.	.	37.39	33.95[b]	36.21	35.24[d,e,f]
Gp 12	31.92	31.95	32.44	33.22	35.48	34.09[b]	34.58	34.17[e]

Table 1.12 continued

Yr	97	98	99	00	01	02	all yrs
Gp 1	37.61	34.64[b,c,d,e]	35.32	37.57	35.71	.	36.03[a,c]
Gp 2	36.41	38.86[a]	37.47	33.73	.	34.86	35.68[a,b,c]
Gp 3	37.59	35.00[b,c,d,e]	36.02	38.63	.	.	36.98[c]
Gp 4	36.01	33.89[b,c,d,e]	38.80	35.58	35.14	.	35.06[a,b,c,d]
Gp 5	35.81	.	38.28	.	.	.	36.18[a,b,c]
Gp 6	36.13	35.58[b,c,d]	35.04	35.84	34.77	33.32	35.12[a,b]
Gp 7	36.33	36.15[a,b,c]	35.07	35.42	31.96	34.25	35.73[a,c,e]
Gp 8	36.34	33.76[b,c,d,e]	34.47	.	.	.	36.05[a,c]
Gp 9	36.03	33.80[b,c,d,e]	33.53	32.76	33.59	34.77	34.73[b,e]
Gp 10	36.08	33.78[b,c,d,e]	35.81	31.24	33.73	34.80	34.52[b,d]
Gp 11	34.83	31.91[d,e]	36.28	36.84	31.81	.	34.84[a,b,d]
Gp 12	34.96	33.41[e]	33.91	34.31	32.23	30.87	33.78[d]

Table 1.13 Progeny ultrasound rib fat thickness in cm by Angus bull EPD grouping

AN RRF_S TO RF_P						
Yr	99	00	01	02	03	all yrs
Gp 1	0.27[a]	0.36[a]	.	0.19	0.20	0.23
Gp 2	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.
Gp 7	.	.	.	.	.	.
Gp 8	.	.	.	.	.	.
Gp 9	.	.	.	.	.	.
Gp 10	.	.	.	.	.	.
Gp 11	.	.	.	.	.	.
Gp 12	0.17[b]	0.22[b]	0.21	0.20	0.22	0.2

[a,b] RF means within a column without common superscripts differ P > 0.05
Gp=Group; Yr=Year; AN=Angus Breed; RRF_S=Rank Rib Fat Sire;

Table 1.14 Progeny ultrasound rib fat thickness in cm by Red Angus bull EPD grouping

RA RRF_S TO RF_P						
Yr	99	00	01	02	03	all yrs
Gp 1	.	0.23	.	0.27[a]	0.24[a]	0.26[a]
Gp 2	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.
Gp 7	.	.	.	.	.	.
Gp 8	.	.	.	.	.	.
Gp 9	.	.	.	.	.	.
Gp 10	.	.	.	.	.	.
Gp 11	.	.	.	.	.	.
Gp 12	0.20	0.17	0.16	0.20[b]	0.19[b]	0.18[b]

[a,b] RF means within a column without common superscripts differ P > 0.05
Gp=Group; Yr=Year; RA=Red Angus Breed; RRF_S=Rank Rib Fat Sire;
RF_P=Rib Fat Progeny

Table 1.15 Progeny ultrasound rib fat thickness in cm by Gelbvieh bull EPD grouping

G RRF_S TO RF_P						
Yr	99	00	01	02	03	all yrs
Gp 1	0.18[a]	0.16	0.16[a]	0.20	0.19	0.17[a]
Gp 2	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.
Gp 7	.	.	.	.	.	.
Gp 8	.	.	.	.	.	.
Gp 9	.	.	.	.	.	.
Gp 10	.	.	.	.	.	.
Gp 11	.	.	.	.	.	.
Gp 12	0.15[b]	0.15	0.15[b]	0.18	0.18	0.16[b]

[a,b] RF means within a column without common superscripts differ P > 0.05
Gp=Group; Yr=Year; G=Gelbvieh Breed; RRF_S=Rank Rib Fat Sire;
RF_P=Rib Fat Progeny

Table 1.16 Progeny carcass rib fat thickness in cm by Angus bull EPD grouping

AN RRF_S TO RF_P							
Yr	96	97	98	99	00	01	all yrs
Gp 1	0.44	0.4	0.43	0.20	.	.	0.39
Gp 2	.	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.	.
Gp 7	.	.	.	.	.	.	.
Gp 8	.	.	.	.	.	.	.
Gp 9	.	.	.	.	.	.	.
Gp 10	.	.	.	.	.	.	.
Gp 11	.	.	.	.	.	.	.
Gp 12	0.52	0.53	0.43	0.35	0.37	0.57	0.50

P = 0.05
Gp=Group; Yr=Year; AN=Angus Breed; RRF_S=Rank Rump Fat Sire; RF_P=Rump Fat Progeny

Table 1.17 Progeny carcass rib fat thickness in cm by Red Angus bull EPD grouping

RA RRF_S TO RF_P				
Yr	96	97	02	all yrs
Gp 1	.	.	0.62	0.61[a]
Gp 2	.	.	.	.
Gp 3	.	.	.	.
Gp 4	.	.	.	.
Gp 5	.	.	.	.
Gp 6	.	.	.	.
Gp 7	.	.	.	.
Gp 8	.	.	.	.
Gp 9	.	.	.	.
Gp 10	.	.	.	.
Gp 11	.	.	.	.
Gp 12	0.49	0.50	.	0.50[b]

P = 0.05
Gp=Group; Yr=Year; RA=Red Angus Breed; RRF_S=Rank Rib Fat Sire; RF_P=Rib Fat Progeny

Table 1.18 Progeny carcass rib fat thickness in cm by Gelbvieh bull EPD grouping

G RRF_S TO RF_P									
Yr	73	74	81	82	84	85	86	87	88
Gp 1	0.61	0.45	.	0.56[a]	.	.	.	0.39	0.23
Gp 2	.	.	.	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.	.	.	.
Gp 7	.	.	.	.	.	.	.	.	.
Gp 8	.	.	.	.	.	.	.	.	.
Gp 9	.	.	.	.	.	.	.	.	.
Gp 10	.	.	.	.	.	.	.	.	.
Gp 11	.	.	.	.	.	.	.	.	.
Gp 12	0.48	0.40	0.26	0.47[b]	0.34	0.30	0.32	0.37	0.24

[a,b] RF means within a column without common superscripts differ P > 0.05
Gp=Group; Yr=Year; G=Gelbvieh Breed; RRF_S=Rank Rib Fat Sire;
RF_P=Rib Fat Progeny

Table 1.18 continued

Yr	89	90	91	92	93	94	95	96	97
Gp 1	.	0.10	.	0.39[a]	0.40	0.31	0.36[a]	0.35[a]	0.33
Gp 2	.	.	.	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.	.	.	.
Gp 7	.	.	.	.	.	.	.	.	.
Gp 8	.	.	.	.	.	.	.	.	.
Gp 9	.	.	.	.	.	.	.	.	.
Gp 10	.	.	.	.	.	.	.	.	.
Gp 11	.	.	.	.	.	.	.	.	.
Gp 12	0.21	0.19	0.18	0.29[b]	0.35	0.28	0.28[b]	0.26[b]	0.30

Table 1.18 continued

Yr	98	99	00	01	02	all yrs
Gp 1	0.33	0.40	0.41	0.48	0.58[a]	0.39[a]
Gp 2	.	.	.	.	.	.
Gp 3	.	.	.	.	.	.
Gp 4	.	.	.	.	.	.
Gp 5	.	.	.	.	.	.
Gp 6	.	.	.	.	.	.
Gp 7	.	.	.	.	.	.
Gp 8	.	.	.	.	.	.
Gp 9	.	.	.	.	.	.
Gp 10	.	.	.	.	.	.
Gp 11	.	.	.	.	.	.
Gp 12	0.33	0.36	0.35	0.40	0.41[b]	0.30[b]

PERMISSION TO COPY

In presenting this thesis in partial fulfillment of the requirements for a master's degree at Texas Tech University or Texas Tech University Health Sciences Center, I agree that the Library and my major department shall make it freely available for research purposes. Permission to copy this thesis for scholarly purposes may be granted by the Director of the Library or my major professor. It is understood that any copying or publication of this thesis for financial gain shall not be allowed without my further written permission and that any user may be liable for copyright infringement.

Agree (Permission is granted.)

Leopoldo Arturo Pacheco 6/21/07

_____ _____

Student Signature Date

Disagree (Permission is not granted.)

_____ _____

Student Signature Date