ASSOCIATIONS OF DNA MARKERS WITH CARCASS AND PRODUCTION TRAITS IN ANGUS SIRED CALVES

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Story In Brief

Six high and six low marbling expected progeny difference bulls were chosen from the 1989 Angus sire summary (accuracies ≥ .5) and were mated at random to MARC II composite cows. Steers (n=120) and heifers (n=120) from each marbling group were produced over a two year period. Offspring were slaughtered at two different times (early and late kills) to establish variance in external fat cover. Traits studied included birth weight, adjusted weaning weight, hot carcass weight, rib-eye area, adjusted fat thickness and marbling scores. The rib section of one half of each carcass was weighed, and the ninth-tenth-eleventh rib section was dissected into lean, seam fat, subcutaneous fat, longissimus dorsi muscle and bone. DNA samples were obtained from all sires (semen) and offspring (blood or muscle). Genotypes (AA,AB,BB) were determined with polymerase chain reaction and restriction fragment length polymorphism analyses of genomic DNA for four genes: Kappa-casein (K-CAS), Beta-lactoglobulin (B-LAC), Growth Hormone (GH), and PIT-1. Associations between genotypes and phenotypes were analyzed. Preliminary results indicate that the GH, PIT-1, and K-CAS genes may influence total carcass weight as well as primal and subprimal lean mass, while also affecting adipose deposition. Alternatively, polymorphisms in GH, PIT-1, and K-CAS may be markers for other linked genes affecting carcass traits. Eventually, these associations between gene polymorphisms and carcass traits could be used to improve livestock through marker assisted selection.

(Key Words: Beef Cattle, Growth, Carcass, DNA Markers, Marbling, EPD.)

Introduction

The grading of beef has been used as an indication of quality since 1917 (Lesser, 1993; Kempster et al., 1982). The development of beef grading was designed to help supply a more consistent product for the consumer. Through

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labeling of meat products with quality and yield grades, consumers are better able to choose a product that will suit their tastes. To date, the most reliable measurement that is positively correlated with overall palatability is the amount of intramuscular adipose tissue (marbling) present in the longissimus dorsi muscle (Jennings et al., 1978; Tatum et al., 1982; Savell et al., 1987; Jeremiah et al., 1992). Therefore, the understanding of why different breeds of beef cattle have different abilities to marble is a subject of interest. Understanding the genetic mechanisms which influence marbling could allow the beef industry to produce a more consistent market animal in terms of carcass characteristics.

The production of a lean, fast growing market animal with a minimum of feed input is a desirable goal for the livestock industry. Often it is difficult to attain these goals simultaneously. The ideal scenario would be a rapid growing market animal that would produce a lean carcass with a minimum of external fat, and enough marbling to grade Choice. Currently, progress in animal breeding is accomplished through selection of superior breeding stock evaluated through testing of progeny and relatives. If DNA markers are identified which have significant effects on carcass and production traits, these markers could be used to evaluate potential breeding stock more accurately and at earlier ages than with present methods. Therefore, marker assisted selection could speed our progress in producing the ideal market animal. With these concepts in mind, the goal of this study is to identify molecular markers associated with carcass and production traits in offspring from Angus sires selected for either high or low expected progeny differences (EPD) for marbling score.

Materials and Methods

Population Design. Twelve bulls were selected from the 1989 Angus sire summary with accuracies greater than or equal to .50 for marbling score EPD. Six sires had high EPDs (mean = +.62), and six sires had low EPDs (mean = -.23) for marbling score. These 12 sires were mated at random to composite MARC II cows (1/4 Angus, 1/4 Hereford, 1/4 Gelbvieh, and 1/4 Simmental) to produce offspring in a two year period. Steers (n=120) and heifers (n=120) were weaned and fed to slaughter weights. Two different slaughter times were designated (early and late kills) during each of the two years so variability in external fat thickness would be attained. Measured production traits included birth weight (BW) and adjusted weaning weight (AWW). Carcass traits collected were hot carcass weight (HCW), rib-eye area (REA), adjusted fat thickness (FAT), and marbling score (MARB). The rib section (RIB) of one half of each carcass was weighed and separated into the ninth-tenth-eleventh (NTERIB) and the remaining rib sections. The ninth-tenth-eleventh rib section was weighed and dissected into subcutaneous fat (NTESC), seam fat (NTESM), lean (NTELEAN), longissimus dorsi muscle (NTEEYE) and bone (NTEB) weights. We focused on the ninth-tenth-eleventh rib section because it serves as a good indicator of total carcass composition (Hankins and Howe, 1946).

Genotyping. DNA samples were collected for all sires from semen samples, and from all offspring from either blood or tissue samples. All animals were genotyped for four loci. Genotyping was accomplished through Polymerase Chain Reaction (PCR) amplification of the DNA region of interest, and restriction enzyme digestion of the resulting PCR product. The different alleles were then visualized on agarose gels stained with ethidium bromide and viewed under ultraviolet light. Genotypes for Kappa-casein and Beta-lactoglobulin, two milk protein genes, were determined according to protocols from Medrano and Aguilar-Cordova (1990a, 1990b). Genotypes for growth hormone were determined according to protocols by Zhang et al. (1992). Genotypes for PIT-1, a protein necessary for expression of the growth hormone gene (Ingraham et al., 1988), were determined according to Moody et al. (1994). Two alleles (A&B) were found for all genes evaluated. Each animal was assigned a genotype of AA, AB, or BB.

Statistical Analysis. Effect of genotype on the measured production and carcass characteristics were tested using two types of statistical methods. Least-squares analysis was performed to test for significant genotype effects on all production and carcass traits. Also, a mixed model analysis was performed under a sire model to test for genotype significance on birth weight, adjusted weaning weight, hot carcass weight, rib-eye area, adjusted fat thickness, marbling score, and total rib section weight. Linear contrasts determined if gene action was dominant or additive in nature.

Results and Discussion

Allele frequencies in both the high (HM) and low (LM) marbling offspring groups are shown in Figure 1. Effects of genotype on measured traits are listed in Table 1 for least-squares analyses, while effects of genotype on measured traits using mixed model analyses are found in Table 2. Utilizing least-squares analyses, as well as the mixed model analyses there were no significant associations between genotype and birth weight or adjusted weaning weight. Several associations were found between genotype and carcass traits using the least-squares analyses. Effects of GH genotype were significant for HCW, RIB and NTEEYE, and approached significance for FAT and NTESC. PIT-1 genotype significantly affected RIB, NTERIB, NTESM and NTEB, while effects approached significance for HCW and NTESC. The K-CAS genotype significantly affected REA, FAT, HCW, RIB and NTEEYE, and approached significance for NTESC and NTEB. B-LAC significantly affected RIB. The results from the mixed model analyses were consistent with results from the least-squares analyses. The mixed model analyses detected a significant additive effect of growth hormone on marbling score, and a significant dominant effect of growth hormone on rib-eye area, both of which were not detected by the least-squares analyses.

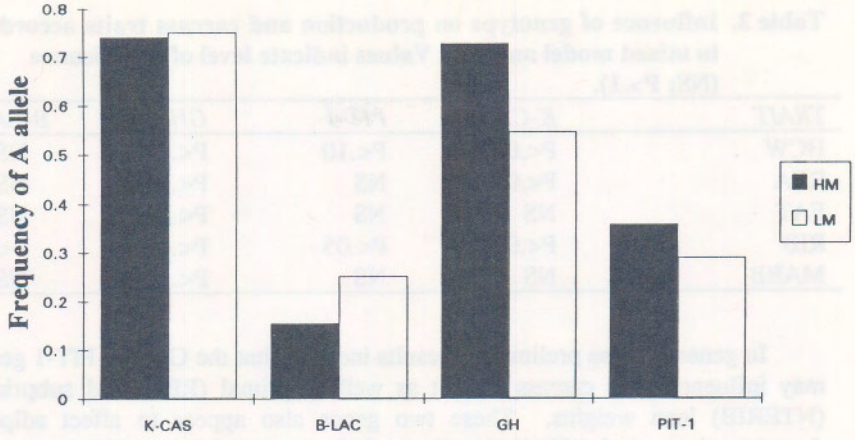

Figure 1. Allele (A) frequencies in calves for K-CAS (n=240), B-LAC (n=240), GH (n=239), and PIT-1 (n=235). B allele frequencies can be calculated as (1 - A allele frequency). HM = fequency for calves sired by high marbling bulls. LM = frequency for calves sired by low marbling bulls

Table 1. Influence of genotype on production and carcass traits according to least-squares analysis. Values indicate level of significance (NS: P>.1).

TRAIT	*K-CAS*	*PIT-1*	*GH*	*B-LAC*
BW	NS	NS	NS	NS
AWW	NS	NS	NS	NS
HCW	P<.05	P<.10	P<.05	NS
REA	P<.05	NS	NS	NS
FAT	P<.05	NS	P<.10	NS
RIB	P<.05	P<.05	P<.05	P<.05
NTEEYE	P<.05	NS	P<.05	NS
NTESC	P<.10	P<.10	P<.10	NS
NTEB	P<.10	P<.05	NS	NS
NTERIB	NS	P<.05	NS	NS
NTESM	NS	P<.05	NS	NS
MARB	NS	NS	NS	NS

Table 2. Influence of genotype on production and carcass traits according to mixed model analysis. Values indicate level of significance (NS: P>.1).

TRAIT	*K-CAS*	*PIT-1*	*GH*	*B-LAC*
HCW	P<.05	P<.10	P<.05	NS
REA	P<.05	NS	P<.10	NS
FAT	NS	NS	P<.10	NS
RIB	P<.05	P<.05	P<.10	P<.10
MARB	NS	NS	P<.10	NS

In general, these preliminary results indicate that the GH and PIT-1 genes may influence total carcass weight as well as primal (RIB), and subprimal (NTERIB) lean weights. These two genes also appear to affect adipose deposition in several different locations. Influences of GH and PIT-1 genes on carcass traits was not unexpected. Previous research has shown that the administration of exogenous growth hormone to livestock increases carcass protein and decreases carcass fat deposition (Dunshea, 1993). Similar results have been seen in transgenic animals possessing a growth hormone gene from a different species (Pomp et al., 1992). These previous studies implicate growth hormone in the control of body composition. Therefore, a polymorphism in the growth hormone gene, or the PIT-1 (a protein responsible for growth hormone transcription) gene, could influence the function of their respective protein products which affect body composition. Alternatively, the polymorphisms in GH and PIT-1 may be markers for other unidentified genes located nearby in the DNA sequence which are affecting carcass traits, as is likely the scenario for K-CAS and B-LAC.

Associations between genotypes and economically important traits in livestock, such as those discussed here, could eventually be used for marker assisted selection. If animals are selected based on their genetic make-up, the producer could expect accurate and rapid improvement in traits of interest. Present methods used for selection such as EPD measurements require many years of expensive testing before accurate prediction of an animal's true breeding value can be made. At present, there is a lack of data on which to base marker assisted selection for production and carcass composition traits. However, the accumulation of information relating genotype to important traits, such as those presented in this study, may eventually make marker assisted selection for carcass and production traits a possibility for the cattle industry.

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