# ASSOCIATION OF SINGLE NUCLEOTIDE POLYMORPHISMS IN THE LEPTIN GENE AND SEGREGATION BY ULTRASOUND BACKFAT AT WEANING ON CARCASS PERFORMANCE IN STEERS

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# Abstract

One hundred ninety-three crossbred steers from two herds were used to determine the association of leptin gene polymorphisms and effects of feedlot management of lean and fat steers on carcass performance. Steers were sorted into FAT and LEAN groups by ultrasound backfat at weaning and randomly assigned to a finishing phase. Steers were assigned to a backgrounding phase (BACK) and were fed a forage-based diet for 90 days or directly entered a feedlot phase (FEED). Genotypes were determined by IGENITY® (Atlanta, GA) for a panel of nine single nucleotide polymorphisms (SNP) in the leptin gene (UASMS1, UASMS2, C963T, E2FB, A1457G, and A252T), leptin receptor (T945M), growth hormone receptor (G200A), and fat metabolism enzyme (K232A). Initial backfat (BF) means for the FAT and LEAN group were 3.4 mm and 1.8 mm, respectively. Mean on-test weight was heavier for FAT (306.5 kg) than LEAN (292.9 kg). Age-adjusted hot carcass weights (HCWT) were heavier for LEAN/BACK when compared to FAT/FEED and FAT/BACK ($P<0.05$). Dressing percent for the FAT/FEED group tended to be higher ($P<0.10$) over all groups except LEAN/BACK. Steers that went directly to the feedlot had higher marbling scores than backgrounded groups. FAT/FEED had higher 12$^{th}$ rib BF than the other contemporaries. None of the SNPs were useful for predicting ultrasound BF at weaning. Some association was detected with UASMS2 and HCWT ($P<0.10$) resulting in an 11 kg difference between genotype CC and CT ($P<0.05$). Five of the leptin polymorphisms (UASMS1, UASMS2, A1457G, C963T, and E2FB) were associated with adjusted carcass BF ($P=0.01$, 0.06, 0.01, 0.01, and 0.01, respectively) and calculated yield grade ($P<0.01$). A252T was associated with REA, and genotype TT was larger than AA and AT ($P<0.05$). This study suggests that segregation by initial fatness estimates and feedlot management strategies has the opportunity to increase HCWT by 35 kg. Sorting cattle upon

feedlot entry by ultrasound BF and segregation using genetic markers are useful tools that can assist in the estimation of carcass composition in the live animal. With additional research, the possibility exists to incorporate genetic markers into feedlot selection to assist in marketing decisions.

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# CHAPTER 1 - Review of Literature

## Introduction

Historically, feedlot operators have long used visual external back fat indicators to determine the proper marketing date for cattle on feed. This was sometimes effective but it causes cattle to be marketed on averages, leading to lost revenue from cattle not being harvested near their ideal compositional endpoint. With the advent of ultrasound technology, managers gained an effective tool to determine and group harvest-ready cattle. The technology has been found to be an objective and economical way to estimate live body composition. Brethour (1992) found a correlation of 0.975 between 12$^{th}$ rib backfat thickness and carcass backfat measurements at harvest. Ultrasound estimates of intramuscular fat made on feedlot cattle several months in advance of harvest have been positively correlated with carcass marbling (Brethour, 1990).

More recently, the use of DNA markers to predict future carcass composition has also demonstrated positive results. Schenkel et. al. (2005) found select genotypes significantly influenced lean yield, fat yield, and carcass fat, but did not affect quality grade in feedlot steers. These markers have the ability to transform the industry by shedding light on carcass and performance attributes of cattle at a young age. These methods may eliminate the need to feed non-conforming and outlier cattle and shift the focus to cattle that have the capacity to perform to the standards that are desirable.

## Ultrasound

Ultrasound has rapidly become one of the more popular methods of live animal carcass evaluation in recent years, mostly due to the fact that it is non-invasive in nature, collection and data analysis is simple and the results are accurate and repeatable.

The basic principle of ultrasound uses the measurement of time and distance as a sound wave returns from reflection off of soft tissue. When the transducer comes into contact with the animal's skin, the ultrasound machine converts electrical impulses into high-frequency sound waves. As these waves travel into and throughout the body, different boundaries and tissues are defined by sound waves reflecting off of soft tissues of differing densities and returning to the transducer, where it is converted into the image that is viewed on the screen and measurements can be taken.

Wild (1950) first characterized the use of ultrasonic imaging to quantify muscle and fat in the live animal. In 1959, Stouffer found that fat thickness and rib eye area can be accurately measured using ultrasound. Many technological advancements, including more efficient machines and better imaging methods, led to rapid advancements in the field during the 1970s and 1980s.

Faulkner et. al. (1990) from the University of Illinois, tested the accuracy of ultrasound fat thickness measurements against the actual carcass measurements taken off the harvested animal. They scanned 371 head of steers and heifers and, five days later, harvested the cattle three different ways. The first group was harvested at the University of Illinois Meat Lab using only skinning knives, the second group was harvested at a commercial facility using air knives and a hide puller, and only a hide puller was used on the third group. Results show that 72% of cattle harvested had +/- 2 mm difference in ultrasound fat to carcass fat measurements at the $12^{th}$ rib. They concluded that ultrasound is an accurate and precise method of measuring $12^{th}$ rib fat

(Faulkner et. al., 1990). Brethour (1992) later confirmed this finding, showing the correlation between 12th rib ultrasound fat measurements and carcass measurements taken at the same location to be 0.975.

Brethour (1990) devised a subjective, but repeatable, scoring system to measure "ultrasound speckle", the salt-and-pepper appearance of the cross-sectional scan of the longissimus muscle that is normally associated with intramuscular fat. The objective of this study was to be able to accurately determine marbling scores of animals before they are harvested. Brethour scanned 619 head from 14 groups of cattle just before slaughter up to 148 days pre-harvest using an Aloka 210 with a 3 MHz transducer. The steers were scanned within two weeks of slaughter and all measurements were taken on the right side of the animal at the 12th rib. Marbling scores are expressed as 4.0=Slight$^{00}$ and 5.0=Small$^{00}$. Speckle scores in 11 of the 14 groups of cattle were highly correlated ($P<0.01$) with carcass marbling score. Live animal speckle scores classified carcasses as Select or Choice with 77% accuracy, and similar accuracy was achieved as much as 148 days before slaughter by adjusting for the regression of speckle scores with days on feed. While this method was highly subjective and only useful to a trained, experienced technician, these findings were an important stepping stone to computer-generated models interfaced with an ultrasound machine to accurately and repeatedly estimate quality grade of the live animal weeks to months from their optimal endpoint. This was further studied by Brethour (2000) and he found that projections of carcass marbling improved as the evaluation date neared slaughter date. Early projections from the onset of feeding allowed tentative categorization of candidates for Choice or not Choice but were only 64% accurate; as the date of evaluation was pushed back in the feeding period, the rate of distinguishing Choice from Select neared 75% accuracy.

Ultrasound estimates for backfat thickness and marbling score, when combined with economic data into a computer model that maximizes profitability, can be a powerful tool for feedlot operators concerned about their bottom line. Basarab et. al. (1999) conducted a study using the Kansas State University (KSU) feeder cattle sorting system to track and predict future carcass merit on 4,101 head of yearling steers in two commercial feedlots in Alberta, Canada. The KSU sorting system combines initial body weight, ultrasound backfat thickness, and marbling score with economic data such as local carcass price matrices and production costs to project the number of days on feed that maximizes performance. This system is usually applied three to four months prior to slaughter, or in most cases at re-implant time in the feedlot. Steers in Feedlot 1 were randomly assigned to two treatment groups; sorted by weight (n=856) into low, medium and high weight groups and sorted by the KSU sorting system (n=849) into short, medium, and long days on feed groups. In Feedlot 2, steers were randomly assigned to two groups; not sorted or control (n=798) and sorted by the KSU system (n=1598) into short, medium, and long days on feed groups. Initial ultrasound scans were taken up to three to four months prior to harvest. Whole pens were marketed when a majority of the steers in the pen reached a carcass weight and grade characteristics required for optimal returns.

Feedlot 1 steers sorted by the KSU sorting system were 22.4% ($P<0.01$) less uniform in body weight, 24.5% ($P<0.01$) more uniform in backfat thickness and equally uniform in marbling score as compared to steers sorted by weight. Steers in Feedlot 2 were more ($P<0.01$) uniform in body weight and equally uniform in backfat thickness and marbling score as compared with the unsorted control steers. Performance measures including days on feed, dry matter intake, and feed:gain were not significantly different between groups or feedlots. However, average daily gain (ADG) in Feedlot 1 was higher (0.12 kg/d) for the KSU sorted

group compared to the control ($P<0.05$). As well, ADG in Feedlot 2 was higher (0.05 kg/d) for the KSU sorted group than the unsorted control group ($P<0.05$). Carcasses from KSU sorted steers in Feedlot 1 tended to have more marbling ($P<0.10$) and lean meat yield ($P<0.05$) than carcasses from weight-sorted steers. As well, sorted steers had a higher AAA% (USDA Choice) acceptance rate when compared to unsorted steers in Feedlot 1 ($P<0.01$) In Feedlot 2, carcasses from KSU sorted steers had higher ($P< 0.01$) YG1 acceptance rates and higher ($P< 0.01$) AA% (USDA Select) carcasses. This was mainly due to the differences in fat endpoint and carcass weight desired by each feedlot manager. It was found that the strategy employed by the sort system attempts to project carcasses into the higher-valued tiers of the pricing structure without causing them to be over-weight or over-fat. Using the KSU sort system produced an average profit of $27.67 per head in Feedlot 1 and $15.22 per head in Feedlot 2 as compared with controls when carcass premiums and discounts were taken into account. The increased net return was primarily due to increased ADG and a more desirable distribution of carcass yield and quality grades (Basarab et. al., 1999).

## Leptin

Leptin is a 16-kDa protein hormone secreted from white adipocytes that has been implicated in the regulation of food intake, energy expenditure, and whole-body energy balance in rodents and humans (Houseknecht et. al., 1998). Much of the early research involving the protein was conducted in mice while looking for a cure for obesity. One of the early models found was the *ob/ob* mouse (Ingalls et al., 1950) that had a recessive genetic mutation that resulted in sterile adult mice with over 50% body fat.

In 1994, the leptin gene was discovered in Jackson Laboratory C57BL/6J and SM/Ckc$_{-+DAC}$ mice (Zhang et. al. ,1994). The leptin gene has three exons, and the coding region

is located in exons 2 and 3, while exon 1 is non-translated (Zhang et. al., 1997). The helical structure of the leptin receptor implied similarity to helical cytokine family members interleukin(IL)-6, which was later confirmed due to its resemblance in its signal transduction (Houseknecht et. al., 1998). The members of the IL-6 family of cytokines interact with their receptors through three different binding sites; I, II, and III. Leptin contains a single disulfide bond that links two cystines (Cys96 and Cys146) within the C and D helices. This bond is imperative to the stability and structural support of leptin (Rock et.a., 1996). The leptin gene has been mapped to bovine chromosome 4 and has been associated with serum leptin concentrations, feed intake and body fatness (Nkrumah et. al., 2005).

Leptin has been considered a candidate gene for performance, carcass, and meat quality traits in beef cattle (Schenkel, 2005). More specifically, the role of leptin in metabolic regulation has been demonstrated through its action on the hypothalamic-pituitary adrenal axis, and results seem to suggest that leptin plays an integral role in the growth process (Delavaud et. al., 2002). Much of this research is devoted to differences and associations of single nucleotide polymorphisms (SNP) in the leptin gene with carcass, performance, and meat quality characteristics. A SNP is a DNA sequence variation that occurs when a single nucleotide (A, C, T, or G) in the genome differs between members of a species in the population. Results from many of these studies do in fact confirm findings from previous publications, yet some report quite different conclusions, showing the need for further exploration into the subject.

Buchanan et. al. (2002) identified several alleles of the BM1500 microsatellite in the leptin gene and found they were associated with carcass fat measures in a population of 154 unrelated beef bulls. Six unrelated bulls for phenotype and 34 unrelated bulls for genotype were selected to screen for polymorphisms in the leptin gene. A SNP was found in the exon 2 region

of the leptin gene and is a cytosine to thymine transition. It changes the commonly reported amino acid at that position, an arginine (encoded by the C allele) into a cysteine (encoded by the T allele). All three bulls selected for sequencing based on high fat phenotype were homozygous for the T allele, while the three bulls selected for lean phenotype were homozygous for the C allele, thus associating the T allele with higher fat carcasses and the C allele with leaner carcasses. Genotype significantly affected average fat and grade fat ($P<0.05$). Leptin mRNA expression was higher in cattle homozygous for the thymine (T) allele, suggesting that the exon 2 SNP could be the causative mutation and this could reflect a feedback response compensating for reduced biological function.

Schenkel et. al. (2005) wanted to evaluate the association of previously reported SNP in the bovine leptin gene with carcass and meat quality traits in a large sample of 1,111 crossbred bulls, steers, and heifers. Five SNP were genotyped (UASMS1, UASMS2, UASMS3, E2JW, and E2FB) and economically-important traits such as fat, lean and bone yield, grade fat, longissimus muscle area (LMA), hot carcass weight (HCW), quality grade (QG), longissimus muscle intramuscular fat (LM i.m. fat), and tenderness evaluations of LM and semitendinosus muscle were compiled. UASMS3 was not included in the study because it was tightly linked with UASMS1. Results found that the two leptin exon 2 SNP were associated with fat and bone yield and carcass fat (E2JW, $P<0.01$; E2FB, $P<0.05$). E2JW and E2FB interacted together on their effect on LM tenderness ($P<0.01$). Three haplotypes made up 88% of the population (TCAC, CCAT, TTAC) and had similar effects in all the traits. However, when compared to these common haplotypes, one (CCTT) showed a significant decrease in fat yield and grade fat, as well as a corresponding increase in lean yield ($P<0.01$). In that same manner, another haplotype (TTTT) showed a significant decrease in LM tenderness at 2 and 14 days postmortem

and for the average shear force over the 21 d postmortem (Schenkel et. al., 2005). These findings were similar to others (Nkrumah et. al., 2004, Buchanan et. al., 2002) in the fact that animals carrying the T allele instead of a C allele in E2FB produce carcasses with poorer grades and lower lean meat yields, but are not different in regards to marbling (Schenkel et. al., 2005). In this study, UASMS2 was not significantly correlated with any of the carcass traits. However, this study upholds the findings of Nkrumah et. al. (2005) of a significant association of UASMS1 (or UASMS3) with carcass fat yield and tended to have relationships with grade fat and carcass lean yield (Schenkel et. al., 2005).

Previous studies have focused on the relationship between polymorphisms in the coding regions of the leptin gene and traits of interest to livestock producers, yet studies in humans have shown that polymorphisms in the leptin promoter may be of major importance. Nkrumah et. al. (2005) set out to evaluate associations between economically important traits and polymorphisms in the promoter region of the leptin gene. Sixteen bulls and steers with extreme phenotypes for feed intake and ultrasound backfat thickness were selected out of 150 animals in the study and used to determine SNP and genotype through polymerase chain reaction (PCR) methods. Three SNP in the bovine leptin promoter were found, namely UASMS1, UASMS2, and UASMS3. In this study, results found from UASMS1 were not used because its inheritance and trait associations were identical to UASMS3. Results presented with respect to UASMS2 showed that final weight was 17 kg and 38 kg higher in TT animals than CT and TT animals, respectively, and ultrasound backfat thickness was 39 and 31% higher for TT animals than that for CC and CT animals. As well, marbling score was also 13 and 9% higher for TT animals that for CC or CT animals, respectively. With respect to UASMS3, animals owning the GG genotype (when compared to CC or CG, respectively) were found to have higher values

concerning midpoint weight, final bodyweight, growth rate, daily dry matter intake (DMI), and longer feeding duration (Nkrumah et. al., 2005). In conclusion, animals having the TT genotype of UASMS2 generally had higher serum leptin concentrations and higher levels of carcass fatness, both subcutaneous and intramuscular. Nkrumah et. al. (2005) differed from Schenkel et. al. (2005) as the authors found no association of UASMS2 with any carcass measures. Yet, animals with the GG genotype of UASMS3 generally achieved higher performance standards in terms of weight when compared to contemporaries.

Polymorphisms in the leptin gene have been linked to many different aspects of the individual animal, yet little has been done to quantify their effect on specific economically important traits in market-ready steers and heifers. Feedlot operators continually search for tools that can accurately predict and quantify market-ready characteristics of animals upon feedlot entry and sort into more optimum and efficient feeding groups. A slaughter trial consisting of over 1,500 head of crossbred finished steers and heifers was conducted by Kononoff et. al. (2005) to determine the effect of a leptin SNP on the quality grade (QG), yield grade (YG), and carcass weight of the steers and heifers. Genotyping was performed using real-time capillary PCR via the LighCycler1 model (Roche Molecular Biochemicals, Mannheim, Germany), where allelic variation in the leptin gene was due to a single nucleotide transition (cytosine[C] to thymine [T] that results in a Arg25Cys. QG and YG were taken according to Canadian Beef Grading Agency standards. Genotypic frequency in this study was found to be 24.9, 50.5, and 24.6% for CC, CT, and TT, respectively, and was found to be similar to observations found by Buchanan et. al. (2002). The proportion of carcasses grading AAA or higher (equivalent to USDA Choice QG) was 7.6% higher with a TT genotype when compared to the CT genotype ($P<0.05$), and tended to be 7.1% higher in TT genotypes than CC genotypes, while not

significant. On the other hand, 12.5 and 15.1% more carcasses graded YG 1 (equivalent to USDA YG 1) in animals of the CT and CC genotypes, respectively, when compared to TT genotype animals ($P<0.01$). Thus, Kononoff et. al. (2005) supports prior work done that describes cattle with the TT genotype being associated with more carcass fat and, in turn, higher quality grade scores. As well, this work associates cattle with the CC and CT genotypes with more lean meat yield and a lower numerical yield grade. It is important to note that the proportion of carcasses grading AAA or higher and the observed proportion of carcasses for each YG was significantly affected by sex. But, in this study where the continuous response variable was carcass weight, the interaction between sex and genotype was tested and found to be insignificant ($P=0.89$) While these results uphold conclusions found in earlier studies, the thought process by the authors takes this information a step further to a more practical level. If the animal's genotype for the leptin SNP is given to feedlot operators, it is possible to think those operators could use that information to sort cattle of similar genotypes into harvest groups and manage those cattle to their genetic potential. For instance, cattle with the TT genotype could be accelerated through the feedlot phase, and might have an increased chance of qualifying for a lower numerical yield grade. With these observations and the ability of identifying functional differences in the leptin gene, it could be suggested that identification of the leptin genotype may be an important part in those strategies (Kononoff et. al., 2005).

Research has shown differences in carcass characteristics in beef cattle across SNP in the leptin gene at slaughter, however little is known about when those changes happen. That timeline is important for feedlot operators if this information is to be used to sort and select feedlot animals to optimize feeding efficiency. Lusk (2007) genotyped 1,653 feedlot steers and heifers to determine the effect of two leptin SNP (UASMS2 and R25C (sometimes referred to as

EXON2FB or E2FB)) on growth curve parameters for body weight (BW) and backfat thickness (BF). Up to 4 measures of BW and ultrasound estimates of BF were taken from placement up until slaughter on each animal. The independent effect of each SNP and the interaction between the 2 SNP on growth curve parameters was studied. For UASMS2, genotypic frequency was 50, 41 and 9% for CC, CT, and TT, respectively, while R25C frequencies were 32, 48, and 20% for CC, CT, and TT, respectively. R25C did not significantly affect growth parameters individually or in combination with UASMS2 SNP. Genotype CC of UASMS2 had the heaviest on-test weights and subsequently largest mature BW. UASMS2-TT cattle, while having the lowest initial BW at placement, exhibited the fastest rate of BW growth throughout the test. BW gain, directly related to feedlot profitability, was not significantly different between UASMS2-CC and UASMS2-CT, but both mentioned genotypes were significantly higher in average daily gain by 0.047 kg/d than UASMS2-TT genotypes ($P<0.01$). Serial BF measures were fit to a modified power function and the model that included both R25C and UASMS2 SNP provided the best fit to the data ($P<0.01$) than did either single SNP model. R25C-CC/UASMS-TT genotype had the lowest average BF at placement. R25C-CT/UASMS2-CT exhibited the greatest rate of BF growth, while R25C-CC/UASMS-CC genotype had the lowest rate of BF growth. Lusk (2007) fit probability data to an equation that would conclude when certain genotypes would encounter a ceiling when that carcass would not receive a premium for leanness. Based upon this, he found a 30-day difference between when a feedlot might expect the R25C-CC/UASMS2-TT genotype to stop receiving yield grade premiums versus when R25C-CC/UASMS2-CC would stop receiving yield grade premiums. Ultimately, this equation is based on assumption, but it brings new potential to use genetic information in selecting and sorting cattle to optimize feeding strategy and marketing decisions. In conclusion, because of differences in growth parameters

and fat indicators across genotype, the opportunity exists to use that information to a feedlot operators' advantage.

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# CHAPTER 2 - Association of Single Nucleotide Polymorphisms in the Leptin Gene and Segregation by Ultrasound Backfat at Weaning on Carcass Performance in Steers

## Introduction

The cattle industry has changed rapidly toward marketing based on carcass merit. Feedlot managers are continually searching for ways to acquire, feed, and market cattle that are of similar kind in order to take advantage of premiums in value-based marketing grids. This change has induced great interest in technology that evaluates future carcass composition in live animals. Traditionally, feeder cattle were fed and marketed as mixed groups, which results in almost 30% of cattle being more than 25 days from their optimal endpoint (Brethour, 2001). This type of batch marketing affected some cattle with undesirable quality grades, loss of potential gain, or near or at a yield grade discount. Yet ultrasound technology has the capability to determine carcass merit early in the feeding period, allowing managers to sort cattle into outcome groups based on an animal's optimal days on feed. It also facilitates identification of outlier animals that will not achieve quality targets or will exceed packer limitations and allows managers to cull these animals earlier in the cycle.

At the same time, margins in the industry are shrinking, and managers are forced to become more efficient. One solution is to increase carcass weight at a constant backfat thickness, thereby increasing pounds of product produced and diluting fixed operating costs of the feedlot. This requires the use of backgrounding or deferred-feeding to hold those cattle to lower daily gains until it is time to admit them to a full feeding program.

Many single nucleotide polymorphisms (SNP) have been identified in the bovine leptin gene (Buchanan et. al., 2002; Lagonigro et. al., 2003; Liefers et. al., 2004, Nkrumah et. al., 2005;

Liefers et. al., 2005). Genetic markers for leptin SNP have been found to be alternative and sometimes effective ways to forecast carcass fat level in cattle (Kononoff et. al., 2005; Schenkel et. al, 2005). Differences in leptin polymorphisms have shown potential to be used as selection criteria for optimizing animal endpoints and maximizing feeding potential (Lusk, 2007). This genetic information may shed insight into individual animal performance and allow for more informative decisions concerning animal composition and time of harvest.

The use of technology that aids in the prediction of future carcass composition and groups cattle accordingly has the opportunity to not only streamline production efficiency, but also increase product quality, uniformity and consumer acceptance. Previous research has focused on how certain carcass characteristics are affected by leptin genotypes, yet more knowledge is needed before feedlot operators can economically utilize marker information

The objective of this study was to investigate the association of nine leptin gene polymorphisms and the effects of feedlot management of lean and fat steers on carcass performance.

## Materials and Methods

One hundred ninety-three crossbred steers from two herds were used in this study. Steers originated from the Kansas State University commercial cow/calf units (CCU) and the Western Kansas Agricultural Research Center – Hays (ARCH) herds. Thirteen Angus, Hereford, and South Devon bulls were artificial insemination (AI) sires to nearly 60% of the steers, and the rest were born to cows pasture-bred to Angus or Hereford herd bulls. Cows were of mixed age and predominately Angus. Steers were weaned in early November and sorted into FAT and LEAN groups by ultrasound backfat, measured at the 12$^{th}$ rib on the sagittal plane using an ALOKA 210 with a 5 MHz transducer (ALOKA Ultrasound Systems, Wallingford, CT). Steers within the FAT and LEAN groups were randomly assigned to a backgrounding phase (BACK) and fed a forage-based diet for 90 days with an expected gain of 1 kg/d or directly entered a feedlot phase (FEED) (Table 2.1). Both diets consisted of grain sorghum and sorghum silage fed at differing levels to reflect the feeding strategy. Diets also contained soybean meal, urea and ammonium sulfate, as well as included 100 g calcium carbonate, 50 g urea, 50 g Rumensin®/Tylan® premix, 25 g sodium chloride, and 20 g ammonium sulfate per steer daily. Herd origin, fatness assessment, and feeding management were evenly distributed. The trial started on November 16, 2004 when animals were weighed and ultrasounded for backfat after 12 hours of feed deprivation. Cattle were fed treatment diets until February 16, 2005, where mid-weight was recorded and steers were implanted with Synovex-Plus and ultrasounded for backfat using an ALOKA 500v (ALOKA Ultrasound Systems, Wallingford, CT) diagnostic real-time machine with a 17 cm, 3.5 MHz linear array transducer equipped with appropriate software (Cattle Performance Enhancement Company, CPEC, software). Starting February 17, 2005, cattle were fed a finishing ration similar to FEED diet to a target backfat level until harvest. Cattle were

weighed and ultrasounded for backfat before being harvested at a commercial facility (National Beef, Dodge City, Kansas) and carcass data were collected after a 24-hour carcass chill.

Tail hair follicles were collected in February 2005 on individual steers so that the root bulb was intact and inserted into a collector for genetic analysis by Igenity® (a business unit of Merial Ltd., Atlanta, GA). Genotypes were determined using Igenity® L Test for a panel of nine single nucleotide polymorphisms (SNP) in the leptin gene (UASMS1, UASMS2, C963T, E2FB, A1457G, and A252T), leptin receptor (T945M), growth hormone receptor (G200A), and fat metabolism enzyme (K232A). Four SNP were located within the leptin promoter region; UASMS1 and UASMS2 (Nkrumah et. al., 2005), A1457G and C963T (Liefers et. al., 2005). Two SNP, E2FB and A252T (Buchanan et. al., 2002, and Lagonigro et. al., 2003, respectively), were located within exon 2 of leptin. T945M (Liefers et. al., 2004) was located within exon 20 of the leptin receptor. G200A (Ge et. al., 2000) was located within exon 10 of the growth hormone receptor. K232A (Winter et. al., 2002, and Thaller et. al., 2003) was located within the diacylglycerol O-acyltransferase (DGAT1) gene. Genotypic effects for each SNP were analyzed for ultrasound backfat assessed at weaning and for carcass traits: hot carcass weight (HCWT), dressing percentage (DRESS%), yield grade (YG), marbling score (MARB), kidney-pelvic-heart fat (KPH), ribeye area (REA), backfat (BF), adjusted fat (ADJFAT), and carcass yield grade (CYG).

## Statistical Analysis

All analyses were performed using Statistical Analysis Software (SAS Inst., Inc., Cary, NC). Descriptive characteristics of quantitative traits were garnered using the means procedure. The model for the effect of feeding management and initial fatness assessment on carcass traits included contemporary group as fixed effect and herd origin as a random effect using the mixed

procedure. Four treatment groups were formed and analyzed by cross-classification in respect to feeding management (FEED/BACK) and initial fatness assessment (FAT/LEAN). HCWT were adjusted to a constant BF basis to reflect standard commercial feeding practices; all other traits were adjusted to an age-constant basis for comparison. The model used to determine effects of leptin genotypes on carcass traits included contemporary group as a fixed effect and age at harvest as a covariate using the mixed procedure. Eight treatment groups were investigated due of the differences in herd source, initial fatness assessment, and feeding strategy. Means for fixed effects were estimated using least square means, and pair-wise comparisons were made when effects tended to be significant.

## Results and Discussion

### *Feeding Management*

Table 2.2 conveys preliminary measures at the beginning of the study. Initial BF means for the FAT and LEAN groups were 3.42 mm and 1.82 mm, respectively. Mean on-test weight was heavier for FAT (306.5 kg) than LEAN (292.9 kg). No differences in ultrasound estimates of (UEO) MARB were evident between the two groups. Initial weights of ARCH steers were 15.2 kg heavier than CCU steers. There was no difference in initial BF assessment between the two herds, but ARCH had higher initial UEO MARB scores than CCU.

When sorted into treatments, both FAT/BACK and FAT/FEED had heavier initial weights than LEAN/BACK and LEAN/FEED (Table 2.3). At the end of the trial period, weights and ultrasound BF were recorded and average daily gain (ADG) was calculated when steers were adapted to a common finishing ration. FEED groups were heavier ($P<0.05$) at mid-weight than BACK groups. FAT/FEED had a 64.9 kg advantage in weight over LEAN/BACK ($P<0.01$). BF measurement was different between all groups ($P<0.01$) at this point. Re-ranking in BF was evident between FAT/BACK and LEAN/FEED, as FAT/BACK increased less than 1 mm, while LEAN/FEED increased over 4 mm. Mid-ADG was heavier ($P<0.05$) for FEED than BACK with no difference evident among fatness assessment by treatment. At this point in the feeding period, it was apparent that differences in initial fatness assessment and feeding strategy played a key role in performance measures in the feedlot phase.

Before harvest, weights and ultrasound BF were recorded and ADG was calculated for steers. LEAN/BACK recorded the heaviest final weight and was significant over all groups except LEAN/FEED ($P<0.05$). FAT/FEED had the lowest body weight before harvest. Final ultrasound BF was highest in FAT/BACK and lowest in LEAN/FEED, but interestingly, overall

ADG was highest in LEAN/FEED and lowest in FAT/BACK. Schoonmaker et. al. (2004) saw similar results in a study to determine whether different sources and amounts of energy in the growing phase could extend the growth curve in early-weaned steers. Groups of steers were allotted to one of four growing-phase regimens and results showed that feeding early-weaned steers an ad-libitum high-concentrate (ALC) diet accelerated physiological maturity to a point where those steers had the lightest HCWT at slaughter. The authors found ADG was highest in the ALC group and least for backgrounded steers. Data from the current study suggest that ADG is higher ($P<0.05$) in both FEED groups than BACK treatments. In summary, FAT groups continued to have higher BF measurements than LEAN, and FEED groups had higher ADG than BACK. LEAN groups had heavier final weights than FAT, but could be attributed to more days on feed. Decisions made at the onset of the feeding period with respect to initial fatness assessment and feeding management of steers have the potential to drastically alter the physiological composition of the animal near its endpoint.

Of interest in this study was how initial fatness estimation and subsequent feeding strategy affected hot carcass weight (HCWT) adjusted to a constant BF thickness. Since most cattle are commercially fed to fat-constant endpoints, it is logical to make comparisons (Klopfenstein et. al., 2000) in the same manner. LEAN/BACK had the heaviest (406.2 kg) HCWT of the treatments and had a 25, 35, and 17 kg advantage over FAT/BACK, LEAN/FEED, and FAT/FEED, respectively ($P<0.01$). As well, LEAN/FEED had 17 kg heavier HCWT than FAT/FEED ($P<0.01$). These findings agree with Schoonmaker et.al. (2004), who found that steers who consumed a full-silage diet for 50 days before being switched to a 70% concentrate diet had heavier ($P<0.01$) carcasses at slaughter than steers who were fed a 50% concentrate diet for 140 days and then were switched to a 70% concentrate diet until slaughter. Murphy and

Loerch (1994) found that restrictively-fed steers had greater lean tissue accretion as a percentage of their total gain than steers fed high concentrates ad-libitum. When adjusted for age, LEAN/BACK mean HCWT was still heaviest. Harvest ages ranged from 429 d for FAT/FEED to 491 d for LEAN/BACK. According to harvest age, LEAN/BACK was the farthest from their pen-wise optimal harvest date according to a pre-set backfat threshold. This could be one explanation for the difference in HCWT, as those cattle were fed longer to reach target BF levels, thus expectedly had heavier carcass weights at similar BF levels. Initial fatness assessment also affected HCWT when cattle were subjected to similar diets throughout the feeding period. LEAN groups had 17 and 25 kg heavier HCWT than FEED groups when cattle were subjected to FEED and BACK diets, respectively ($P<0.01$). While age at harvest and differences in physiological maturity affect growth rate and fatness at slaughter, these findings suggest that both initial fatness and management during the feeding period play a role in increasing HCWT at a constant BF.

LEAN/FEED had lower ($P<0.05$) 12$^{th}$ rib BF than the other groups. Interestingly, by the end of the trial period LEAN/FEED had the second-highest BF measurement of the groups. It was only after groups were switched to a common finishing ration that both BACK groups surpassed LEAN/FEED in respect to BF. FAT/FEED had the greatest 12$^{th}$ rib BF thickness, but was not significant over FAT/BACK and LEAN/BACK. Schoonmaker et. al. (2004) found that early weaned steers fed high concentrate diets had the greatest ($P<0.01$) fat depth at 260 d of age. KPH was also significantly lower ($P<0.05$) in LEAN/BACK than other treatments. Dressing percentage was highest in FAT/FEED group and tended to be significant ($P<0.10$) over all groups except LEAN/BACK. One point of interest is the fact that FAT/FEED had the lowest HCWT, but the highest dressing percentage. Steers that went directly to the feedlot had higher

USDA marbling scores than BACK groups. LEAN/FEED had significantly higher marbling than both BACK groups ($P<0.05$), and LEAN/BACK was the lowest. This finding is different than Klopfenstein et. al. (2000), who found that backgrounding programs had no effect on quality grade when adjusted to a fat-constant basis. As well, Schoonmaker et. al. (2004) saw no difference in carcass marbling score, but further analysis showed steers fed high-concentrate diets for extended time periods had the lowest percentage of fat in the longissimus muscle. However, Murphy and Loerch (2004) reported lower carcass quality grades and less $12^{th}$ rib BF in steers fed restricted-energy diets when compared to high-concentrate diets. In a practical sense, the differences in marbling in the current study translate to the distinction between high Select and low Choice. Yet, this information shows that cattle do have the opportunity to have above adequate intramuscular fat while staying relatively lean at the $12^{th}$ rib, indicating that feeding management does influence the ability to reach quality grade targets. LEAN/FEED had significantly less adjusted carcass fat as well as numerically-lower carcass yield grades than other treatments ($P<0.05$). No differences were found between other groups for adjusted fat and carcass yield grade. Again, data indicate that feeding to a fat-constant endpoint can be achieved by feeding strategies regardless of initial fat level or management.

### *Genetic markers*

None of the SNPs were useful for predicting ultrasound BF at weaning or dressing percentage (Table 2.5 and 2.6). Some association was detected with UASMS2 and HCWT ($P<0.10$) resulting in an 11 kg difference between genotype CC and CT ($P<0.05$). This tendency agrees with some research in respect to the growth potential found in UASMS2-CC, as Kononoffet. al. (2005) reported that CC genotype tended to have heavier ($P<0.10$) carcass weights than those of the TT genotype. Lusk (2007) showed that CC had the highest average

daily gains (ADG) over CT and TT and gained 0.047 kg/d more than UASMS2-TT ($P<0.01$). Nkrumah et. al. (2005) found the opposite, that CT and TT genotypes had 9 and 6% greater ADG than CC, but TT genotypes tended to have higher final body weights than CC or CT ($P<0.10$), although the frequency of the T allele of UASMS2 was lower in one specific line of cattle than others in that study. Schenkel et.al. (2005) showed that genotypes for UASMS2 did not significantly affect HCWT.

In the present study, none of the SNPs were predictive of marbling. This coincides with Schenkel et. al. (2005) who found that genotypes for five leptin SNP (UASMS1, UASMS2, UASMS3, E2JW, and E2FB) did not significantly influence quality grade. Nkrumah et.al. (2005) saw animals with the TT genotype of UASMS2 had 13 and 9% increases in marbling score ($P<0.01$) compared with CC or CT genotypes, respectively.

A252T was associated with ribeye area, and genotype TT was larger than AA and AT ($P<0.05$). However, as was found by Schenkel et. al. (2005), a very small percentage of the population has the TT genotype. TT was excluded in the Schenkel study, and 1% of the animals in the current study have genotype TT. Thus, more research needs to be explored in a population with a higher incidence of TT genotypes for its effect on carcass traits.

Four leptin polymorphisms (UASMS1, A1457G, C963T and E2FB) were associated with adjusted fat ($P < 0.05$). TT genotypes were fatter ($P<0.05$) than CC or CT genotypes. For A1457G, AA had greater adjusted fat than AG or GG genotypes. For both C963T and E2FB, CC genotypes were fatter ($P<0.05$) than CT and TT. These results concur with findings about increased carcass fatness and the corresponding genotypes with each SNP (Buchanan et. al, 2002; Lusk, 2007; Nkrumah et. al., 2005; Schenkel et. al., 2005). UASMS2 was moderately associated with adjusted fat ($P<0.10$), and TT genotypes had 2 cm more BF than CC genotypes

($P<0.05$). UASMS2-TT genotypes are associated with increased carcass fat levels by Nkrumah (2004), and Lusk (2007) hypothesized that UASMS-TT cattle deposit fat more quickly than the other genotypes. Those same SNPs were associated with CYG ($P<0.01$). TT genotypes were associated with higher numerical YG in UASMS1 and UASMS2 when compared to CC and CT genotypes ($P<0.05$). As well, AA (A1457G) and CC (C963T and E2FB) genotypes were linked to fatter carcasses.

In conclusion, this study suggests that segregation by initial fatness estimates and feedlot management strategies has the opportunity to increase HCWT by 35 kg when adjusted to a fat-constant endpoint. Data presented revealed significant differences between management practices that could aid in increasing the production efficiency of feedlots. Sorting cattle upon feedlot entry by ultrasound BF and segregation using genetic markers are not competing technologies; both are useful tools that can assist in the estimation of carcass composition in the live animal. With additional research, the possibility exists to incorporate genetic markers into feedlot selection and segregation practices to pinpoint optimal days on feed and assist in marketing decisions.

**Table 2.1 Diet components of full-fed (FEED) and background (BACK) diets**

Full-feed (FEED)

| Ingredient | % DM |
|---|---|
| Rolled Milo | 80.2 |
| Sorghum silage | 14.2 |
| Soybean meal | 3.5 |
| Limestone | 0.9 |
| Rumensin®/Tylan® premix | 0.4 |
| Urea | 0.4 |
| Salt | 0.2 |
| Ammonium Sulfate | 0.2 |

Background (BACK)

| Ingredient | % DM |
|---|---|
| Rolled Milo | 17.0 |
| Sorghum silage | 71.9 |
| Soybean meal | 8.5 |
| Limestone | 1.1 |
| Rumensin®/Tylan® premix | 0.5 |
| Urea | 0.5 |
| Salt | 0.3 |
| Ammonium Sulfate | 0.2 |

**Table 2.2 Characteristics of steers by fatness assessment and herd of origin**

| Item | FAT | LEAN |
|---|---|---|
| Initial weight, kg | 306.5 | 292.9 |
| Initial backfat, mm | 3.42 | 1.82 |
| Initial UEO marbling, score[y] | 4.01 | 3.89 |
| | | |
| | ARCH | CCU |
| Initial weight, lb | 308.5 | 293.3 |
| Initial backfat, mm | 2.52 | 2.66 |
| Initial UEO marbling, score[y] | 4.06 | 3.87 |

[y]Scale of marbling score: 3.0 = Trace 00, 4.0 = Slight 00, 5.0 = Small 00, etc.

**Table 2.3 Steer performance and carcass characteristics**

| | Treatment | | | |
|---|---|---|---|---|
| Item | FAT/BACK | FAT/FEED | LEAN/BACK | LEAN/FEED |
| No. of steers | 46 | 47 | 52 | 48 |
| Means | | | | |
| Initial wt, kg | 306.5 | 307.5 | 292.7 | 294.8 |
| Initial backfat, mm | 3.4 | 3.5 | 1.8 | 1.9 |
| Initial age, d | 251 | 251 | 246 | 247 |
| Harvest age, d | 471 | 429 | 491 | 444 |
| Estimates | | | | |
| Mid-weight, kg | $408.2^{a}$ | $459.9^{b}$ | $395.1^{a}$ | $451.3^{b}$ |
| Mid-backfat, mm | $4.2^{a}$ | $7.2^{b}$ | $2.6^{c}$ | $5.9^{d}$ |
| Mid-ADG, kg/d | $1.12^{a}$ | $1.68^{b}$ | $1.06^{a}$ | $1.70^{b}$ |
| Final wt, kg | $606.0^{a,b}$ | $593.3^{b}$ | $639.6^{c}$ | $617.3^{a,c}$ |
| Final backfat, mm | $11.5^{a}$ | $10.9^{a,b}$ | $10.5^{a,b}$ | $10.0^{b,c}$ |
| Final ADG, kg/d | $1.43^{a}$ | $1.65^{b}$ | $1.50^{a}$ | $1.70^{b}$ |
| Hot carcass wt, kg | $381.0^{a,b}$ | $370.6^{a}$ | $406.0^{c}$ | $388.3^{b}$ |
| $12^{th}$-rib backfat, cm | $1.5^{a}$ | $1.6^{a}$ | $1.3^{a}$ | $1.2^{b}$ |
| Kidney, pelvic, and heart fat, % carcass wt | $2.5^{a}$ | $2.5^{a}$ | $2.5^{a}$ | $2.1^{b}$ |
| Dressing percent, % | $64.1^{a}$ | $66.4^{b}$ | $65.3^{b,c}$ | $65.1^{c}$ |
| Marbling score[y] | $4.9^{a,b}$ | $5.4^{a,c}$ | $4.7^{b}$ | $5.4^{c}$ |
| Ribeye area, $cm^2$ | 88.4 | 91.0 | 89.7 | 92.9 |
| Adjusted backfat, cm | $1.6^{a}$ | $1.5^{a}$ | $1.5^{a}$ | $1.1^{b}$ |
| USDA Yield grade, score[z] | $3.3^{a}$ | $3.1^{a}$ | $3.3^{a}$ | $2.7^{b}$ |

Superscripts across a row are different at $P \leq 0.05$.

[y] Scale of marbling score: 3.0 = Trace 00, 4.0 = Slight 00, 5.0 = Small 00, etc.

[z] Yield grade calculated using the official USDA formula = 2.5 + (2.5 x adjusted $12^{th}$ rib back fat thickness) + (0.0038 x hot carcass weight, lb) + (0.2 x percentage kidney, pelvic, and heart fat) – (0.32 x ribeye area, square inches).

**Table 2.4 Genotypic percentages of SNP markers by sire**

| | | T945M | | | UASMS1 | | | UASMS2 | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Sire | n | CC | CT | TT | CC | CT | TT | CC | CT | TT |
| 234 | 4 | 100 | 0 | 0 | 0 | 75 | 25 | 0 | 75 | 25 |
| 276 | 3 | 100 | 0 | 0 | 0 | 66.7 | 33.3 | 0 | 66.7 | 33.3 |
| 42 | 14 | 100 | 0 | 0 | 7.1 | 35.7 | 57.1 | 7.1 | 42.9 | 50 |
| 692 | 13 | 53.8 | 46.1 | 0 | 61.5 | 30.8 | 7.7 | 81.8 | 18.2 | 0 |
| 808 | 7 | 100 | 0 | 0 | 14.3 | 42.9 | 42.9 | 14.3 | 57.1 | 28.6 |
| 962 | 15 | 100 | 0 | 0 | 21.4 | 42.9 | 35.7 | 35.7 | 28.6 | 35.7 |
| EXP | 2 | 100 | 0 | 0 | 50 | 50 | 0 | 50 | 50 | 0 |
| GEE | 11 | 90.9 | 9.1 | 0 | 66.7 | 33.3 | 0 | 63.6 | 36.4 | 0 |
| GENC | 7 | 100 | 0 | 0 | 14.3 | 57.1 | 28.6 | 28.6 | 57.1 | 14.3 |
| GPD | 11 | 100 | 0 | 0 | 0 | 81.8 | 18.2 | 20 | 70 | 10 |
| GT | 20 | 90 | 10 | 0 | 36.8 | 47.4 | 15.8 | 55 | 25 | 20 |
| PBA | 27 | 96.3 | 3.7 | 0 | 25.9 | 55.6 | 18.5 | 51.8 | 48.1 | 0 |
| PBT | 56 | 96.4 | 3.6 | 0 | 31.5 | 38.9 | 29.6 | 33.3 | 44.4 | 22.2 |
| PE | 8 | 100 | 0 | 0 | 0 | 50 | 50 | 62.5 | 25 | 12.5 |
| Rito | 2 | 100 | 0 | 0 | 0 | 100 | 0 | 0 | 100 | 0 |
| TOTAL | 200 | 94 | 6 | 0 | 26.8 | 46.9 | 26.3 | 39.2 | 42.8 | 18.1 |

| | | A1457G | | | C963T | | | E2FB | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Sire | n | AA | AG | GG | CC | CT | TT | CC | CT | TT |
| 234 | 4 | 25 | 75 | 0 | 25 | 75 | 0 | 25 | 75 | 0 |
| 276 | 3 | 33.3 | 66.7 | 0 | 33.3 | 66.7 | 0 | 0 | 100 | 0 |
| 42 | 14 | 57.1 | 35.7 | 7.1 | 57.1 | 35.7 | 7.1 | 57.1 | 35.7 | 7.1 |
| 692 | 13 | 7.7 | 30.8 | 61.5 | 7.7 | 30.8 | 61.5 | 7.7 | 30.8 | 61.5 |
| 808 | 7 | 42.9 | 42.9 | 14.3 | 42.9 | 42.9 | 14.3 | 28.6 | 57.1 | 14.3 |
| 962 | 15 | 33.3 | 46.7 | 20 | 40 | 40 | 20 | 33.3 | 46.7 | 20 |
| EXP | 2 | 0 | 50 | 50 | 0 | 50 | 50 | 0 | 50 | 50 |
| GEE | 11 | 0 | 45.4 | 54.6 | 0 | 45.4 | 54.6 | 0 | 36.4 | 63.6 |
| GENC | 7 | 28.6 | 57.1 | 14.3 | 28.6 | 57.1 | 14.3 | 14.3 | 42.9 | 42.8 |
| GPD | 11 | 18.2 | 81.8 | 0 | 18.2 | 81.8 | 0 | 18.2 | 72.7 | 9.1 |
| GT | 20 | 15 | 45 | 40 | 15 | 45 | 40 | 5 | 45 | 50 |
| PBA | 27 | 14.8 | 55.6 | 29.6 | 18.5 | 55.6 | 25.9 | 14.8 | 55.6 | 29.6 |
| PBT | 56 | 30.9 | 40 | 29.1 | 30.9 | 38.2 | 30.9 | 30.3 | 39.3 | 30.4 |
| PE | 8 | 50 | 50 | 0 | 50 | 50 | 0 | 50 | 50 | 0 |
| Rito | 2 | 0 | 100 | 0 | 0 | 100 | 0 | 0 | 100 | 0 |
| TOTAL | 200 | 25.6 | 47.7 | 26.6 | 26.6 | 46.7 | 26.6 | 23 | 47 | 30 |

**Table 2.4 Genotypic percentages of SNP markers by sire (continued)**

| | | A252T | | | G200A | | | K232A | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Sire | n | AA | AT | TT | AA | AG | GG | PP | PQ | QQ |
| 234 | 4 | 100 | 0 | 0 | 0 | 0 | 100 | 33.3 | 33.3 | 33.3 |
| 276 | 3 | 66.7 | 33.3 | 0 | 0 | 66.7 | 33.3 | 0 | 66.7 | 33.3 |
| 42 | 14 | 100 | 0 | 0 | 0 | 21.4 | 78.6 | 84.6 | 15.4 | 0 |
| 692 | 13 | 100 | 0 | 0 | 0 | 23.1 | 76.9 | 84.6 | 15.4 | 0 |
| 808 | 7 | 100 | 0 | 0 | 0 | 14.3 | 85.7 | 83.3 | 16.7 | 0 |
| 962 | 15 | 93.3 | 6.7 | 0 | 0 | 20 | 80 | 86.6 | 13.3 | 0 |
| EXP | 2 | 100 | 0 | 0 | 0 | 100 | 0 | 100 | 0 | 0 |
| GEE | 11 | 90.9 | 9.1 | 0 | 0 | 54.5 | 45.5 | 20 | 70 | 10 |
| GENC | 7 | 71.4 | 14.3 | 14.3 | 0 | 28.6 | 71.4 | 100 | 0 | 0 |
| GPD | 11 | 81.8 | 18.2 | 0 | 0 | 18.2 | 81.8 | 81.8 | 18.2 | 0 |
| GT | 20 | 80 | 15 | 5 | 5 | 29 | 75 | 77.8 | 16.7 | 5.6 |
| PBA | 27 | 88.9 | 11.1 | 0 | 3.7 | 37 | 59.3 | 64 | 28 | 8 |
| PBT | 56 | 96.4 | 3.6 | 0 | 3.6 | 25 | 71.4 | 95.9 | 4.1 | 0 |
| PE | 8 | 100 | 0 | 0 | 0 | 0 | 100 | 100 | 0 | 0 |
| Rito | 2 | 100 | 0 | 0 | 0 | 50 | 50 | 0 | 100 | 0 |
| TOTAL | 200 | 92 | 7 | 1 | 2 | 26.5 | 71.5 | 79.2 | 17.5 | 3.3 |

**Table 2.5 Prediction of ultrasound backfat at weaning using SNP markers**

| SNP | P-Value | GENOTYPES | MEANS (mm) | SE |
|---|---|---|---|---|
| T945M | 0.91 | CC | 2.6 | 0.08 |
| | | CT | 2.6 | 0.31 |
| | | TT | - | - |
| UASMS1 | 0.13 | CC | 2.6 | 0.15 |
| | | CT | 2.7 | 0.11 |
| | | TT | 2.4 | 0.14 |
| UASMS2 | 0.59 | CC | 2.6 | 0.12 |
| | | CT | 2.7 | 0.12 |
| | | TT | 2.5 | 0.18 |
| A1457G | 0.27 | AA | 2.4 | 0.15 |
| | | AG | 2.7 | 0.11 |
| | | GG | 2.6 | 0.15 |
| C963T | 0.25 | CC | 2.4 | 0.15 |
| | | CT | 2.7 | 0.11 |
| | | TT | 2.6 | 0.15 |
| E2FB | 0.40 | CC | 2.4 | 0.16 |
| | | CT | 2.7 | 0.11 |
| | | TT | 2.7 | 0.14 |
| A252T | 0.79 | AA | 2.6 | 0.08 |
| | | AT | 2.7 | 0.28 |
| | | TT | 3.0 | 0.76 |
| G200A | 0.46 | AA | 3.2 | 0.53 |
| | | AT | 2.7 | 0.15 |
| | | TT | 2.6 | 0.09 |
| K232A | 0.95 | PP | 2.6 | 0.09 |
| | | PQ | 2.6 | 0.19 |
| | | QQ | 2.6 | 0.43 |

**Table 2.6 Prediction of dressing percentage using SNP markers**

| SNP | P-Value | GENOTYPES | MEANS (%) | SE |
|---|---|---|---|---|
| T945M | 0.96 | CC | 65.3 | 0.11 |
| | | CT | 65.3 | 0.46 |
| | | TT | - | - |
| UASMS1 | 0.27 | CC | 65.2 | 0.22 |
| | | CT | 65.2 | 0.16 |
| | | TT | 65.6 | 0.21 |
| UASMS2 | 0.50 | CC | 65.3 | 0.18 |
| | | CT | 65.1 | 0.17 |
| | | TT | 65.4 | 0.26 |
| A1457G | 0.35 | AA | 65.5 | 0.21 |
| | | AG | 65.2 | 0.16 |
| | | GG | 65.1 | 0.22 |
| C963T | 0.20 | CC | 65.6 | 0.21 |
| | | CT | 65.1 | 0.16 |
| | | TT | 65.2 | 0.21 |
| E2FB | 0.21 | CC | 65.6 | 0.23 |
| | | CT | 65.2 | 0.16 |
| | | TT | 65.1 | 0.20 |
| A252T | 0.79 | AA | 65.3 | 0.11 |
| | | AT | 65.1 | 0.41 |
| | | TT | 65.7 | 1.09 |
| G200A | 0.55 | AA | 66.1 | 0.76 |
| | | AT | 65.2 | 0.21 |
| | | TT | 65.3 | 0.13 |
| K232A | 0.91 | PP | 65.3 | 0.13 |
| | | PQ | 65.4 | 0.29 |
| | | QQ | 65.4 | 0.64 |

**Table 2.7 Prediction of hot carcass weight using SNP markers**

| SNP | P-Value | GENOTYPES | MEANS (kg) | SE |
|---|---|---|---|---|
| T945M | 0.18 | CC | 387.8 | 2.23 |
| | | CT | 375.3 | 9.04 |
| | | TT | - | - |
| UASMS1 | 0.22 | CC | 390.4 | 4.26 |
| | | CT | 383.8 | 3.16 |
| | | TT | 392.2 | 4.21 |
| UASMS2 | 0.08 | CC | 393.6[a] | 3.53 |
| | | CT | 382.6[b] | 3.33 |
| | | TT | 388.5 | 5.15 |
| A1457G | 0.30 | AA | 390.7 | 4.26 |
| | | AG | 383.6 | 3.13 |
| | | GG | 389.9 | 4.27 |
| C963T | 0.26 | CC | 390.8 | 4.15 |
| | | CT | 383.5 | 3.13 |
| | | TT | 390.5 | 4.25 |
| E2FB | 0.20 | CC | 390.5 | 4.49 |
| | | CT | 383.0 | 3.12 |
| | | TT | 391.0 | 4.01 |
| A252T | 0.77 | AA | 386.9 | 2.27 |
| | | AT | 388.0 | 8.14 |
| | | TT | 402.5 | 21.67 |
| G200A | 0.28 | AA | 365.7 | 14.97 |
| | | AT | 389.9 | 4.18 |
| | | TT | 386.6 | 2.55 |
| K232A | 0.35 | PP | 387.0 | 2.49 |
| | | PQ | 391.6 | 5.44 |
| | | QQ | 373.0 | 11.93 |

Within a column, superscripts a and b differ $P \leq 0.05$.

**Table 2.8 Prediction of carcass marbling score using SNP markers**

| SNP | P-Value | GENOTYPES | MEANS (score) | SE |
|---|---|---|---|---|
| T945M | 0.85 | CC | 5.1 | 0.06 |
| | | CT | 5.2 | 0.24 |
| | | TT | - | - |
| UASMS1 | 0.94 | CC | 5.1 | 0.11 |
| | | CT | 5.1 | 0.08 |
| | | TT | 5.1 | 0.11 |
| UASMS2 | 0.88 | CC | 5.1 | 0.10 |
| | | CT | 5.2 | 0.09 |
| | | TT | 5.1 | 0.14 |
| A1457G | 0.97 | AA | 5.1 | 0.11 |
| | | AG | 5.1 | 0.08 |
| | | GG | 5.1 | 0.11 |
| C963T | 0.93 | CC | 5.2 | 0.11 |
| | | CT | 5.1 | 0.08 |
| | | TT | 5.1 | 0.11 |
| E2FB | 0.86 | CC | 5.2 | 0.12 |
| | | CT | 5.1 | 0.08 |
| | | TT | 5.1 | 0.11 |
| A252T | 0.69 | AA | 5.1 | 0.06 |
| | | AT | 5.3 | 0.22 |
| | | TT | 5.0 | 0.57 |
| G200A | 0.51 | AA | 4.8 | 0.40 |
| | | AT | 5.2 | 0.11 |
| | | TT | 5.1 | 0.07 |
| K232A | 0.65 | PP | 5.1 | 0.07 |
| | | PQ | 5.2 | 0.15 |
| | | QQ | 5.2 | 0.33 |

**Table 2.9 Prediction of kidney, pelvic and heart fat using SNP markers**

| SNP | P-Value | GENOTYPES | MEANS (%) | SE |
|---|---|---|---|---|
| T945M | 0.29 | CC | 2.4 | 0.04 |
| | | CT | 2.6 | 0.15 |
| | | TT | - | - |
| UASMS1 | 0.19 | CC | 2.4 | 0.07 |
| | | CT | 2.3 | 0.05 |
| | | TT | 2.5 | 0.07 |
| UASMS2 | 0.17 | CC | 2.4 | 0.06 |
| | | CT | 2.4 | 0.06 |
| | | TT | 2.6 | 0.09 |
| A1457G | 0.20 | AA | 2.5 | 0.07 |
| | | AG | 2.3 | 0.05 |
| | | GG | 2.4 | 0.07 |
| C963T | 0.16 | CC | 2.5 | 0.07 |
| | | CT | 2.3 | 0.05 |
| | | TT | 2.4 | 0.07 |
| E2FB | 0.15 | CC | 2.5 | 0.08 |
| | | CT | 2.3 | 0.05 |
| | | TT | 2.4 | 0.07 |
| A252T | 0.95 | AA | 2.4 | 0.04 |
| | | AT | 2.4 | 0.14 |
| | | TT | 2.3 | 0.37 |
| G200A | 0.10 | AA | 2.9 [a,c] | 0.25 |
| | | AT | 2.3 [b] | 0.07 |
| | | TT | 2.4 [d] | 0.04 |
| K232A | 0.49 | PP | 2.4 | 0.04 |
| | | PQ | 2.3 | 0.09 |
| | | QQ | 2.4 | 0.20 |

Within a column, superscripts a and b differ P≤0.05, and c and d differ P≤0.10.

**Table 2.10 Prediction of ribeye area using SNP markers**

| SNP | P-Value | GENOTYPES | MEANS ($cm^2$) | SE |
|---|---|---|---|---|
| T945M | 0.61 | CC | 90.6 | 0.58 |
| | | CT | 89.4 | 2.39 |
| | | TT | - | - |
| UASMS1 | 0.71 | CC | 90.8 | 1.16 |
| | | CT | 90.8 | 0.84 |
| | | TT | 89.7 | 1.10 |
| UASMS2 | 0.56 | CC | 91.2 | 0.97 |
| | | CT | 90.5 | 0.90 |
| | | TT | 89.4 | 1.35 |
| A1457G | 0.98 | AA | 90.3 | 1.10 |
| | | AG | 90.6 | 0.84 |
| | | GG | 90.6 | 1.10 |
| C963T | 0.89 | CC | 90.1 | 1.10 |
| | | CT | 90.6 | 0.84 |
| | | TT | 90.8 | 1.10 |
| E2FB | 0.89 | CC | 90.1 | 1.16 |
| | | CT | 90.6 | 0.84 |
| | | TT | 90.8 | 1.03 |
| A252T | 0.06 | AA | 90.6 [a] | 0.58 |
| | | AT | 88.1 [a] | 2.06 |
| | | TT | 102.0 [b] | 5.55 |
| G200A | 0.33 | AA | 85.2 | 3.87 |
| | | AT | 91.2 | 1.10 |
| | | TT | 90.5 | 0.65 |
| K232A | 0.41 | PP | 90.5 | 0.71 |
| | | PQ | 91.6 | 1.48 |
| | | QQ | 86.9 | 3.29 |

Within a column, superscripts a and b differ $P \leq 0.05$.

**Table 2.11 Prediction of adjusted carcass fat using SNP markers**

| SNP | P-Value | GENOTYPES | MEANS (cm) | SE |
|---|---|---|---|---|
| T945M | 0.71 | CC | 1.4 | 0.03 |
| | | CT | 1.5 | 0.13 |
| | | TT | - | - |
| UASMS1 | 0.01 | CC | 1.4 [a] | 0.05 |
| | | CT | 1.4 [a] | 0.05 |
| | | TT | 1.6 [b] | 0.05 |
| UASMS2 | 0.06 | CC | 1.4 [c] | 0.05 |
| | | CT | 1.4 | 0.05 |
| | | TT | 1.6 [d] | 0.05 |
| A1457G | 0.01 | AA | 1.6 [a] | 0.05 |
| | | AG | 1.4 [b] | 0.05 |
| | | GG | 1.4 [b] | 0.05 |
| C963T | 0.01 | CC | 1.6 [a] | 0.05 |
| | | CT | 1.4 [b] | 0.05 |
| | | TT | 1.4 [b] | 0.05 |
| E2FB | 0.01 | CC | 1.6 [a] | 0.05 |
| | | CT | 1.4 [b] | 0.05 |
| | | TT | 1.4 [b] | 0.05 |
| A252T | 0.98 | AA | 1.4 | 0.03 |
| | | AT | 1.4 | 0.13 |
| | | TT | 1.4 | 0.30 |
| G200A | 0.14 | AA | 1.8 | 0.20 |
| | | AT | 1.4 | 0.05 |
| | | TT | 1.4 | 0.03 |
| K232A | 0.15 | PP | 1.4 | 0.03 |
| | | PQ | 1.3 | 0.08 |
| | | QQ | 1.4 | 0.18 |

Within a column, superscripts a and b differ P≤0.05, and c and d differ P≤0.10.

**Table 2.12 Prediction of carcass yield grade using SNP markers**

| SNP | P-Value | GENOTYPES | MEANS (score) | SE |
|---|---|---|---|---|
| T945M | 0.77 | CC | 3.1 | 0.04 |
| | | CT | 3.2 | 0.16 |
| | | TT | - | - |
| UASMS1 | 0.002 | CC | 3.1 | 0.07 |
| | | CT | 3.0 [a] | 0.05 |
| | | TT | 3.4 [b] | 0.07 |
| UASMS2 | 0.01 | CC | 3.1 [a] | 0.06 |
| | | CT | 3.1 [a] | 0.06 |
| | | TT | 3.4 [b] | 0.09 |
| A1457G | 0.01 | AA | 3.3 [a] | 0.07 |
| | | AG | 3.1 [b] | 0.05 |
| | | GG | 3.1 [b] | 0.07 |
| C963T | 0.004 | CC | 3.3 [a] | 0.07 |
| | | CT | 3.0 [b] | 0.05 |
| | | TT | 3.1 [b] | 0.07 |
| E2FB | 0.01 | CC | 3.3 [a] | 0.07 |
| | | CT | 3.0 [b] | 0.05 |
| | | TT | 3.1 [b] | 0.07 |
| A252T | 0.56 | AA | 3.2 | 0.06 |
| | | AT | 3.2 | 0.21 |
| | | TT | 2.6 | 0.57 |
| G200A | 0.45 | AA | 3.4 | 0.26 |
| | | AT | 3.1 | 0.07 |
| | | TT | 3.1 | 0.04 |
| K232A | 0.45 | PP | 3.1 | 0.04 |
| | | PQ | 3.1 | 0.10 |
| | | QQ | 3.4 | 0.21 |

Within a column, superscripts a and b differ $P \leq 0.05$.

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# CHAPTER 3 - Effect of Adding Aureomycin® or Rumensin® to Mineral Supplements on Summer Beef Cowherd Performance


## Abstract

Two hundred forty-six head of commercial Angus-based cows were used to determine the effect of adding Aureomycin® or Rumensin® to mineral supplements on summer beef cowherd performance. Cow/calf pairs were randomly allotted to summer native pasture groups by treatment and fed an industry-standard mineral/trace mineral supplement for the duration of the trial. The study consisted of three treatments: (1) negative control fed a base mineral/trace mineral supplement with no medication added, (2) cattle fed same base supplement with the addition of Aureomycin (0.5 mg/45.3 kg cow body weight daily), and (3) cattle fed same base supplement with the addition of Rumensin (200 mg/hd/d). Feed additives were mixed in to provide recommended average daily consumption. Treatments were initiated May 6 and cows were weighed, body condition scored (BCS) and calves were weighed. Cow and calf weights and cow BCS were recorded on June 6 and October 6.Cow and calf performance data and herd health records were recorded and used as response variables to treatments. Mineral intake was consistent with no statistical difference between treatments. Cow and calf weight gains were similar among treatments during the first 32 days of the study and no significant differences in cow body condition score gains and pregnancy rates were found. Total calf gains for the duration of the trial were similar for Aureomycin- and Rumensin-supplemented groups, and both were 9 and 7 kg greater, respectively, than for control calves ($P < 0.01$). Overall herd health was enhanced by feeding Aureomycin when compared to control or Rumensin ($P < 0.01$). Foot rot was the main health concern in this trial, and the addition of Aureomycin to mineral supplements reduced foot rot ($P < 0.01$) by 50 to 67% over other treatments.

## Introduction

Mineral supplementation is an important practice for cow/calf operations in order to meet cow mineral requirements that are not satisfied by summer grazing practices. Lack of specific minerals can lead to decreased cow weights, calf gains, and reproductive rates. Still, the addition of medicated mineral premixes over and above standard mineral packages has the benefit of increasing cowherd performance and weight gains while reducing herd health concerns. The objective of this study was to show that cow/calf pairs fed medicated mineral supplements would have greater cow and calf weights, cow body condition scores and decreased incidence of sickness when compared to standard mineral supplements.

## Materials and Methods

To evaluate the effect of including Aureomycin or Rumensin to mineral supplements on summer cowherd performance, two hundred forty-six commercial Angus-based cow/calf pairs were used and randomly allotted to three treatment groups that were balanced for dam and calf age. Cows were weighed and body condition scored April 26 to establish baseline measures. Cows were weighed, body condition scored and calves were weighed again May 6 then sorted into treatment pastures. Pasture groups were allotted randomly to treatments. All animals grazed native pastures with water available at all times. Cattle were rotated among the pastures on a two- to four-week schedule. A standard mineral/trace mineral supplement was provided to all pastures throughout the duration of the trial. All treatments were administered on a hand-fed basis in an industry-standard mineral supplement, and feed additives were included to provide recommended average daily consumption. Treatments consisted of: (1) negative control fed a base mineral/trace mineral supplement with no medication added, (2) cattle fed same base supplement with the addition of Aureomycin-90 (chlortetracycline HCl, 0.5 mg/ 45.3 kg body

weight), and (3) cattle fed same base supplement with the addition of Rumensin (monensin sodium, 200 mg/head/d). All cattle had free-choice access to mineral feeders throughout the trial. Mineral supplement consumption was monitored weekly, orts recorded, and concentrations of medications were maintained within manufacturer recommended levels. On October 5, cows were weighed and body condition scored, and calf weaning weight was recorded as their individual weaning weight. Cowherd performance data was used as response variables to treatments. Cow weights, gains, body condition scores, and pregnancy rates were measured. Cow weight and condition score were measured at the beginning of the trial, immediately prior to the breeding season, and on the weaning date. Cow/calf pairs were gathered in the late afternoon one day prior to measuring cattle weights and fed 4.5 kg/pair of prairie hay in drylots with no access to water. Cows and calves were separated just before weighing and body condition scoring, which began early the next morning. Body condition (scale 1 to 9, 1=emaciated, 9=obese) was determined by averaging the estimates obtained from four independent observers. Observers used both visual and palpation techniques to determine their score.

Blood samples were taken May 16 and May 26 to determine the percentage of cows cycling prior to estrous synchronization and breeding. Estrous synchronization consisted of two shots of $PGF_{2\alpha}$ on May 26 and June 6 to initiate the breeding season. Cows were artificially inseminated to three purebred Angus bulls from June 7 through June 11 using heat detection and the AM/PM rule. Polled Hereford bulls were then turned out on June 15 for natural service. Natural breeding season lasted 65 days. Pregnancy confirmation by rectal palpation occurred from October 14 to October 22.

In addition, cow and calf incidence of bovine respiratory disease, foot rot, pinkeye, and general health concerns for cattle grazing pastures were measured throughout the study. Nasal swabs were collected from 15 cows and their calves in the control group and 15 cows and calves in the Aureomycin group on May 6, the initiation of the trial. At weaning and weighing, nasal swabs were taken again from cows and calves that had shown positive results from the first swabs. Sickness, health treatments, and mortality records were kept on the entire herd. Cows and calves were vaccinated and processed according to protocol designed by our consulting veterinarian.

Data were hand recorded and transferred to digital format for statistical analysis. Pasture groups were the experimental units. Appropriate models and procedures were developed for statistical analysis of least squares means' comparisons using the PROC GLM procedure in SAS version 8.2. Beginning weights and body condition scores were included as covariates. Models developed to analyze calf weight gain included date of birth and sex as independent variables. More specifically, orthogonal contrasts that compared the medication versus non-medication and Aureomycin versus Rumensin were used for statistical analysis. The PROC CATMOD procedure is SAS version 8.2 was used to determine the probability of differences between treatments' least squares means recorded as categorical response variables (health and pregnancy).

## Results and Discussion

Mineral intake was consistent between treatments. Table 3.1 indicates daily mineral consumption was between 124.7 and 147.4 g per cow/calf pair. Mineral intake was similar among treatments, but numerically the Rumensin-containing mineral was consumed in lesser amounts than the other mineral mixes. Records show that mineral intake remained fairly constant from the beginning to the end of the trial. Rumensin intake averaged 216 mg/hd/d. Aureomycin intake averaged 910 mg/hd/d. The average weight of the Aureomycin fed cows was 492 kg. Therefore, cows consumed an average of 84 mg Aureomycin/45.3 kg body weight throughout the trial.

Cattle performance was measured for both cows and calves. Table 3.2 lists the weights, body condition scores, and pregnancy rate of the cows. Remarkably, cows gained nearly 1.7 kg/d during the first 32 d of the trial. These dates correspond to the 32 d prior to the start of the breeding season. Much of the weight gain can be attributed to gut fill as pasture quality improved over this period due to warming temperatures and rainfall of the month of May 2004. Cow and calf weight gains increased similarly among treatments during the first 32 d of the experiment. Cows in T3 (Rumensin) gained about 0.1 body condition score more than T2 (Aureomycin) cows. However, by weaning time all treatments had similar gains in body condition score. Body condition scores remained similar between treatments throughout the trial. Pregnancy rates were similar between treatments, ranging from 88.9 to 92.0% successful diagnosis of pregnancy.

Calf gains were similar among treatments during the first 32 d of the trial (Table 3.2). Total calf gains for the duration of the experiment were similar for T2 and T3 (Aureomycin and Rumensin), and both were 8 kg greater than for T1 calves. It appears that summer pastures along with mineral supplementation containing medication will increase the amount of saleable

product without sacrificing cowherd weight, body condition or reproductive rates. This is extremely important to cow/calf producers looking to reduce the unit cost of production.

Table 3.3 shows the experimental results concerning herd health. Herd health was greatly enhanced by feeding Aureomycin when compared to the control or Rumensin-fed cattle ($P < 0.01$). The most common illness detected and treated was foot rot. It appears from our data that adding Aureomycin to mineral supplements have the possibility of reducing the incidence of foot rot ($P < 0.01$) by 50 to 67%. Pinkeye and respiratory diseases were minimal throughout the trial period. Combining all categories of illness, cattle fed Aureomycin incurred much fewer bouts of sickness ($P < 0.01$). Five cattle were treated for injuries not considered to be related to treatments. These injuries included snakebite, cuts and other irregularities.

In summary, the addition of either Aureomycin or Rumensin to mineral supplements fed to cow/calf pairs grazing summer pastures will increase calf weaning weights without sacrificing cowherd weight, body condition, or reproductive rates. The addition of Aureomycin to mineral supplements reduced the incidence of foot rot. This can lead to substantial savings in medical costs, labor costs, and animal handling.

**Table 3.1 Average intake of mineral mixes used in experiment**

| | Treatment | | |
|---|---|---|---|
| Item | Control | Aureomycin | Rumensin |
| No. of cow/calf pairs | 62 | 91 | 93 |
| No. of pasture groups | 2 | 3 | 3 |
| Mineral intake, gm/pair/d | 138.9 | 147.4 | 124.7 |
| Medication intake, mg/pair/d | 0 | 910 | 216 |

**Table 3.2 Effects of mineral medication treatments on cowherd performance**

| | Treatment | | | Contrast | |
|---|---|---|---|---|---|
| Item | Control | Aureomycin | Rumensin | Control vs. Medicated | Aureomycin vs. Rumensin |
| *Cowherd data* | | | | | |
| Initial cow weight, kg | 461 | 443 | 443 | | |
| Initial BCS[a] | 5.0 | 4.8 | 4.7 | | |
| Initial calf weight, kg | 99 | 98 | 100 | | |
| *Performance from the start of the trial to the beginning of breeding season (32 days)* | | | | | |
| Cow breeding weight, kg | 503 | 498 | 503 | .25 | .07 |
| Cow breeding BCS | 5.0 | 5.0 | 5.1 | .52 | .19 |
| Calf weight, kg | 137 | 137 | 137 | .82 | .73 |
| Cow wt gain, kg | 55 | 52 | 54 | .61 | .32 |
| BCS change | .15 | .18 | .30 | .08 | .03 |
| Calf wt gain, kg | 38 | 38 | 38 | .87 | .45 |
| *Performance from the start of the trial to weaning (152 days)* | | | | | |
| Weaning cow weight, kg | 542 | 536 | 535 | .14 | .95 |
| Weaning cow BCS | 5.1 | 5.1 | 5.0 | .40 | .18 |
| Calf weaning wt, kg | 254 | 263 | 264 | .01 | .74 |
| Cow wt gain, kg | 93 | 90 | 87 | .28 | .60 |
| BCS change | .2 | .2 | .2 | .52 | .98 |
| Calf wt gain, kg | 156 | 164 | 164 | .01 | .97 |
| Pregnancy rate, % | 90.2 | 92.0 | 88.9 | .95 | .49 |

[a]BCS is body condition score, estimated on a scale of 1 = emaciated to 9= obese.

**Table 3.3 Effect of mineral treatments on the incidence of cowherd health problems**

| | Treatment | | | |
|---|---|---|---|---|
| Item | Control | Aureomycin | Rumensin | P-value |
| | (Number of Cattle Treated for Illness) | | | |
| Foot rot | 26 | 12 | 36 | .0006 |
| Pink eye | 1 | 0 | 1 | .99 |
| Respiratory diseases | 0 | 0 | 1 | .99 |
| All illnesses | 27 | 12 | 38 | .003 |
| Other (injury, etc.) | 3 | 0 | 2 | .99 |