Southern Branch ADSA Graduate Student Paper Competition

218 Effect of length of cut and degree of kernel processing of corn silage on production characteristics of lactating Holstein cows. K. M. Cooke* and J. K. Bernard, *The University of Georgia, Tifton*.

Forty mid-lactation Holstein cows were used in a 9-wk randomized block trial to determine the effect of the degree of kernel processing (KP) and theoretical length of cut (TLC) on nutrient intake and digestibility and milk yield and composition. Corn was harvested at 3/4 milk line stage of maturity at either 1.90 or 2.54-cm TLC. At each TLC, corn was processed at either 2 or 8-mm roll clearance. A control was harvested at 1.90-cm TLC without processing. All treatments were stored in 2.4 m plastic bags and allowed to ferment approximately 5 mo before feeding. Corn silage provided 38% of the DM in the experimental diets which were fed once daily behind Calan doors. No differences in DM or nutrient intake were observed among treatments. Milk yield tended to be higher ($P = 0.07$) for cows fed processed versus unprocessed corn silage (36.0 vs. 35.4 kg/d, respectively). No differences were observed in milk fat (3.88%) or protein (3.10%) due to TLC or KP. However, an interaction between TLC and KP was observed for yield of milk ($P = 0.09$), fat ($P = 0.09$), protein ($P = 0.01$), and energy-corrected milk ($P = 0.03$) because of high yield for cows fed diets containing corn silage processed at 2 mm versus 8 mm at 2.54-cm TLC. Whole tract NDF digestibility tended to be higher ($P = 0.06$) for cows fed processed versus unprocessed corn silage (60.9 vs. 50.1%, respectively) and for animals fed corn silage chopped at 2.54 vs. 1.90-cm (64.4 vs. 54.9%, respectively). Starch digestibility was greater ($P = 0.003$) for corn silage processed at 2 versus 8-mm (92.1 vs. 86.0%, respectively). These results indicate that as TLC increases, the degree of KP becomes more critical for maintaining fiber digestibility and milk yield.

Key Words: Corn Silage, Kernel Processing, Theoretical Chop Length

219 Evaluating the effectiveness of decreasing the dosage of GnRH for ovulation synchronization and timed AI in dairy cows. L. E. McKee*, W. M. Graves, and J. D. Clark, *The University of Georgia, Athens*.

The objective of this study was to determine the effectiveness of decreasing the dose of GnRH (Cystorelin, Merial Limited, Duluth, GA) used in the ovulation synchronization (Ovsynch) protocol. First service lactating Holstein cows (n=100) at the University of Georgia Dairy Center in Athens were randomly assigned to 1 of 4 treatment groups (25/trt). All cows received 25 mg of PGF2α (Lutalyse, Pfizer Animal Health, New York, NY) 11 days (d -11) prior to starting Ovsynch. Cows in treatment 1 received 100 μg GnRH on day 0, 25 mg PGF2α on day 7, and 100 μg GnRH on day 9. Treatment 2 received 50 μg GnRH on day 0, 25 mg PGF2α on day 7, and 100 μg GnRH on day 9. Treatment 3 received 100 μg GnRH on day 0, 25 mg PGF2α on day 7, and 50 μg GnRH on day 9. Treatment 4 received 50 μg GnRH on day 0, 25 mg PGF2α on day 7, and 50 μg GnRH on day 9. All injections were given i.m. Blood samples were collected on days -11 and 0 for progesterone analysis. All cows were artificially inseminated (AI) 16-20 hours after the second GnRH injection. Pregnancy was checked via ultrasound at 35-40 days and 55-60 days after AI. Data was analyzed by Chi Square. The 100 cows averaged 2.3 lactations, 68 days in milk and 88 lb of milk on DHIA. Pregnancy rates at 35-40 days were 52%, 32%, 44%, and 56% for treatments 1, 2, 3, & 4 respectively (P>.05, NS). At 55-60 days, the rates were 36%, 28%, 36%, and 48% (NS). Embryonic losses between days 40 and 60 were 16%, 4%, 8%, & 8%. Overall pregnancy rates were 46% at 40 days and 37% at 60 days (NS). A total of 14 of the 100 cows were considered to be noncyclic (both samples < 1.0 ng/ml), and only 2 of these were pregnant at 35-40 days versus 44 of the 86 cyclic cows (either or both samples > or = 1.0 ng/ml). A total of 28.8% of 28 were pregnant at 55-60 days when the highest temperature-humidity index (THI) on the day bred was > or = 80, 45.2% of 31 when the THI was between 70-79 and 36.6% of 41 when the THI high was 69 or < (NS). During the 11 months of this study, days open on DHIA decreased 34 days.

Key Words: Ovulation Synchronization, Timed AI, GnRH

Physiology of Lactation

220 Use of serial analysis of gene expression (SAGE) for gene transcript profiling in lactating bovine mammary gland. E. E. Connor*, A. V. Capuco, and T. S. Sonstegard, *USDA-ARS, Bovine Functional Genomics Laboratory, Beltsville, MD*.

Serial analysis of gene expression (SAGE) methodology permits quantitative analysis of global gene expression in a given tissue and is useful for comparison of gene expression patterns across physiological states and identification of novel transcripts. At present, only three SAGE libraries have been produced in cattle from cultured kidney, cultured aorta and immature B cells, and are publicly available in the NCBI SAGEMap database (http://www.ncbi.nlm.nih.gov/SAGE/). Our interest is in characterizing gene expression in bovine mammary parenchyma during lactation; however, the disproportionate abundance of milk protein transcripts during this physiological stage hinders the use of microarrays for transcript profiling. To evaluate gene expression during early lactation, a SAGE library was produced from pooled RNA (n=3 multiparous Holstein cows) isolated from biopsied mammary parenchyma at approximately Day 7 of lactation. Preliminary sequencing of SAGE tags identified the greatest abundance of α-, β- and κ-casein, α-lactalbumin, β-lactoglobulin and ribosomal protein transcripts, as expected. However, a number of tags corresponding to bovine expressed sequence tags and genes involved in metabolism, intracellular signaling and proteolysis were detected in lower abundance. Our results suggest that SAGE is a feasible approach to study gene expression in lactating mammary gland.

Key Words: Mammary Gland, Gene Expression, Cattle

221 Differential effects of ovarian hormones on epithelial proliferation in the porcine mammary gland. A. S. Barndollar*, J. M. Scudder, J. F. Trott, and R. C. Hovey, *University of Vermont, Burlington*.

Development of the mammary gland (MG) architecture in gilts must occur prior to pregnancy and lactation. Ultimately this development is of major importance as it influences a sows milk production and growth of her piglets. Here we investigated the regulation of cell division in the MG of gilts by ovarian steroid hormones. Based on data from other species, we hypothesized that estrogen (E) would stimulate greater proliferation of mammary epithelial cells compared to progesterone (P). Five-month-old female Yucatan miniature pigs were treated with either E (0.1mg/kg), P (0.25mg/kg) or saline (SAL) by daily sc injection (n=4 per group) for five days. Prior to euthanasia, animals were injected with bromodeoxyuridine (BrDU, 5mg/kg), a nucleotide analog incorporated into newly synthesized DNA. MG tissues were sampled, fixed and prepared as paraffin sections. In order to localize dividing cells, an immunohistochemical procedure was developed using a biotinylated anti-BrDU antibody, followed by chromogenic detection of a red precipitate (Vector Red) in nuclei of hematoxylin-counterstained sections. To determine cellular proliferation rates, two hundred cells were counted from each of five ducts in two MGs for each pig. The percent of cells dividing was determined as the proportion of total cells counted that were BrDU-positive. Hormone treatment significantly altered epithelial cell proliferation in the mammary ducts. Proliferation rate following treatment with SAL, E or P was 5.77±1.8%, 13.7±.8% and 1.5±.9%, respectively, indicating that proliferation was increased by E (P=.007) and decreased by P (P=.078). These changes were also accompanied by alterations in both parenchymal morphology and histology. Taken together, these results indicate a positive effect of E and a negative effect

of P on epithelial proliferation in the MG of gilts. This knowledge may be lead to enhanced mammary growth in gilts and milk production by sows.

Key Words: Mammary Gland, Estrogen, Progesterone

222 Effects of continuous milking and bST on mammary cell proliferation, milk yield and composition in primiparous cows. E. L. Annen*, A. C. Fitzgerald, P. C. Gentry, and R. J. Collier, *University of Arizona, Tucson.*

Continuous milking (CM) of bST-treated cows resulted in no loss of production in multiparous cows, but a 20 to 25% loss in primiparous cows suggesting mammary development in primiparous cows is inhibited by CM. Objectives were to determine effects of CM and bST 1) on mammary epithelial cell (MEC) proliferation during late gestation and early lactation and 2) on milk yield and composition. Primiparous cows were randomly assigned to either continuous (throughout late gestation and early lactation) bST (+bST; n=4) or no bST (-bST; n=4) treatment. Within each animal, udder halves were randomly assigned to CM or a 60-d dry period (CTL) treatment. CTL glands were dried 60 d prior to expected parturition date. CM glands were milked twice daily and yield recorded until parturition or spontaneous dry-off. In the subsequent lactation, daily milk yield and weekly milk composition was measured until 30 d postpartum. Mammary biopsies were taken at -20, -8, +2, +7, and +20 d relative to parturition. CTL+bST and CTL-bST udder halves were dry for 54.4 and 63.3 d and CM+bST and CM-bST halves were dry for 5.6 and 3.1 d due to spontaneous dry-off. Prepartum half-udder milk yield was greater ($P < 0.01$) in +bST cows than -bST cows (11.0 vs. 8.9 kg/d). Postpartum half-udder milk yields (10.6 vs. 22.2 kg/d) were dramatically reduced ($P < 0.01$) in CM halves compared to CTL halves, regardless of bST treatment. Postpartum milk yield in CM and CTL udder halves was not altered by bST treatment. Milk composition (fat, protein, SCC linear score) was not affected by CM or bST treatment. MEC proliferation (Ki67 antigen index) was greater in CM than CTL glands at d -20 (3.7 vs 2.3%; $P < 0.05$), but less at d -8 (4.6 vs. 2.7 %; $P < 0.05$). MEC proliferation was not affected by CM at d +2, +7, and +20 and was not altered by bST at any time point. Results indicate that CM reduced subsequent half-udder milk yield in primiparous cows and MEC proliferation near parturition (-8 d). Negative effects of CM were not overcome by bST supplementation.

Key Words: No Dry Period, Continuous Milking, bST

223 Effects of continuous milking and prostaglandin E_2 on milk yield and composition. E. L. Annen*[1], C. M. Stiening[1], M. E. Dwyer[1], B. A. Crooker[2], A. C. Fitzgerald[1], and R. J. Collier[1], [1]*University of Arizona, Tucson,* [2]*University of Minnesota, St. Paul.*

Continuous milking (CM; no dry period) of primiparous cows reduces milk yield in the subsequent lactation regardless of bST treatment while CM of multiparous cows results in no decrease in yield when treated with bST. This parity effect may be caused by CM inhibiting mammogenesis in primiparous cows. Reduced mammary epithelial cell (MEC) growth has been demonstrated in CM glands. Stimulation of mammogenesis in CM glands may alleviate reduced milk yields. Prostaglandin E_2 (PGE) in mammary secretions rises during the last 3 wk of gestation and returns to basal levels by 2 d postpartum (PP). This rise in PGE corresponds with a period of rapid MEC growth and differentiation. Prepartum (PR) intramammary infusions (IMI) of PGE were mammogenic in late-pregnant heifers. The objectives of this study were to determine effects of CM and PGE on milk yield and composition. The study used first or second lactation cows (n=8). Within each cow, udder halves were randomly assigned to CM or a 60-d dry period (CTL) and PP IMI of PGE (+PGE) or no PGE (-PGE). Cows were on study from 67 d PR to 28 d PP. At 60 d PR the CTL udder half was dried. Milk yield was recorded daily and milk composition determined weekly. PGE treatment (875 μg/10 ml medium chain triglyceride oil) was administered by IMI at parturition and at 72 h PP. CTL halves were dry 64.0 d and CM halves were dry 12.6 d as a result of spontaneous dry-off of some CM halves. Milk yield was reduced ($P < 0.01$) in CM udder halves compared to CTL halves (13.2 vs. 22.1 kg/d), but reductions were less substantial in second lactation cows compared to first lactation cows (33% vs. 53%). Milk composition (fat, protein, SCC linear score, and lactose) was unaltered by CM. No effect of PGE on milk yield or composition was detected in CTL or CM glands. Results confirm that CM reduces milk yield of cows with a mammary growth requirement. Reduced milk yield was not alleviated by PGE suggesting PGE concentrations in CM glands are not limiting mammary growth or milk synthesis.

Key Words: No Dry Period, PGE_2_

224 Influence of leptin single nucleotide polymorphism on lactation curve traits for lactating dairy cows. H. W. Soita*, D. A. Christensen, F. C. Buchanan, T. L. Heck, and J. J. McKinnon, *University of Saskatchewan, Saskatoon, SK, Canada.*

DHI test day records of milk production of 48 cows(TT=15,TC=14 CC=19) from the University of Saskatchewan dairy research unit during the years 2000 to 2001 were used to study the influence of leptin single nucleotide polymorphism (C/T transition that results in an Arg25Cys)) on lactation curve traits. Phenotypic traits of the milk yield lactation curve were estimated by fitting Woods (1967) gamma function to data recorded monthly by DHI. The traits of interest included rates of incline to reach peak yield b, rates of decline after peak yield c, peak yield, days to peak yield, persistency and total yield. Only data from animals with lactation period over 280d were included. The genotype structure of the herd based on leptin SNP showed that of the 134 cows genotyped 27.6, 44.0 and 28.4 % were TT, TC and CC respectively. Days to peak yield was defined as b/c, Peak yield was calculated as a $(b/c)^{be}$-b, persistence was calculated as -(b+1)ln(c). The area under the lactation curve was taken to represent the total yield of the 305d lactation. The influence of leptin SNP on lactation curve's rate of incline, days to peak and persistency depended on parity. The TT/TC cows in their first lactation exhibited steeper ($P<0.05$) incline rates consequently they (TT/TC) reached peak lactation earlier ($P<0.05$) as compared to the CC. Persistency tended to be higher ($P<0.1$) for the first calf TT/TC cows as compared to the CC. Similarly total 305-d lactation milk yield showed trends for higher yields for the TT/TC younger cows. We also note here that total 305-d milk yield is negatively correlated with rate of decline c implying that the TT/TC cows with less steeper decline have higher milk production potential. It is concluded that a phenotypic variation with reference to lactation curve exists due to the leptin SNP in dairy cows in the first lactation.

Key Words: Leptin SNP, Lactation Curve

225 Identifying positive effectors of milk protein synthesis: amino acids and glucose. C. A. Toerien*, D. R. Trout, and J. P. Cant, *University of Guelph, Guelph, ON, Canada.*

In eukaryotic cells, nutrients play an important role in activating the cell signalling cascades that regulate protein synthesis. To assess the effect of amino acids and glucose in the mammary gland, Holstein cows were fasted to quench protein synthesis before re-supplying nutrients. In a 6x6 Latin Square design, cows (initial: 69±4 DIM; 43.4±0.5 kg milk/d) were subjected every 14 d to a 31-h fast. For the last 9 h of the fast, cows were infused iv with EAA+Glc (positive control), Glc, Met+Lys, His, Leu, or saline (Sal; negative control). Blood samples were collected at 1 d, -1 min and hourly during the infusion, and at +1 d. Milk production response to infusion was calculated from milk produced in the front quarters between +1 and +7 h of the 9-h infusion. At +9 h, an approximately 1.5-g biopsy sample of mammary tissue was harvested from a hindquarter (HQ). In successive periods, HQs were alternated so that each HQ was allowed 28 d to recover. Post-biopsy, cows were refed and infused with AA+Glc for 5 h. Relative to Sal, infusion of EAA+Glc increased ($P<0.05$) total milk, lactose and protein yields by 83, 106 and 45% respectively. Infusion of glucose alone resulted in similar responses (83, 98 and 41% respectively; $P<0.05$), implicating Glc as a powerful activator of protein synthesis. Infusion of His elevated milk (29%) and lactose (36%) yields above Sal (P#88040.07). Met+Lys-, His- and Leu-stimulated protein yields did not differ from Sal ($P>0.05$). Nor did His-stimulated protein yield differ from EAA+Glc ($P>0.05$). The effect of His on protein yield equalled 57% of the effect of EAA+Glc, which was far greater than its 5% proportion in the EAA of the EAA+Glc infusate. In conclusion, both glucose and His affected changes in milk synthesis

that implies responses in signal cascades in the mammary epithelial cell.

	Treatments					
Milk	Sal	EAA+Glc	Glc	Met+Lys	His	Leu
Total, kg	$1.71^{a}\pm0.1$	$3.13^{b}\pm0.1$	$3.13^{b}\pm0.1$	$2.06^{a}\pm0.1$	$2.2^{a}\pm0.1$	$1.95^{a}\pm0.1$
Lactose, g	$69^{a}\pm4.9$	$141^{b}\pm5.7$	$136^{b}\pm5.5$	$83^{a}\pm5.5$	$93^{a}\pm5.6$	$84^{a}\pm5.3$
Protein, g	$59^{a}\pm2.8$	$82^{b}\pm3.3$	$80^{bc}\pm3.2$	$67^{ac}\pm3.2$	$71^{ab}\pm3.2$	$61^{a}\pm3$
Fat, g	$132^{a}\pm7.7$	$147^{a}\pm9$	$163^{a}\pm8.7$	$143^{a}\pm8.8$	$150^{a}\pm8.9$	$153^{a}\pm8.4$

^{a,b,c} Significance ($P<0.05$)

Key Words: Milk Protein Regulation, Amino Acids, Glucose

226 Cloning and expression of bovine glucose transporter GLUT8.

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GLUT8 is a new member of the facilitative glucose transporter family, exhibiting high-affinity glucose transport activity. The expression of GLUT8 has been shown to depend on gonadotropin secretion and may be regulated by insulin. To study the role of GLUT8 in glucose uptake and maintenance of glucose homeostasis in lactating bovine tissues, we cloned and sequenced the full length cDNA of bovine GLUT8 (GenBank accession no. AY208940) by RACE (rapid amplification of cDNA ends). The 2073 base pair cDNA sequence is predicted to encode a protein of 478 amino acids, with a molecular weight of approximately 51 kDa. The deduced amino acid sequence of bovine GLUT8 has 90%, 84%, 84% and 58% identity to human, mouse, rat and chicken GLUT8, and is 26%, 27% and 24% identical with bovine GLUT1, GLUT3 and GLUT4. Bovine GLUT8 retains the characteristic structural features of GLUT8 proteins previously identified from other species including membrane spanning helices, glucose transporter motifs, an N-linked glycosylation site on loop 9 and a putative dileucine internalization motif. The major in vitro transcription and translation product of bovine GLUT8 cDNA migrated at an apparent molecular weight of 38 kDa similar to the sizes reported for GLUT8 from other mammalian species. In the presence of canine microsomal membranes, the translation product increased to 40 kDa suggesting glycosylation. Transient transfection studies in COS-7 and MAC-T 11A cells using a FLAG epitope tagged construct revealed that bovine GLUT8 is localized to the cytoplasm in non-stimulated conditions. A 2.1 kb GLUT8 mRNA transcript was detected at the highest levels in bovine testes, at medium levels in lactating bovine mammary gland, lung, kidney, spleen, intestine and skeletal muscle, and at lower levels in bovine liver. GLUT8 mRNA expression in bovine mammary gland increased about ten-fold ($P<.001$) during late pregnancy and early lactation, similar to changes in expression of GLUT1. These results indicate that GLUT8 expression may be regulated by lactogenic hormones and GLUT8 may play a role in glucose uptake in the lactating bovine mammary gland.

Key Words: Glucose Transport, Glucose Uptake, Mammary Gland

227 Effects of a shorter duration of photoperiod treatment during the dry period on cellular immune function in dairy cattle.

T. L. Auchtung*, E. D. Reid, D. E. Morin, and G. E. Dahl, *University of Illinois, Urbana.*

The periparturient period is a time of increased immunosuppression and risk of mastitis in cows. Previously, our laboratory has observed an enhanced cellular immune function in cows treated with short day photoperiod (SDPP) while dry, relative to long day photoperiod (LDPP). However, comparisons have not been made with natural photoperiod, or with further manipulations of photoperiod during the dry period. The objective of this experiment was to determine the effect of natural photoperiod during the dry period on cellular immune function, relative to current photoperiod management practices. In addition, we were interested in investigating the effects of modifications of the standard SDPP during the dry period. Holstein cows ($n = 30$) were assigned randomly to one of four dry period treatments: LDPP (16 h light: 8 h dark), SDPP (8 h light: 16 h dark), AMB (natural lighting schedule during dry period), and SD21 (AMB until 21 d prepartum followed by SDPP). After parturition, cows were exposed to AMB. Blood was collected at dry off and every 4 wk until 21 d prepartum, at which time sampling occurred weekly until calving. Mitogens used were concanavalin A and pokeweed mitogen. Neutrophil chemotaxis was measured in response to interleukin-8. At dry off, there was no difference for either lymphocyte proliferation or neutrophil chemotaxis. After 4 wk on treatment, SDPP had enhanced ($P < 0.05$) neutrophil chemotaxis and lymphocyte proliferation than cows on LDPP or AMB. Cows on SD21 at 4 wk were on the same photoperiod treatment as AMB and had similar responses to AMB and LDPP groups. In conclusion, SDPP improves cellular immune function compared with both LDPP and AMB treatments. These data suggest that SDPP has beneficial effects on cellular immune function during the first month of the dry period, whereas LDPP has no effect on immune function of the dry period. The consequences of shortening the duration of SDPP during the dry period on immune function is being examined.

Key Words: Cattle, Photoperiod, Immune Function

228 Comparison of gene expression changes in the two subunits of bovine IgG1 receptor during colostrogenesis.

D. G. Martinez*, R. Thomason, and T. B. McFadden, *University of Vermont, Burlington.*

Massive transfer of IgG1 into bovine colostrum is mediated by the mammary Fc receptor. This receptor consists of two light and two heavy chains, β_2-microglobulin and FcRn, respectively. Previous studies have suggested that FcRn is up-regulated three weeks before parturition to facilitate the transfer of plasma IgG1 into colostrum. Conversely, another study has reported that β_2-microglobulin is the regulated component of the receptor. To resolve this discrepancy we quantified changes in gene expression of the two units of FcRn receptor in heifers undergoing colostrum formation. Twelve non-pregnant Holstein heifers were fed melengesterol acetate (.5 mg/day) for 14 d to synchronize estrus and were then induced into lactation by treatment with estrogen and progesterone (E+P; .1 and .25 mg/kg/d) for 7 d. Twice-daily milking was initiated 21d after the initial E+P injection. Mammary biopsies were obtained at 0, 5 and 10 d relative to the initial E+P treatment. Gene expression of FcRn and β_2-microglobulin in mammary tissue was measured by quantitative real time PCR and normalized to β-actin mRNA expression. IgG1 concentrations were determined in plasma and secretion as colostrogenesis markers. Circulating IgG1 concentrations began to decrease from about day 5 ($3.7\pm.3$ mg/ml)relative to the initial injection of E+P to reach a minimum around day 12 ($2.8\pm.3$ mg/ml; $P<.01$). A high concentration of IgG1 in secretions was detected on day 12 (54.6 ± 4.3 mg/ml) and then decreased progressively through the initiation of milking (14.9 ± 3.5 mg/ml; $P<.01$). Abundance of $_2$-microglobulin mRNA did not change over time ($P>.05$). In contrast, FcRn gene expression increased about tenfold on day 5 ($P<.01$), coinciding with the initial decrease of plasma IgG1, and then declined about sixfold by day 10 ($P<.01$). We conclude that FcRn (heavy chain) is the hormonally regulated unit of the bovine mammary epithelial Fc receptor during colostrum formation whereas β_2-microglobulin is constitutively expressed.

Key Words: FcRn, β_2-Microglobulin, Colostrum

229 Changes in expression of vitamin receptors in bovine mammary gland during hormone induced colostrogenesis.

D.G. Martinez*, R. Thomason, and T.B. McFadden, *University of Vermont, Burlington.*

The objective of this study was to quantify changes in gene expression of megalin, low-density lipoprotein receptor (LDL-R) and folic acid receptor during hormone-induced colostrum formation to determine whether they may be involved in the transport of their ligands (vitamin A, β-carotene and folic acid) from maternal circulation into colostrum. Twelve non-pregnant Holstein heifers were fed melengesterol acetate (0.5 mg/day) for 14 d to synchronize estrus and were then induced into lactation by treatment with estrogen and progesterone (E+P; .1 and .25 mg/kg/d) for 7 d. Twice-daily milking was initiated 21d after the initial E+P injection. Mammary biopsies were obtained at 0, 5 and 10 d relative to the initial E+P treatment. β-carotene concentrations were determined in plasma and mammary secretions as an indicator of colostrogenesis. Concentrations of α-lactalbumin in plasma were measured for use as a functional marker of lactogenesis. Expression of megalin, LDL-R, and folic acid receptor mRNA in mammary tissue was determined by quantitative real time PCR and normalized to β-actin mRNA expression. Plasma β-carotene concentrations declined between -2d ($3.6\pm.3$ ug/ml) and 10d ($3.1\pm.3$ ug/ml; $P<.01$) relative to initial E+P injection, indicating colostrum formation. Concentrations of β-carotene in mammary secretions averaged $.78\pm.09$ ug/ml at 12d, then decreased through the initiation of milking ($.49\pm.08$ ug/ml;

P<.01). Plasma α-lactalbumin concentrations increased about fivefold from 10d to 15d (P<.01), indicating onset of lactation. Megalin expression increased about 3-fold from 0d to 5d (P=.01), then decreased 2.8-fold by 10d (P=.01). Gene expression of LDL-R decreased 4.5-fold (P<.06) from 5d to 10d while folic acid receptor mRNA decreased about twofold (P<.05). We conclude that temporal changes in expression of megalin, LDL-R and folic receptor mRNA during colostrogenesis may be related to the transport of their ligands into colostrum. Hormonal induction of lactation provided a useful model for studying the regulation of colostrogenesis.

Key Words: Colostrum, Vitamins, Induced Lactation

Meat Science and Muscle Biology

230 Conjugated linoleic acid (CLA) concentrations in beef tissues from cattle finished on pasture initially with limited grain. R. N. Sonon Jr.*[1], D. C. Beitz[1], A. H. Trenkle[1], J. R. Russell[1], and R. Rosmann[2], [1]*Iowa State University, Ames,* [2]*Rosmann's Family Farms*.

Thirty Red Angus cross yearling steers and heifers (initial BW = 394±54 kg) were fed to choice grade in an on-farm study to compare the concentrations of CLA in beef tissues and to evaluate beef quality of cattle finished on pasture initially or on drylot diet entirely. The cattle on the pasture group grazed by rotation forages consisting primarily of endophyte-free tall fescue grass for 207 d and then, were shifted to the drylot diet for 59±15 d, whereas the drylot cattle were fed ground alfalfa-orchardgrass hay for 183±16 d. In addition to the basal forage, a corn-soybean concentrate mixture was fed at 0.5 to 1.0% of BW to the pasture group of cattle while grazing, and at 2.0% of BW to the drylot group of cattle. After harvest of cattle, steaks were removed from the 12th-13th rib of the carcasses of sixteen animals for fatty acid analysis and sensory evaluation. Results showed that cis9, trans11 CLA concentration in ribeye steak of pastured cattle (0.44 g/100 g of fatty acids) was significantly higher (p#88040.05) than in steak of cattle fed the drylot diet (0.17 g/100 g of fatty acid). Linolenic acid (C18:3n-3) concentration in ribeye steak of pastured cattle (0.79 g/100 g of fatty acids) was significantly higher (p#88040.05) than in the ribeye steak of drylot cattle (0.61 g/100 g of fatty acids). The Warner-Bratzler shear test of tenderness of ribeye steak from pasture-fed cattle was 2.85±0.61 kg and did not differ with that of the drylot cattle (2.60±0.65 kg). Sensory evaluation of ribeye steaks (pasture vs drylot) included juiciness (5.83 vs 5.43), tenderness (6.61 vs 7.00), chewiness (3.14 vs 2.43), flavor (2.08 vs 2.43) and off-flavor (5.56 vs 5.55) and these attributes were not different (p>0.05) between the two groups of cattle. Data from this on-farm study indicate that pasture-feeding contributed to the production of a potentially healthier beef without diminishing eating qualities.

Key Words: CLA, Beef Quality, Pasture

231 Effects of two supplementation levels of linseed combined with CLA or tallow on meat quality traits and fatty acid profile of adipose tissue and longissimus muscle in pigs. G. Bee*, S. Jacot, G. Guex, and W. Herzog, *Swiss Federal Research Station for Animal Production and Dairy Products 1725 Posieux, Switzerland*.

Linseed is an efficient dietary supplement to increase 18:3n-3 concentration in meat and adipose tissue in pigs. Increased concentration of highly unsaturated PUFA can lead to quality deterioration due to lipid oxidation. We hypothesize that inclusion of conjugated linoleic acids (CLA) or tallow could limit the potential for lipid oxidation. In the present study we evaluated the effect of CLA or tallow combined with linseed on carcass characteristics, longissimus muscle (LM) quality traits, and the fatty acid profile of the LM and adipose tissue. From 18 to 104 kg BW, 32 Swiss Large White barrows were fed a grower finisher diet supplemented either with: 1) 3% linseed (L3); 2) 2% linseed (L2); 3) 2% linseed + 1% CLA (L2C); or 3) 2% linseed + 1% tallow (L2T). The amount of omental fat was higher (P < 0.05) in the L3 (2.09%) compared to the L2 and L2T group (1.60% for each). Initial pH in the LM was higher (P < 0.05) in the L2T (6.30) compared with the L2 (6.06) and L2C (6.03) group, but did not differ from the L3 group (6.14), whereas no dietary effects were observed for ultimate pH, color, drip, cooking losses, and shear force values. Inclusion of CLA (L2C) did not affect PUFA level but increased (P < 0.05) the concentration of saturated and decreased (P < 0.05) that of monounsaturated fatty acids in the tissues compared to the other treatments. Neither CLA nor tallow altered the concentration of 18:3n-3, 20:3n-3, 20:5n-3, and 22:5n-3 compared to the L2 group. Consequently, in the 3 dietary groups the n-6/n-3 ratio was similar in the LM (2.9) and adipose tissue (3.6). As expected, the higher linseed supply (L3) resulted in increased (P < 0.05) 18:3n-3 and 20:3n-3 concentrations in the tissues, whereas from the higher unsaturated fatty acids of the n-3 family only 22:5n-3 level was increased (P < 0.05) in the adipose tissue compared to the L2, L2C, and L2T group. The present results indicate, that CLA, but not tallow, combined with linseed could help reduce the potential for lipid oxidation by decreasing the unsaturation level without affecting the improved n-6/n-3 ratio.

Key Words: Linseed, CLA, Pig

232 Consumer acceptance of beef from steers finished on ryegrass forage or a high-concentrate diet. C. R. Kerth*, K. W. Braden, R. B. Cox, and J. Alexander, *Department of Animal Sciences, Auburn University, Auburn, AL*.

Charlais-Angus crossbred steers were fed one of three finishing diets to determine consumer acceptance of forage-fed or concentrate-fed beef. When steers (n = 30) reached 340 kg, they were randomly assigned to one of three finishing treatments consisting of ryegrass only for 178 d (RG), ryegrass for 125 d followed by 98 d of a high-concentrate, feedlot-type diet (RGC), or a high-concentrate, feedlot-type diet for 82 d (CON). Steers from RGC and CON groups were harvested when estimated backfat thickness reached 1.0 cm and steers from the RG group were harvested when the amount of forage was insufficient to maintain animal growth. To determine consumer acceptance, 153 consumers at an outdoor festival in Auburn, AL were asked to taste steaks from each of the three treatments. Boneless, strip loin steaks were cooked (71C) on clam-shell-style electric grills, cut into 1.0 X 1.0 cm cubes and placed in double boilers kept warm over a small flame. Overall acceptability scores were determined by marking an "X" on a continuous line anchored with frowning (score of 0) and smiling (score of 100) faces and scored by interpolation. Pricing acceptability was determined in the same manner with $7.46/kg and $16.26/kg anchoring the line and $11.86/kg as the midpoint of the line, representing the typical market value of a strip loin steak at the time. Consumers were then asked which steak they preferred. The demographics of those participating in the survey were evenly distributed across income levels and gender, with almost half (46.6%) being younger than 30 y and the remainder evenly distributed from 31-80 y of age. Overall acceptability scores and price per pound were higher (P < 0.05) for steaks from cattle finished on CON compared to steaks from cattle finished on RG or RGC. Additionally, a higher (P < 0.05) percentage of consumers preferred steaks from CON (63.9%) compared to RGC (13.9%) or RG (22.2%). Consumers that preferred RG beef were willing to pay $1.17/kg more for RG beef compared to CON beef. These results indicate that a significant market exists for forage-fed beef and consumers are willing to pay a premium for it.

Key Words: Grass-Fed Beef, Consumer Acceptance, Price

233 Mechanisms of beef carcass tenderness. R. Johnson*, J. Sawdy, J. M. Reddish, M. S. Updike, and M. Wick, *The Ohio State University, Columbus*.

This study advanced a model that was developed to investigate the potential for relating changes in electrophoretic protein patterns derived from the L. dorsi of beef cattle 36 hr postmortem with tenderness at 7 d. Previous research done in this lab showed a significant association (R^2 = 0.82) between tenderness at 7 days, as determined by Warner Bratzler Shear analysis, and the relative intensities of 7 bands from L. dorsi myofibrillar fingerprints of proteins/peptides derived from the same tissue at 36 hr postmortem. Mass spectrometric analyses was used to identify one of the bands, significantly associated with tenderness, as bovine fast myosin light chain-1 (bMLC1) (P < 0.001). The method was previously used to identify fragments of bovine myosin heavy chain as being associated with tenderness. These combined findings suggest the presence of at least two distinct mechanisms contributing to tenderness. One mechanism proposes a relationship between myosin heavy chain proteolysis and tenderness. The most recent finding indicates a positive correlation with the amount of intact bMLC1 and tenderness.