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