Tuesday, July 11, 2006

POSTER PRESENTATIONS

Animal Health II

T1 Release of CD14 by bovine neutrophils results in down-regulation of IL-8. M. Paape*[1], E. Sohn[2], E. Connor[1], R. Fetterer[1], R. Peters[2], and D. Bannerman[1], [1]*USDA-ARS*, *Beltsville, MD*, [2]*University of Maryland*, *College Park*.

CD14, the leukocyte receptor for lipopolysaccharide (LPS), is important in the response of PMN to infection by Gram-negative bacteria. IL-8 is a potent chemoattractant of PMN. The objective of the present study was to characterize bovine PMN cell surface expression and shedding of CD14 molecules, and its effect on secretion of IL-8 by PMN. PMN were isolated from blood collected from 16 lactating cows. PMN ($5x10^6$ /ml) were cultured in RPMI and stimulated with 0, 1, 10 and 100 µg/ml of LPS for 20 h at 37°C. The percentage of PMN expressing membrane (m) CD14 was determined by flow cytometry. Concentrations of CD14 and IL-8 in RPMI were quantitated by ELISA. To determine the effect of cell density of PMN on release of CD14 and IL-8, varying concentrations of PMN were stimulated with either 0.1 or 10 µg/ml of LPS, and supernatants assayed for CD14 and IL-8. Expression of mCD14 decreased from 35% (control PMN) to 25% after exposure to 100 µg/ml of LPS. Secretion of CD14 increased with increasing cell density and with increasing concentrations of LPS, whereas secretion of IL-8 decreased. Results from quantitative real-time PCR indicated that CD14 gene expression did not increase after stimulation of PMN with LPS. Results from this study indicate that release of CD14 suppressed secretion of IL-8, and that the increase in CD14 resulted from either the shedding of mCD14 or originated from an intracellular pool of sCD14. The suppression of IL-8 by CD14 may be an important mechanism to control influx of PMN into the bovine mammary gland.

Key Words: CD14, IL-8, Neutrophil

T2 Assessing changes in gene expression in mammary tissue following experimental induction of *Staphylococcus aureus* mastitis using a cDNA microarray. J. Kelsey*[1], K. Bayles[2], L. Fox[3], and M. McGuire[1], [1]*University of Idaho*, *Moscow*, [2]*University of Nebraska Medical Center*, *Omaha*, [3]*Washington State University*, *Pullman*.

To determine gene expression changes in the mammary gland following experimental induction of mastitis, two previously uninfected lactating Holstein cows were experimentally infected. Two consecutive daily 10 mL infusions containing 5000 CFU *S. aureus* 305 bacteria diluted in PBS in one rear quarter of each cow induced the infection. The opposite rear quarter was infused with PBS and used as a control. Milk somatic cell count and *S. aureus* plate counts were monitored to determine if subclinical mastitis infections had occurred. Counts of *S. aureus* increased in the infected quarter of each cow to about 500 CFU/mL milk. Milk somatic cell counts also increased with each infected quarter 80% higher than the control. Two days following infusions, mammary biopsies were taken from both rear quarters, and tissue was immediately snap frozen. Total RNA was isolated, amplified, converted to cDNA and labeled with Cy3 or Cy5 dye before hybridization to the NBFGC bovine microarray (Michigan State University). Comparisons were made within cow, infected vs non-infected tissue. Total intensity values were background subtracted, log transformed, and normalized using a lowess normalization. Normalized values were then averaged for each gene and a t-test was conducted to determine which genes were changing significantly ($P < 0.05$). The genes that changed significantly ($P < 0.05$) were almost all up-regulated (about 750 genes). Some of these genes were associated with lipid metabolism including bile salt-stimulated lipase, lipase A and thioesterases. There were also many immune-related genes upregulated including MHC class I, cytokines, and immunoglobulins. This study demonstrates that *S. aureus*-induced mastitis leads to the induction of genes involved in lipid metabolism and immune function in the mammary gland.

Key Words: *S. aureus*, Mastitis, Gene expression

T3 High growth rate fails to enhance adaptive immune responses of neonatal calves and is associated with decreased T cell viability. M. Foote*[1], B. Nonnecke[2], W. Waters[2], D. Beitz[1], M. Fowler[3], T. Johnson[3], and B. Miller[3], [1]*Iowa State University*, *Ames*, [2]*USDA, ARS, National Animal Disease Center*, *Ames, IA*, [3]*Land O'Lakes Inc. Research Farm*, *Webster City, IA*.

The objective of the study was to evaluate the effects of three targeted growth rates [No Growth (or maintenance, NG), Low Growth (LG), and High Growth (HG)] on adaptive (antigen-specific) immune responses of preruminant calves vaccinated with Mycobacterium bovis, strain bacillus Calmette Guerin (BCG) and ovalbumin (OVA) 3 wk after initiation of dietary treatments. Growth rates for NG (0.11 kg/d), LG (0.58 kg/d), and HG (1.16 kg/d) calves differed ($P \leq 0.001$) throughout the experimental period. Blood leukocyte populations from HG calves

had lower (P≤.05) mononuclear leukocyte (MNL) percentages and higher ($P \leq 0.05$) granulocyte percentages than maintenance-fed (NG) calves. CD4 T cell percentages increased ($P \leq 0.05$) with age in NG and LG calves, typical of maturing calves, but failed to increase in HG calves. Growth rate did not affect ($P \geq 0.05$) percentages of CD45RO (memory) CD4 and CD8 T cells, OVA-specific serum IgG concentrations, or PPD-induced interferon-γ and inducible nitric oxide. Cutaneous delayed-type hypersenitivity responses of NG and HG calves to antigen were comparable and exceeded ($P \leq 0.05$) responses of LG calves. In resting and antigen stimulated MNL cultures, viabilities of CD4, CD8, and γδ TCR T cells from HG calves were lower ($P \leq 0.05$) than those of T cell subsets from NG and LG calves. In conclusion, adaptive immune responses were affected minimally by growth rate. Results suggest that protein-energy malnutrition in the absence of weight loss is not detrimental to antigen-specific immune responses of preruminant calves and that an increased growth rate does not enhance these responses. Negative effects of high growth rate on T cell viability may influence the resistance of the preruminant calf to infectious disease.

Key Words: Calf nutrition, Adaptive immunity, Neonatal immunity

T4 Determination of endoparasites population in water buffalos (*Bubalus bubalis*) in Magdalena Medio, Colombia. G. A. Prada-Sanmiguel*, *Universidad de La Salle, Facultad de Medicina Veterinaria*, *Bogotá, Distrito Capital, Colombia*.

The objective was to determine gastrointestinal, pulmonary, hepatic and hematic parasite populations in water buffalo (*Bubalus bubalis*) in La Suiza; a ranch located in Magdalena Medio, Colombia. 600 buffalo were evaluated in order to determine presence and prevalence of hemoparasites, and 150 buffalo were analyzed once per month to determine gastrointestinal, pulmonary and hepatic parasite populations. Techniques used in this study included: blood frotis, fecal sedimentation-flotation, coproculture, MacMaster, Baermann and Dennis techniques. The hemoparasite prevalence found was the follows: *Anaplasma* spp 54.6%, *Trypanosoma* spp 1.2 % and *Babesia* spp 0.2%. The gastrointestinal parasites observed were: *Nematodirus* sp, *Cooperia* sp, *Ostertagia* sp, *Trichuris* sp, *Oesofagostomum* sp, *Bunostomum* sp, *Trichostrongylus* sp, *Strongyloides* sp, *Eimeria* spp, *Moniezia* sp, *Toxacara* sp and *Haemonchus* sp. Egg counts per gram of feces curves were also analyzed during the 12 months of 2004. No pulmonary or hepatic parasites were found in *B. bubalis* of Magdalena Medio, Colombia.

Key Words: Bubalus bubalis, Endoparasites, Colombia

T5 Lymphocyte, neutrophil, and mineral responses to *S. aureus* and *E. coli* mastitis. H. R. Springer*[1], J. P. Goff[2], D. D. Bannerman[3], and M. J. Paape[3], [1]*Iowa State University*, *Ames*, [2]*USDA-ARS National Animal Disease Center*, *Ames, IA*, [3]*Bovine Functional Genomics Laboratory*, *Beltsville, MD*.

We hypothesized mastitis would elicit systemic immune suppression. Primiparous Holstein (n=10) and Jersey (n=10) cows were infected with 220 cfu of *S. aureus* in one quarter of the mammary gland. Blood and milk samples were taken at 6-24 hr intervals after infection. Infected quarters were treated with pirlamycin on day 10 for 9 days; clearing the infection in 16 cows. Seven wks later, in a separte study, the same cows were infected in a different quarter with 270 cfu of *E. coli* and blood and milk samples again taken. All cows cleared *E. coli* from the milk within 7 d without antibiotic. Time after *S. aureus* infection had significant effect on IFN-γ production by lymphocytes ($P < 0.001$), with nadir in IFN-γ response at 24 hrs post infection. Neutrophil function, measured by neutrophil iodination, was not significantly depressed by *S. aureus* challenge, but was in *E. coli* infection ($P < 0.001$). No significant febrile response was elicited in response to *S. aureus* infection, but *E. coli* infection resulted in elevated rectal temperatures 12 and 18 hrs post-infection ($P < 0.0001$). Circulating lymphocyte populations showed a more pronounced drop with *E. coli* compared to *S. aureus* challenge ($P < 0.02$). Time after infection had significant, but opposite effects on blood neutrophil populations in the two infections ($P < 0.0001$). *E. coli* lowered this population while *S. aureus* increased it. Serum iron decreased significantly during infection; by 18 hrs with *E. coli* and by 24 hrs with *S. aureus*. Iron levels with *E. coli* infection decreased to a greater extent than with *S. aureus* ($P < 0.01$). *E. coli* infection caused a greater increase in unsaturated iron binding capacity than *S. aureus* ($P < 0.0001$). Both infections decreased plasma calcium ($P < 0.05$) with *E. coli* causing a greater reduction than ($P < 0.0001$). These data suggest that both *S. aureus* and *E. coli* mastitis elicit a systemic immune response with a stronger, earlier inflammatory response to *E. coli* infection.

Key Words: Mastitis, Immune response, *Staphylococcus aureus*

T6 Development of a ruminant fescue toxicosis model. S. S. Block*, P. H. Doane, and M. J. Cecava, *ADM Animal Nutrition Research*, *Decatur, IN*.

Sixteen male lambs (average weight 27.0 kg) were used to develop a fescue toxicosis model. Lambs were fed a pelleted diet containing 20% fescue seed during the study. Control diets used ergovaline-free fescue seed while the contaminated diet used fescue seed containing 2,800 ppb ergovaline. The complete diet fed to lambs during the toxin challenge period of the study contained 615 ppb ergovaline, 1041 ppb ergot alkaloids, and no additional ergotamines. Complete diets were supplemented with feed additives to assess whether the response to induced toxicity was affected by the presence of additives. The study was divided into four periods; adaptation (A), supplementation (S), elevated ambient temperature with supplementation (HS), elevated ambient temperature and fescue seed feeding with supplementation (HFS). Temperature and humidity were adjusted to maintain a relative heat index of 38°C. Supplements had no effect on any parameter measured during S. During the HS period, rectal temperature (RT), heart rate (HR), and breathing rate (BR) of lambs increased whereas feed intake decreased. Signs of toxicosis were apparent in HFS, including reduced feed consumption and weight gain ($P < 0.01$), elevated HR, BR, and RT ($P < 0.01$). Clinical markers of toxicosis included a significant reduction in circulating prolactin (477 ng/ml to 18 ng/ml; $P < 0.01$) after introduction of ergovaline-containing feed. Symptoms of toxicosis occurred only when the sheep were fed ergovaline-contaminated fescue seed in the presence of elevated ambient temperature. The inclusion of test supplements had no effects on the appearance of alkaloids in the urine ($P > 0.62$) or any parameters of fescue toxicity, with the exception of body temperature. Rectal temperature tended to be lower in animals consuming one supplement compared with control (40.5 vs. 40.7°C; $P < 0.11$). Induction of fescue toxicosis was successfully achieved, using a combination of high ambient temperature and inclusion of 20% ergovaline-contaminated fescue seed into the diet.

Key Words: Fescue, Ruminant, Toxicosis

T7 The relationship of copper and zinc with hematological parameters in beef cattle. M. Soch*[1], P. Srejberova[2], and J. Broucek[3], [1]*University of South Bohemia, Faculty of Agriculture*, *Ceske Budejovice, Czech Republic*, [2]*Czech Beef Breeders Association*, *Praha, Czech Republic*, [3]*SCPV*, *Nitra, Slovakia*.

The objective of this study was to define the relationship between copper (Cu) and zinc (Zn) and the hematological parameters of hemoglobin (HB) and hematocrit (HT) in beef cattle. Seventy two (in spring and autumn seasons of 2004) blood (jugular), faeces (grab samples), and pasture (collected at the time blood was taken) samples were collected from two herds of beef cattle (Aberdeen Angus) from the Sumava (Czech Republic) mountains region (elevation=675-910 m above sea level). Blood was kept cold (+3°C) and analysed within 24 hours. The content of HB was estimated photometrically (540 nm) using a spectrometer UV/VIS Unicam 5625. HT was determined by the capillary microhematocrit method. The concentrations of Cu and Zn in plasma, feces, and pasture (DM) were analysed by flame atomic absorption (Spectrometer Unicam 969). The data were analyzed using STATISTIX 8. The normal distribution of data was evaluated by Wilk-Shapiro/Rankin Plot procedure. All data were normally distributed. Pearson Correlation was used for the evaluation of relationships. Concentrations of Cu and Zn in plasma (Cu 11.2 ± 3.87 mmol.L-1; Zn 13.01 ± 3.86 mmol.L-1) and feces (Cu 17.97 ± 10.17 mmol.L-1; Zn 113.02 ± 64.78 mmol.L-1) were below reference values (RfV). The lack of Cu and Zn in beef cattle was due to deficiency of both elements in the diet which provided only 86 % and 89 % of the needed Cu and Zn, respectively. Hematological parameters (HB, HT) were in the range of RfV (HB 110.90 ± 16.89 mmol.L-1; HT 0.32 ± 0.06 mmol.L-1). The low concentrations of Cu and Zn in plasma of cattle did not have negative influence on HB and HT. There were significant ($P <$ 0.05) correlations between hematological parameters and mineral elements (HB:Cu, r=0.622*; HB:Zn, r=0.520*; HT:Cu, r=0.606*; HT:Zn, r=0.688*).

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Key Words: Microelements, Hematological parameters, Beef cattle

T8 Production of bacteriocins by bacterial isolates from dairy cattle. M. A. V. P. Brito*[1] and G. A. Somkuti[2], [1]*EMBRAPA Dairy Cattle Research Center*, *Juiz de Fora, Brazil*, [2]*Eastern Regional Research Center, USDA-ARS*, *Wyndmoor, PA*.

A collection of 116 bacterial strains recovered from healthy cows in 41 dairy herds in Brazil was surveyed for the production of bacteriocins. The bacteria included 106 strains of staphylococci (87 coagulase positive and 19 coagulase negative) and 10 strains classified as streptococci. All cultures were grown in tryptic soy broth for 18 h at 37°C and cell-free supernatants were tested for antimicrobial activity against several target organisms by the agar diffusion method. Filtrates of 58 staphylococci and a culture identified as *Streptococcus uberis* showed strong activity against *Listeria monocytogenes* ScottA, whereas a *S. bovis* isolate was active against *S. agalactiae*. Filtrates of 53 staphylococci also inhibited the growth of *Staph. aureus* strain 305, a major causative agent of bovine mastitis in the United States. Although plasmids were apparently absent in the streptococcal isolates, the plasmid profiles of staphylococci invariably included an 8 kb plasmid. Staphylococcal isolates were tested for the production of aureocins A70 and A53, two bacteriocins of coagulase positive staphylococci known to be associated with 8 kb and 10.2 kb plasmids, respectively. The presence of either the A70 or A53 bacteriocin gene was checked by PCR techniques using forward and reverse primers flanking the structural gene of each bacteriocin. Agarose gel analysis of amplified PCR products of plasmid templates from all 58 isolates showed only a 525 bp fragment that corresponded to the structural gene of the bacteriocin aureocin A70. The results indicated that the apparently widespread association of A70-producing staphylococci with healthy cows in Brazil may be beneficial in controlling undesirable bacteria in dairy herds.

Key Words: Bacteriocins, Aureocin A70, *Staphylococcus aureus*

T9 Evaluation of C. elegans as a pharmacogenetic model to study antihelminthic drugs. M. Worku*, C. Gerard, O. Alexander, I. Abdus-Saboor, and P. Matterson, *North Carolina Agricultural and Technical State University*, *Greensboro*.

Parasite drug resistance is recognized globally as one of the greatest threats to the health of grazing livestock. Macrocyclic lactones are chemical compounds that represent the main treatment. The free-living nematode Caenorhabditis elegans (C. elegans) is a well established biological model. Chemotaxis is an important behavior in enabling it to locate food sources such as E.coli. This study evaluates the effects of Moxidectin exposure on the life cycle and chemotactic behavior of C. elegans. A ring of bacteria (food) on NGM agar medium served as attractive signals to encourage C.elegans to move. Nematodes were placed in the center of the agar plate in 0, 0.25 or 0.50 micromoles of Moxidectin. Over the three day life cycle the reproduction (number of worms), movement (yes or no) and chemotaxis (Number migrating to the ring of bacteria through the Moxidectin) was recorded. Nematodes that had reached the food were picked individually to new seeded plates and allowed to recover and reproduce. The progeny of were tested for Moxidectin sensitivity to determine if the apparent Moxidectin resistance of the parent had bred true. Averages of three experiments are presented. There was a 40 % reduction in total number of worms following first time exposure. A 60% reduction was observed in the second generation. Migration of worms to a food source was reduced by 10% on first time exposure; exposure to 25micromoles of Moxidectin and 25% reduction for second time exposure in treated versus control nematodes. Exposure to 50 micromoles of Moxidectin killed all nematodes. Exposure to Moxidectin affected the life cycle, inhibited chemotaxis to a food source and resulted in the development of resistant phenotypes. This C. elegans model can be used to better understand the molecular basis of resistance to anti-helminthics, drug screening and for identifying molecular targets or biochemical pathways mediating resistance.

Key Words: C. elegans, Cydectin, Drug resistance

T10 Effects of source of supplemental Se on health and immune status of periparturient dairy cows. H. M. Rutigliano*[1], R. L. A. Cerri[1], F. S. Lima[1], L. F. Vettorato[1], D. B. Araujo[1], J. Hillegass[1], W. W. Thatcher[2], and J. E. P. Santos[1], [1]*University of California Davis*, *Tulare*, [2]*University of Florida*, *Gainesville*.

Objectives were to determine the effect of source of supplemental Se on postpartum health, immune responses and Se status of periparturient Holstein cows. Treatments were sodium selenite (SS, n=291) or Se yeast (SY, Sel-Plex®, n=286) supplemented at 0.3 ppm from d 25 prior to calving to 80 d in milk. Health of dairy cows was monitored daily in the first 80 d in milk, and rectal temperature was taken for the first 10 d postpartum. A subset of 15 primiparous and 24 multiparous in the SS group and 10 primiparous and 26 multiparous in the SeY group was used to evaluate cellular and humoral immune responses. A colostrum

sample at the first milking after calving was analyzed for total IgG concentrations. Concentrations of Se in plasma were determined at -45, 0, 21, 42 and 60 d relative to calving. Glutathione peroxidase activity in plasma, neutrophil phagocytic activity and its oxidative metabolism were determined on days 0 and 42 postpartum. Each animal received an i.m. injection of 1 mg of ovalbumin at -45, -25 and 0 d relative to calving. Anti-ovalbumin IgG concentrations in serum were analyzed at every injection and at 21 and 42 d postpartum. Concentration of Se in plasma was similar ($P = 0.38$) for SY and SS throughout the study (0.107 vs 0.101 μg/mL). Glutathione peroxidase activity in plasma was not affected ($P = 0.70$) by source of Se. Concentration of IgG in colostrum was similar ($P = 0.24$) for SY and SS (60.9 vs 71.0 g/dL). Phagocytic and killing activities of neutrophils were influenced ($P < 0.01$) by days postpartum, but not ($P > 0.10$) by source of Se. Similarly, the ability of neutrophils to reduce nitroblue tetrazolium was not ($P > 0.10$) influenced by source of Se in stimulated and nonstimulated neutrophils. Incidence of retained placenta (SY=9.4 vs SS=8.6%), fever (SY=47.0 vs SS=44.7%), clinical ketosis (SY=22.1 vs SS=22.3%), displacement of abomasum (SY=2.5 vs SS=3.8%), and mastitis (SY=27.3 vs SS=25.1%) were not affected ($P > 0.10$) by source of supplemental Se, but a greater ($P < 0.01$) proportion of cows fed SY experienced acute metritis (21.3 vs 13.4%). Source of Se did not influence health or immunological status of periparturient dairy cows.

Key Words: Selenium, Health, Dairy cow

Breeding & Genetics II

T11 The effect of inbreeding on litter size in Chicago miniature pigs. Y.-C. Jung[1], S.-H. Oh*[2], M. T. See[2], T. E. del Rosario[1], and Y.-B. Kim[3], [1]*Jung P&C Institute*, *Seongnam, Gyeonggi, South Korea*, [2]*North Carolina State University*, *Raleigh*, [3]*Rosalind Franklin University of Medicine and Science/Chicago Medical School*, *North Chicago, IL*.

Pedigree and litter size data for a miniature pig population were collected from 1968 to 2004. The objectives of this study were to investigate the genetic characteristics of the miniature pig population maintained at the Chicago Medical School, and to calculate and estimate inbreeding effects on litter size as well as estimate heritability and breeding values by year and generation. A single trait animal model was used to estimate genetic parameters. The model for litter size records included year and parity as fixed effects, and the random genetic effect of animal. Variance and covariance components were estimated by a derivative-free REML algorithm using the MTDFREML computer programs. As a result of analysis of 2227 individuals, inbreeding coefficients ranged from 0 to 0.43, and averaged 0.10 ± 0.08 over 29 generations. Estimation of variance components for litter size resulted in 0.63 and 3.50 for genetic and environmental variances, respectively. Heritability of litter size was estimated as 0.15 ± 0.04. As a result, from inference through the analyses in this study, inbreeding in the Chicago miniature pig population increased on average 0.0068 per year, phenotypic litter size decreased 0.0781 per year, and breeding value of litter size decreased 0.0168 per year. In other words, a 10% increase in inbreeding resulted in 0.25 pig reduction in breeding value and 1.148 pig decrease in litter size.

Key Words: Miniature pigs, Inbreeding, Litter size

T12 Relationship between sire tenderness EPD and progeny carcass performance. J. W. Bolsen*, J. Minick Bormann, D. W. Moser, and T. T. Marston, *Kansas State University*, *Manhattan*.

The objectives of this study were to determine how well a bull's tenderness Expected Progeny Differences (EPD) actually predicted his progeny's carcass performance, and to evaluate the effect of selection for tenderness EPD on other carcass measurements. In 2002, eight Hereford bulls with divergent tenderness EPD were mated randomly to crossbred cows. These EPD were developed from the NCBA Carcass Merit Project, and the accuracies ranged from 0.20 to 0.43. Steers, bulls, and cull heifers that were weaned in two groups were fed out and harvested with complete carcass data collected. Measurements collected on all cattle (n = 91) included feedlot in-weight (IW), final weight (FW), dressing percent (DP), hot carcass weight (HCW), ribeye area (REA), 12-13th rib fat thickness (FT), marbling score (MS), kidney pelvic heart fat (KPH), and yield grade (YG). A sub-set of cattle (n = 39) were evaluated for tenderness and sensory traits, including Warner-Bratzler shear force (WBSF), myofibril tenderness (MT), overall tenderness (OT), color (CO), purge loss (PL), juiciness (JU), flavor (FL), and average pH (PH). Data were analyzed using the GLM procedure of SAS. The model for all carcass and sensory traits included fixed effects of weaning group, sex, kill group, and sire EPD level. Sire tenderness EPD level did not have an effect ($P > 0.05$) on WBSF, MT, OT, CO, PL, JU, FL, or PH. Low accuracies on the sire EPD and small progeny numbers probably contributed to the lack of difference in tenderness between EPD levels. The regression of actual sire tenderness EPD on progeny WBSF was 0.32 ± 0.44. In the larger data set, IW, FW, DP, HCW, REA, FT, MS, KPH, and YG were unaffected ($P > 0.05$) by sire tenderness EPD level. These results from a larger sample of progeny indicate that selection on tenderness EPD should not affect other carcass traits.

Key Words: Tenderness, EPD, Carcass traits

T13 Carcass characteristics of different breeds on beef cattle. A. A. Souza*, L. Suguisawa, H. N. Oliveira, and A. C. Silveira, *São Paulo State University*, *Brazil*.

Different breeds of beef cattle may show different carcass composition, so it's possible to combine breed development and markets. Beef consumers from europe have preference for thiner cuts than americans and japanese consumers do. Other point is the worrying about health. People look for thiner cuts to avoid saturate fat consume. So, we could work with specific breeds for specific markets and consumers, optimizing production and the satisfaction of consumers. Forty two bullocks approximately 8 months and 240 kg, from Nellore, Angus, Angus Nellore crossbred, Brangus, Simmental x Nellore crossbred, Simbrasil and Simmental were evaluated for liveweight, ribeye area (REA), backfat thickness (BF), marbling and intramuscular lipids. Animals were housed with high concentrate diet and slaughtered at an approximate 3 mm of backfat thickness. Angus and its crossbred had thicker backfat and marbling, but smaller ribeye area than Simmental and its crossbred, and Nellore showed intermediate values.