

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 $\mu\text{g/mL}$). 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. Jung¹, S.-H. Oh^{*2}, M. T. See², T. E. del Rosario¹, and Y.-B. Kim³, ¹Jung P&C Institute, Seongnam, Gyeonggi, South Korea, ²North Carolina State University, Raleigh, ³Rosalind 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. Sugisawa, 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 thinner cuts than Americans and Japanese consumers do. Other point is the worrying about health. People look for thinner 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.

Table 1. Carcass characteristics of different breeds

Breeds	LW (kg)	REA (cm ²)	REA/100 kg (cm ²)	BF (mm)	BF/100 kg LW	Marbling (1-6)	lipids (%)
Angus	479 ^{ab}	69.9 ^a	14.5 ^a	3.7 ^b	0.78 ^b	2.54 ^b	2.98 ^b
Brangus	477 ^{ab}	74.0 ^{ab}	15.6 ^{ab}	3.7 ^b	0.73 ^b	2.50 ^b	2.36 ^{ab}
½ Angus							
Nellore	506 ^{bc}	88.5 ^b	17.5 ^b	4.0 ^b	0.83 ^b	2.40 ^b	1.56 ^{ab}
Nellore	445 ^a	72.5 ^a	16.3 ^{ab}	3.2 ^{ab}	0.70 ^{ab}	1.44 ^a	1.50 ^{ab}
½ Simmental							
x Nellore	500 ^{bc}	85.7 ^b	17.2 ^b	2.4 ^a	0.49 ^a	1.08 ^a	1.17 ^a
Simbrasil	488 ^{bc}	83.4 ^b	17.0 ^b	2.5 ^a	0.53 ^a	1.16 ^a	0.76 ^a
Simmental	520 ^a	86.0 ^b	16.6 ^{ab}	2.4 ^a	0.47 ^a	1.05 ^a	0.98 ^a
SEM	0.07	0.11	0.10	0.23	0.22	0.27	0.49

*Means with unlike superscripts are different ($P < 0.05$)

Key Words: Carcass composition, Beef cattle, Breeds

T14 Estimation of genetic parameters for growth traits and image analysis traits of carcass cross section in Japanese Black steers.

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M. trapezius is not evaluated in the grading process for beef in Japan, although this muscle greatly affects the carcass unit price. The relationship between growth traits and *M. trapezius* has hardly been reported. The purpose of this study was to estimate the genetic parameters for growth traits and image analysis traits of rib eye and *M. trapezius* with computer image analysis for the carcass cross section in Japanese Black steers. 1,185 Japanese Black steers in progeny testing were used. The growth traits consisted of initial body weight at the beginning of the 364 d fattening period (IBW), final body weight at the end of the 364 d fattening period (FBW), and average daily gain during the 364 d fattening period (ADG). Digital images of the carcass cross section were taken between the 6-7th rib with photography equipment. Muscle area (MAREA), fat area ratio (FATPER), overall coarseness of marbling (O_COARSE), and coarseness of the largest marbling particle (M_COARSE) in the rib eye and *M. trapezius* were calculated as image analysis traits. Genetic parameters for these traits were estimated with the REMLF90 program using an animal model. Included in the model were herd-year-season and birthplace as fixed effects, age at the beginning of the fattening period as a covariate, and random animal genetic effects. Pedigree records were traced back four generations, and the number of animals in the pedigree file was 7,476. For growth traits, the heritability estimates were 0.65, 0.77 and 0.54 for IBW, FBW and ADG, respectively. For the rib eye and *M. trapezius*, the heritability estimates for image analysis traits were 0.09~0.59 and 0.11~0.74. Genetic correlations between IBW and image analysis traits (MAREA, FATPER, O_COARSE and M_COARSE) were 0.35, -0.10, 0.29 and .028 for the rib eye and 0.32, -0.12, 0.08 and 0.02 for *M. trapezius*, respectively. Genetic correlations between ADG and the above image analysis traits were 0.54, 0.15, 0.56 and 0.79 for the rib eye and 0.43, -0.02, 0.24 and 0.09 for *M. trapezius*, respectively.

Key Words: Japanese Black, Growth traits, Image analysis

T15 Genetic parameters estimation of birth weight for cashmere goat in southern Khorasan province of Iran. H. Naeemipour*, H. Farhangfar, and M. R. Asghari, *Birjand University, Birjand, Iran*.

A total of 524 birth weight records obtained from cashmere goat in southern Khorasan province during 2000 - 2003 was used to estimate J. Anim. Sci. Vol. 84, Suppl. 1/J. Dairy Sci. Vol. 89, Suppl. 1

genetic parameters. The number of kids was 524 representing 21 sires and 230 dams. A set of univariate animal models including additive and maternal genetic effects and maternal permanent environmental effect (as random effects) as well as the fixed effects of year and month of birth, sex, birth type and covariate of dam age (up to quadratic order) were utilized. Variance and covariance components were estimated by restricted maximum likelihood procedure using Powel algorithm applied in DFREML software. The results obtained at the present research showed that the effect of maternal permanent random effect contributed a significant part of total variance for birth weight. For the birth weight trait, model six, in which all random effects were included, was recognized as the best model. Based upon the model six, direct and maternal heritabilities were found to be 0.09 and 0.05 respectively. The ratio of permanent maternal variance to total variance was 0.12 and genetic covariance between direct and maternal effects was 0.01.

Key Words: Goat, Genetic parameters, Birth weight

T16 Genetic analysis of weight records at different ages in Baluchi sheep breed of Iran. M. Mollaei¹, H. Farhangfar*², and H. Naeemipour², ¹*Zabol University, Zabol, Iran*, ²*Birjand University, Birjand, Iran*.

A total of 19813 weight records belonging to Baluchi sheep breed of Iran was used to estimate genetic parameters. The traits were birth weight, weaning weight, weight at ages 6, 9, and 12 months, average daily gain at age interval 0-3 and 3-6 months. Genetic and environmental variance and covariance components were estimated by REML method. In order to estimate genetic parameters total six different models were applied. For birth weight and weaning weight, model 2 (additive genetic + maternal permanent environment) was considered to be more appropriate than the other models. The estimates of ht₂, c₂ were 0.058 ± 0.018 and 0.212 ± 0.017 for birth weight and 0.0254 ± 0.0197 and 0.086 ± 0.017 for weaning weight respectively. The best model for the weight at age 6, 9, 12 months was model 1 and the estimates of ht₂ were 0.0423 ± 0.0211, 0.055 ± 0.03, and 0.0549 ± 0.033 respectively. For average daily gain at age 0-3 months, model 2 was more appropriate and the estimates of ht₂, c₂ were 0.0273 ± 0.02 and 0.0844 ± 0.017 respectively. For average daily gain at age 3-6 month model 5 (additive genetic + maternal genetic + permanent environment) was more appropriate and the estimates of ht₂, hm₂ and c₂ were 0.0358 ± 0.012, 0.0099 ± 0.018 and 0.0009 ± 0.08 respectively. The genetic and phenotypic correlations among weight at different ages were also estimated using model 6 (additive genetic + maternal genetic + permanent environment + covariance between additive and maternal genetic effects). The genetic correlations were all positive and ranged between 0.32 and 1.00. The phenotypic correlations were positive and ranged between 0.25 and 0.8.

Key Words: Baluchi sheep, Variance-covariance components, Genetic and phenotypic correlations

T17 Estimation of genetic parameters for weight at different ages in Lori-Bakhtiari sheep breed of Iran. B. Zinvand² and H. Farhangfar*¹, ¹*Birjand University, Birjand, Iran*, ²*Zabol University, Zabol, Iran*.

To estimate genetic parameters for weights at ages 0 (birth), 3 (weaning), 6, 9, and 12 (in month) as well as average daily gains at age interval 0-3 and 3-6, a total of 7038 weight records belonging to 1940 lori-bakhtiari sheep breed of Iran was used. The results of analysis

of variance (GLM) showed that sex, birth year-season and lamb age were significant statistically. Total six different models were applied to estimate genetic parameters using REML statistical method. For birth weight model 2 (additive genetic + maternal permanent environment) was considered to be more appropriate than the other models. The estimates of h^2 , c^2 were 0.19 ± 0.05 and 0.273 ± 0.03 respectively. For weaning weight as well weight at age month 6, model 5 (additive genetic + maternal genetic + permanent environment) was considered to be the best model. The estimates of h^2 , hm^2 and c^2 were 0.009 ± 0.003 , 0.1 ± 0.03 and 0.07 ± 0.003 respectively. The corresponding estimates for weight at age month 6 were 0.1 ± 0.05 , 0.031 ± 0.005 and 0.03 ± 0.005 respectively. The best model for weight at age month 9 was model 6 (additive genetic + maternal genetic + permanent environment + covariance between additive and maternal genetic effects) and the estimates h^2 , hm^2 , c^2 were 0.09 ± 0.05 , 0.05 ± 0.02 , 0.313 ± 0.05 respectively. For weight at age month 12 and average daily gain (0-6), model 1 was found to be the best and the estimates of h^2 were 0.17 ± 0.08 and 0.153 ± 0.06 respectively. For average daily gain 0-3 model 5 was the best model and the estimates of h^2 , hm^2 and c^2 were 0.016 ± 0.06 , 0.1865 ± 0.03 and 0.0394 ± 0.04 respectively.

Key Words: Lori-bakhtiari sheep, Variance-covariance components, Genetic parameters

T18 Genetic analysis of average daily gains in Lori - Bakhtiari sheep breed of Iran using orthogonal legendre polynomials. H. Farhangfar^{*1}, H. Naeemipour¹, M. Zinvand², and M. Hosseini¹, ¹Birjand University, Birjand, Iran, ²Zabol University, Zabol, Iran.

A random regression model including fixed effects of year-season of birth, sex, birth type, dam age and random effects of direct, maternal additive genetic and permanent environment was used to estimate (co)variance components, heritabilities, and additive genetic correlations among average daily gains using a total of 10876 records belonging to 1828 lambs born between 1995 and 2001 in a single large-size flock of Lori-Bakhtiari sheep breed of Iran. Records for lambs were taken as repeated measurements and also a single measurement error variance was also assumed to be constant for all age groups. Orthogonal legendre polynomial regression order 4 was used to model the genetic and permanent environmental (co)variances structure throughout the growth trajectory. Direct and maternal heritability estimates of average daily gains ranged from 0.011 to 0.131 and 0.008 to 0.181 respectively in which pre-weaning average daily gain (0-3) had the lowest and highest direct and maternal heritability estimates among the other age groups.

Key Words: Average daily gain, Random regression, Lori-bakhtiari sheep breed

T19 Genetic analysis of weight records in Zel sheep breed of Iran. A. Vafadar^{*1}, H. Farhangfar², and H. Naeemipour², ¹Zabol University, Zabol, Iran, ²Birjand University, Birjand, Iran.

In this research a total of 4002 weight records obtained from 1767 lambs of Zel breed was used to estimate genetic parameters. The number of flocks was 18 in Mazandaran province of Iran. The fixed environmental factors including flock, year and season of lambing, sex and birth type were statistically significant on weight records at all ages (0,3 and 6 months). (CO)variance components of direct and maternal genetic effects, maternal permanent effect and residual were estimated by REML method by using 6 different model based upon

including or excluding random effects. For birth weight using model 5 (including direct and maternal genetic, and maternal permanent effects) the estimated direct and maternal heritability were 0.0001 and .098 respectively. The corresponding estimates for weight at age 3 were found to be 0.004 and 0.2 respectively using model 6 (as the model 5 plus covariance between direct and maternal genetic effects). The heritability of weight at age 6 was 0.26 as the model 1 (including only direct genetic effect) was applied.

Key Words: Zel breed, Genetic parameter, Growth traits

T20 Correlation of DGAT1 genetic variants with fat content in the Cal Poly Herd. A. Laubscher^{*1}, S. Henderson¹, J. F. Medrano², G. Rincón², and R. Jiménez-Flores¹, ¹California Polytechnic State University, San Luis Obispo, ²University of California, Davis.

The selection of dairy cattle is dictated by improvement of yield and composition of milk. Genotyping tests give breeders the opportunity to use previously unavailable information to increase the frequency of beneficial alleles in their herds. DGAT1 catalyzes the last step in triglyceride biosynthesis. We have analyzed a polymorphisms in exon VII of the DGAT1 gene that produces a K232A substitution (lysine to alanine amino acid change) in the protein. This mutation has been associated with milk production traits and has a significant effect on milk fat content. The two nucleotide polymorphisms in exon VII (AA → GC) give rise to an MwoI restriction fragment length polymorphism (RFLP). The genotype AA of the DGAT1 gene seems to be associated with higher milk fat content. The objective of this study was to examine the association of DGAT1 genotypes with fat content in the Cal Poly Herd. 232 blood samples from 109 Holstein and 123 Jersey cows were analyzed. DNA was extracted from 200 μL of blood using the MoBio Blood Spin Kit. Samples containing 50 ng of DNA were PCR amplified in a total volume of 25 μL for 35 cycles at 94°C, 58°C and 72°C for 30 s at each temperature. A 285 bp fragment from exon VII to intron VIII of the DGAT1 gene was amplified and digested with 5 units of MwoI. Digestion products were separated by electrophoresis on a 3.5% agarose gel stained with ethidium bromide. Comparing the breed difference, the genotype distributions for Holsteins were .06 (AA), .41 (AG) and .53 (GG) (frequency of A=.265, G=.735) vs Jerseys .19 (AA), .49 (AG) and .32 (GG) (frequency A=.435, G=.565). Genotype frequencies were in Hardy-Weinberg equilibrium for both breeds. Our results confirmed that allele A has a significant effect increasing milk fat content in Holstein and Jersey cows as shown in the table below. In addition we detected a significant difference in the phospholipid content between different genotypes.

Table 1. 305-day average % milk fat content in Holstein and Jersey cows in relation to DGAT1 genotypes

Breed	N	AA	AG	GG
Holstein	55	3.7	3.4	3.3
Jersey	60	4.7	4.4	3.9

Key Words: DGAT1, Fat%, Genotyping

T21 Bioinformatics analysis of bovine neuropeptides. A. N. Tegge^{*}, B. R. Southey, A. Andinet, J. V. Sweedler, and S. L. Rodriguez-Zas, University of Illinois, Urbana.

Neuronal communication relies on the release of chemical messengers, or neurotransmitters. Neuropeptides are relatively large neurotransmit-

ters (typically 3 to 39 amino-acids long) that tend to modulate slower, ongoing synaptic functions and activity in the brain or in peripheral target tissues. Using the bovine central nervous system, several studies have reported the effects of neuropeptides on fertility, feed intake, growth (e.g. neuropeptide Y), and milk production (e.g. oxytocin). Neuropeptides are synthesized from larger proteins called prohormone precursors, with the peptides formed from the precursors via a number of enzymatic processing steps. The cleavage of neuropeptides from the prohormone precursors by prohormone convertases is a complex process influenced by multiple factors and the availability of experimental data on bovine neuropeptides is variable. The objective of this study was to integrate the recently available bovine genome sequence, experimental and sequence information from other species and bioinformatics tools to identify prohormone cleavage sites and neuropeptides in the bovine. A total of 27 prohormone sequences were compiled and a logistic regression model based on sequence and experimental information from bovine and other mammals available in NeuroPred (<http://neuroproteomics.scs.uiuc.edu/neuropred.html>) was used to predict cleavage. The average number of neuropeptides per prohormone was 2.4, and ranged from 1 to 9. Of the reported cleavages, 68 cleavages were predicted and 16 cleavages were missed meanwhile 35 non-reported cleavages were predicted. These results suggest that the model offers an adequate description of the bovine prohormone processing. Further comparison of the observed and predicted cleavages indicates that our bioinformatics approach can be used to identify prohormone regions likely to harbor neuropeptides and thus aid the experimental verification.

Key Words: Neuropeptide, Prohormone, Bioinformatics

T22 The allele and genotype frequencies of bovine pituitary-specific transcription factor and leptin genes in Iranian cattle and buffalo populations using PCR-RFLP. A. Javanmard^{*1}, N. Asadzadeh², M. H. Banabazi³, and J. Tavakolian³, ¹*West and North-West Agriculture Biotechnology Research Institute(ABRII-T), TABRIZ, East Azarbyjan, Iran*, ²*Department of Animal Production and Management, Animal Science Research Institution of Iran (ASRI), Tehran, Karaj, Iran*, ³*Department of Biotechnology, Animal Science Research Institution of Iran (ASRI), Tehran, Karaj, Iran*.

The use of polymorphic markers in breeding program could make selection more accurate and efficient. A total of 324 individuals from six Iranian cattle populations (Sarabi, Golpayegani, Sistani, Taleshi, Mazandarani, Dashtiyari), F1 Golpayegani x Brown Swiss and Iranian buffalo populations were genotyped for the Pit-1 *HinfI* and leptin *Sau3AI* polymorphisms by the polymerase chain reaction and restriction fragment length polymorphism (PCR-RFLP). The genotype and gene frequencies for each breed were determined and shown to be quite variable among the breeds. The highest frequencies of allele B for the leptin gene and allele A for the Pit-1 gene were found in Dashtiyari and Sistani cattle, respectively. According to our results, the highest AB genotype frequencies were found in the Taleshi and F1 Golpayegani x Brown Swiss cross for the leptin and Pit-1 genes, respectively. These allele frequencies were comparable to previously published data on exotic breeds. The highest and lowest heterozygosities were found in Taleshi and Dashtiyari cattle for the leptin gene and in F1 Golpayegani x Brown Swiss cross and Sistani cattle for the Pit-1 gene, respectively. The possible association between molecular polymorphisms within these candidate genes and economic traits for the studied populations should be further investigated.

Key Words: Pit-1, Leptin, PCR-RFLP

T23 Polymorphism of bovine lymphocyte antigen DRB3.2 alleles in Iranian Holstein cattle. M. Pashmi^{*1}, A. Salehi¹, A. Ghorash², M. R. Mollasalehi³, and A. Javanamrd⁴, ¹*Department of Animal Science, University of Tehran, Aborahan, Tehran, Iran*, ²*National Research Center for Genetic Engineering and Biotechnology, Tehran, Tehran, Iran*, ³*National Animal Breeding Center, Karaj, Iran*, ⁴*North West and West Agriculture Biotechnology Research Center(ABRII), Tabriz, Iran*.

Breeding goals for dairy cattle have focused mainly on increasing productivity and have ignored disease resistance. Molecular techniques have been developed for identification of bovine genes responsible for production traits and host immunity. In addition, these techniques have been used to clarify the potential association of bovine major histocompatibility (MHC) or bovine leukocyte antigen (BoLA) alleles with disease resistance and production. In this study polymorphism of the second exon of BoLA-DRB3 gene of 96 Iranian cattle was investigated. Genomic DNA extracted from whole blood samples and two-step polymerase chain reaction (PCR) was carried out in order to amplify a 284 bp fragment of target gene. Nested-PCR products were digested with three restriction endonucleases *RsaI*, *BstYI* and *HaeIII*. Digested fragments were analyzed by Polyacrylamid gel electrophoresis. Twenty-two BoLA-DRB3 alleles were distinguished with frequencies ranging from 0.5 to 19.3%. Identified alleles include: BoLA-DRB3.2*3, *6, *7, *8, *9, *10, *11, *12, *13, *14, *15, *16, *20, *21, *22, *23, *24, *25, *27, *28, *32 and *51. Their frequencies found to be 2.6, 2.6, 1.0, 13.5, 0.5, .05, 13.0, 1.6, 1.6, 0.5, 2.6, 14.1, 0.5, 1.6, 7.3, 5.2, 19.3, 2.1, 2.1, 1.6, 0.5 and 5.7% respectively. The most frequent alleles (BoLA-DRB3*8, *11, *16, *22 and *24) accounted for 67.2% of the observed alleles. Results of this study indicate that BoLA-DRB3 locus is highly polymorphic among tested Animals.

Key Words: Bovine leukocyte antigen (BoLA), Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP), Iranian Holstein cattle

T24 Estimation of genome wide haplotype effects in half-sib designs. D. Kolbehdari^{*1,2}, L. R. Schaeffer², and J. A. B. Robinson², ¹*University of Tehran, Tehran, Iran*, ²*University of Guelph, Guelph, Ontario, Canada*.

Methods of scoring haplotype transmission in half-sib designs combined with linear mixed haplotype model were proposed to locate and estimate QTL effects within a 100 cM region of DNA. Precision, average of absolute effects of haplotypes, and correlation between estimated and true breeding values were used to compare scenarios via Monte Carlo simulation of granddaughter designs. Factors studied were the size of QTLs, heritability of quantitative trait, and the positions of QTL. Markers and QTLs were assumed to be bi-allelic. One hundred equally spaced markers (1 cM) with ten QTLs located between markers were simulated. Marker haplotypes were constructed for each pair of contiguous markers. Scores were used to indicate haplotype transmission from sire to son based on marker haplotypes. The scores were used in a linear mixed model across the population. The linear mixed haplotype model was successful model to estimate and locate effects of QTL in granddaughter designs. QTLs of equal magnitude gave slightly higher precision than QTLs of unequal size. Correlations between estimated and true breeding values ranged from 0.72 to 0.85. The linear mixed haplotype model could be used to estimate QTL positions and effects within intervals of 1 cM.

Key Words: Haplotype effects, QTL mapping, QTL detection

T25 Genetic diversity in piracanjuba populations *Brycon orbignyanus* with the random amplified polymorphic DNA (RAPD) markers. N. M. Lopera Barrero^{*1}, R. P. Ribeiro¹, R. N. Siroi², J. A. Povh¹, P. Gomes¹, L. Vargas¹, and D. P. Streit Jr.¹, ¹*Universidade Estadual De Maringá, Maringá, Paraná, Brazil*, ²*Duke Energy International, Geração Paranapanema, Salto Grande, São Paulo, Brazil*.

Brycon species are the most important local fishing source, wherever found, and therefore, are seen as having great economical value. Based on the amplification of genomic DNA by PCR (Polymerase Chain Reaction) with arbitrary nucleotide sequence primers, RAPD can detect high levels of DNA polymorphisms and can produce fine genetic markers. Nowadays, the main concern of researchers and scientific studies, regarding genetics and improvement of fish lineage in Brazil, has been directed to the organization and characterization of genetic banks to study native populations. In order to contribute to restock programs and deeply understand the framework of the piracanjuba *Brycon orbignyanus* the genetic divergence and variability of these stocked populations were estimated by using the RAPD markers. The population of piracanjuba reproducers from Castilho (São Paulo - Brazil) and Porto Ferreira (São Paulo - Brazil) and their offspring were evaluated. Jaccard's similarity coefficient matrix was used in order to elaborate a dendrogram, and the genetic divergence among populations was determined by Mantel's test. The genetic variability was estimated by using both Shannon's index and the polyphormic loci percentage. The genetic divergence in Castilho's population (0.1551) and its offspring (0.1889) and the genetic variability (Shannon's index: 0.3184 in Castilho's population and 0.3433 in offspring; polyphormic loci percentage: 54.02% and 57.47% respectively) were similar, indicating that the control of non-intentional selection was efficient in maintaining reproducers genetic diversity. Porto Ferreira's population showed similar values of genetic divergence (0.1987 and 0.1970) and variability (Shannon's index: 0.3687; polyphormic loci percentage: 58.62%) to Castilho's population and its offspring respectively, therefore, the values of genetic divergence and genetic variability remained uniform, which means that, basically, there was no populations or progeny genetic changes, despite being geographically separated one from the other.

Key Words: Fish, Genetic divergence, Genetic variability

T26 Handling inbreeding and overlapping generations within QTL-mapping. G. Freyer¹ and N. Vukasinovic^{*2}, ¹*Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*, ²*Monsanto Animal AG, St. Louis, MO*.

Approaches of QTL- mapping which are able to deal with complicated pedigrees in dairy cattle such as inbreeding and overlapping generations have hardly been reported so far. Most designs ignore such relationships within a pedigree, simplifying computations but also losing power of QTL detection. A more precise QTL- estimate is expected when inbreeding is accounted for as it occurs. A four-generational pedigree originating from two unrelated great-grand sires was simulated. One of them produced itself 52 out of 420 final offspring, therefore creating a pedigree with overlapping generations. Three different pedigree structures were considered: (a) without inbreeding, (b) with mild inbreeding, where one sire originates from a aunt-nephew-mating, (c) containing a highly inbred sire, originating from a halfsib- mating. These pedigree structures were intended to mimic structures common in dairy populations. In (b) and (c) the number of offspring from

an inbred sire was > 18%. A single QTL explaining 15% of the phenotypic variance was simulated. QTL mapping was considered within a chromosomal segment of 55 cM covered by 11 markers, carrying 2, 4, or 6 alleles, with fine mapping-like marker density around the QTL position for four marker maps. QTL analysis was conducted using varying amount of information content within the data. All analyses were performed by maximum likelihood techniques, mainly by extending the method for calculating identical-by-descent (IBD)- probabilities by Pong Wong et al. (2001) and ASREML. The most precise estimates of QTL location were obtained from the pedigree with mild inbreeding. High level of inbreeding often caused computation problems, likely because of high correlations of IBD values among inbred animals. The results show that taking into account inbreeding and overlapping generations in complicated pedigrees, especially if coupled with increased map density and marker polymorphism, leads to more precise estimates of QTL position and higher power of QTL detection. The benefits of improved precision of QTL mapping are likely to exceed increased computation costs associated with considering all relationships in a pedigree.

Key Words: QTL mapping, General pedigree analysis, Inbreeding

T27 Comparison of the performance of two-dye microarray platforms to characterize gene expression patterns. S. L. Rodriguez-Zas^{*}, R. E. Everts, B. R. Southey, J. K. Drackley, J. J. Looor, and H. A. Lewin, *University of Illinois, Urbana*.

Microarray technology is a well-established tool to simultaneously measure the expression of thousands of mRNA sequences. The objectives of this study were to compare the performance of bovine cDNA and long-oligonucleotide spotted microarray platforms, and to evaluate the impact of various sources of variation. The two platforms considered were a double spotted 7,872 element cDNA array (NCBI GEO GPL2864) and a double spotted 13,257 element long (70-mer) oligo array (NCBI GEO GPL2853). Two experiments using liver biopsies from multiparous cows at 14 DIM in a reference microarray design with reverse labeling were analyzed. The gene expression data were filtered, normalized and described using a mixed effects model including the effects of dye, treatment (ketosis and control), cow, and array. The estimates and significance probability values of 4,791 elements with one-to-one matches between platforms and the ability of selected probes to detect reported differential expression were evaluated. In the first experiment, the correlation between microarrays with reverse labeled samples ranged between 0.93 and 0.95 for the cDNA microarray and between 0.83 and 0.85 for the oligo microarray. The correlation between the log₂ sample-to-reference ratio estimates between platforms ranged from 0.70 to 0.75 in both experiments and increased when elements with high differential expression were considered. The estimates of the log₂ ratios within experimental treatment level from the oligo platform were more dispersed than the estimates from the cDNA platform, however the estimates of the log₂ ratios across treatment levels studied were consistent across platforms. These results indicate that the oligo elements may be more sensitive to variations in gene expression intensity across the conditions studied. The results from selected oligo-probes were more consistent with reported values than the results from the corresponding cDNA-probes.

Key Words: Microarray, cDNA, Mixed model

T28 Relationship between calpastatin gene polymorphism and beef cattle growth, carcass and meat quality traits. L. Suguisawa, A. A. Souza*, H. N. Oliveira, A. C. Silveira, and R. A. Cury, *São Paulo State University, Brazil*.

The Calpastatin polymorphism was associated with performance and meat quality traits, by Chung et al. (2001) methodology, in 300 bullocks. To validate this finding, we looked at a group of animals (126 Angus Nellore, 10 Angus, 18 Brangus, 24 Simmental Nellore, 12 Simmental, 11 Simbrasil, 17 Santa Gertrudes Nellore, 18 Brown Swiss x Nelore, 12 Canchim, 16 Brahman Nellore and 36 Nellore). The animals were weaned at 7 months old at the creep-feeding and raised at the feedlot system for 120 days. The animals were harvested with 450 kg live weight, 3 millimeters of ultrasound fat thickness and 12-15 months old age. The gene polymorphism was analyzed by PCR-RFLP. The animals were classified at three genotypes forms: AA, AB and BB. The higher frequency of AA genotype was from Angus Cattle. Nevertheless, the higher frequency of BB genotype was from Nellore and Brahman Nellore cattle. The genotypes effects on traits were analyzed by General Linear Model of SAS and the Least Square Means of the genotypes were compared by Tukey test. The model included genotype, genetic group x year of feedlot x ranch and interactions. The collected growth traits were: initial and final live weight, average daily gain, ultrasound ribeye area, ultrasound fat thickness and ultrasound rump fat thickness. The collected carcass and meat traits were: dressing percentage, hot carcass weight, carcass ribeye area, carcass fat thickness and Warner Bratzler shear force. Because almost all genetics groups of this research were Zebu crossbreed, these animals could have high Calpastatin quantity. Despite of that, there were not found any relationship between any Calpastatin genotypes and all traits evaluated. The lack of effects of this Calpastatin gene polymorphism indicates that this polymorphism could not be used as a selection tool for improving Animal Breeding.

References:

CHUNG, H.Y.; DAVIS, M.E.; HINES, H.C.; Genetic variants detected by PCR-RFLP in intron VI of the bovine calpastatin gene. *Animal Genetics*, v. 32, p. 40-53, 2001.

Key Words: Calpastatin gene, Meat quality, Cattle growth

T29 Corn oil or Corn grain supplementation to forage-finished steers. IV. Effects on gene expression of lipogenic enzymes in the s.c. adipose tissue. E. Pavan*^{1,2}, S. Joseph¹, K. Robbins¹, S. Duckett³, and R. Rekaya¹, ¹University of Georgia, Athens, ²INTA, Balcarce, Bs. As., Arg., ³Clemson University, Clemson, SC.

Samples of s.c. fat were obtained from 28 Angus steers after slaughter to determine the effect of energy supplementation of steers grazing tall fescue pastures. Steers (n = 8/ treatment; 289 ± 3.8 kg) were supplemented with either corn grain (0.52% BW; PC) or soybean hulls plus corn oil (0.45% BW + 0.10% corn oil; PO). Negative (pasture only; P) and positive (85% concentrate/15% roughage; C) controls were also included in the study. RNA was extracted from the s.c. adipose tissue using TRIzol reagent (Gibco Invitrogen Corp.). RNA from each treatment was pooled (10 µg/steer) and five replicates from the same RNA pool were used for microarray hybridization. GeneChip Bovine Genome array (Affymetrix) was used for hybridization of the extracted mRNA's according to the Affymetrix protocol. The data was normalized and analyzed using a simple linear (ANOVA) model. Treatments effects were compared using non-orthogonal contrasts between all possible comparisons, the Benjamini and Hochberg method of false discovery rate (FDR) was used to control the experimentwise error rate. Genes were identified as being differentially expressed using a FDR of 0.05. At a FDR of 0.01 a total of 89, 39 and 1133 genes were detected to be differently expressed between P and PO, P or C, respectively, 757 and 113 between C and PO or PC, and 183 between PO and PC. Lipoprotein lipase was differently ($P < 0.01$) expressed between PO and C and acetyl-coA carboxylase ($P < 0.01$) between P and C. Fatty acid synthase was differently expressed ($P < 0.01$) between C and either P or PO. Stearoyl-coA desaturase was differently expressed ($P < 0.01$) between PC and P, C or PO and between C and P, whereas did not differ (FDR > 0.05) between PO and either P or C. The gene encoding the soluble form of isocitrate dehydrogenase was differently expressed ($P < 0.01$) between PO and P, PC and C as well among C and either PC or P. The expression of glycerol phosphate acyltransferase differ ($P < 0.01$) between all comparison evaluated. Gene expression of the adipocyte lipogenic enzymes from beef steers may be manipulated through diet.

Key Words: Bovine, Lipogenic enzymes, Gene expression

Companion Animals: Nutrition & Health

T30 Identification of canine markers related to obesity. R. Yamka* and K. Friesen, *Hill's Pet Nutrition, Inc., Topeka, KS*.

Thirty lean and thirty obese neutered/spayed beagles (average age = 7.5 ± 0.7 years) were identified for this study. Fifty percent of the dogs were female (15 lean and 15 obese) and fifty percent were male (15 lean and 15 obese) in order to determine if gender played a role in marker differences. Animals were weighed, given a body condition score (1=lean, 3=ideal and 5=obese) and a blood sample was drawn. Average body condition scores were 4.7 and 2.5 for the obese and lean groups, respectively. Average body weights were 17.3 ± 0.4 and 11.2 ± 0.4 kg for the obese and lean groups, respectively. Serum was analyzed for chemistry screens, obesity markers, thyroid markers and arthritis markers. The obese group had higher levels of alkaline phosphatase ($P = 0.04$), cholesterol ($P = 0.04$), triglycerides ($P = 0.06$), total protein ($P < 0.01$), albumin ($P < 0.01$), thyroxine ($P = 0.05$), calcium ($P < 0.01$), phosphorous ($P = 0.04$), glucose ($P < 0.01$), insulin ($P < 0.01$), insulin like growth factor-1 ($P < 0.01$), low density lipoprotein (P

< 0.01), leptin ($P < 0.01$) and type 2 cartilage synthesis ($P < 0.01$). The obese group had lower levels of creatinine ($P = 0.01$), serum urea nitrogen ($P < 0.01$), chloride ($P < 0.01$) and obese males had lower levels of testosterone ($P = 0.04$). These data indicate that obesity is directly related to other disease states in dogs (i.e. dyslipidemia, arthritis and diabetes). Thus, managing obesity through weight loss and/or calorie restriction may alleviate or prevent the differences observed between lean and obese blood markers.

Key Words: Canine, Obesity, Marker

T31 Identification of feline markers related to obesity. R. Yamka* and K. Friesen, *Hill's Pet Nutrition, Inc., Topeka, KS*.

Thirty lean and thirty obese domestic short hair cats (average age = 7.4 ± 0.5 years) were utilized for this the study. Animals were weighed, given a body condition score (1=lean, 3=ideal and 5=obese) and a