analysis were used as candidates of independent variables. Correlation coefficients between BCS (Beef Color Standard) numbers evaluated by graders and L*, and between BCS and luminance by the image analysis were -0.39 and -0.62, respectively. FATPER of ribeye was classified into 3 levels (S:<19%, M:19%~23% and L:>23%). Correlation coefficients of L* value and luminance of lean were 0.80 for S, 0.50 for M and 0.20 for L. The L* value of lean with a low FATPER level might reflect the accurate lean color. However, the L* value with more marbling meat might not be as accurate as the lean color value. In the multiple regression analysis predicting the L* value by colorimeter, the most affected image analysis traits for S, M and L were the luminance of lean, R component of whole ribeye, and G component of marbling, respectively. The diameter of the colorimeter probe might be oversized for measuring the lean color of beef, marbling included.

Key Words: Beef Color, Image Analysis, Colorimeter

T49   Alternative supplementation strategies for replacement beef heifers grazing dry California foothills annual range during summer. R. B. Monteiro*[1,2], G. D. Cruz[1], D. M. Myers[1], J. W. Oltjen[1], and R. D. Sainz[1], [1]*University of California, Davis,* [2]*University of Sao Paulo, Piracicaba, SP, Brazil.*

California's annual foothill rangelands are the main forage source for the state's range livestock industry and are characterized by marked seasonal variations in forage availability and quality. Due to the inadequate quality of dry forage during summer and fall, cattle require supplemental feed to balance deficiencies in protein, energy and minerals. The objectives of this study were to evaluate the effects of different types of supplementation for weaned heifer grazed in dry range and analyze the cost-benefit within the treatments. The supplements were: a commercial molasses-based tub supplement (COM; 30% CP) and a low-cost protein/energy/mineral formulation (UCD; 58% CP, 60% TDN, 3% P, 500 mg/kg Cu, 3 mg/kg Se). In 2005 and 2006, 60 weaned replacement Angus-Hereford heifers (248 ± 11.8 kg BW) were stratified by BW and allocated randomly to 6 groups of two supplement types with three replicate groups of 10 heifers for each treatment in each year. Heifers were given supplements every 3 d (UCD) or every 20 d (COM) for 70 d, and weighed every 28 d. Average daily gains were determined by regression. The data were analyzed by ANOVA with year and supplement as main effects and pasture group as the experimental unit. Supplement intakes were different (P < 0.05) between years, but ADG only tended to differ (P < 0.10). Across years, supplement intakes and costs per heifer averaged 547 and 398 g/d and $0.331 and $0.184 (P < 0.05) for the COM and UCD groups, respectively. Heifers' ADG were 78 and 246 g/d for the COM and UCD groups, respectively (P < 0.01). The UCD supplement produced greater gains (>3X) compared with a commercial tub supplement, at much lower cost. With appropriate feeders the UCD supplement can be fed free choice to improve calf performance and reduce costs of production.

Key Words: Beef Heifers, Annual Range, Supplementation

T50   Effects of deworming nursing calves 90 days prior to weaning on calf weaning weight. J. E. Rossi*[1], D. T. Ensley[2], and B. G. Mullinix, Jr.[1], [1]*University of Georgia, Tifton,* [2]*University of Georgia, Athens.*

Two trials were conducted to determine the effects of deworming winter born (Jan/Feb) calves 90 days (June) prior to weaning on calf weaning weight. In trial 1, nursing Angus calves (n=117, 174 ± 5.3 kg) were allotted by weight and sex in each of six fescue pastures. Treatments consisted of no deworming (CON) or deworming (DW) with Doramectin injectable (1 mL/50 kg BW). Equal numbers of steers and heifers were in each treatment within each pasture. All cows were dewormed with Doramectin pour-on (1 mL/10 kg BW) on d 0. Calves were weighed on d 0, 30, 60, and 90 of the trial. Data were analyzed using the MIXED procedure of SAS. Overall ADG was greater (P < 0.10) for DW (0.87 kg/d) compared with CON (0.84 kg/d) calves. Daily gain was not different (P > 0.18) from d 0 to 30 (1.03 and 1.00 kg/d for DW and CON; respectively), d 31 to 60 (0.95 and 0.91 kg/d for DW and CON; respectively) or d 61 to 90 (0.68 and 0.66 kg/d for DW and CON; respectively). In trial 2, nursing Angus, Angus × Charolais, and Hereford × Charolais calves (n=209, 175 ± 9.7 kg) were dewormed 90 days prior to weaning. Calves were allotted by weight, sex, and breed to each of three bermudagrass pastures. Treatments consisted of no deworming (CON) or deworming (DW). Equal numbers of steers and heifers were in each treatment within each pasture. Deworming and weighing procedures were the same as in Trial 1. Overall ADG was not different (P = 0.59) between treatments (0.95 and 0.93 kg/d for DW and CON; respectively). Daily gain was not different (P > 0.32) from d 0 to 30 (0.99 and 0.97 kg/d for DW and CON; respectively), d 31 to 60 (0.85 and 0.80 kg/d for DW and CON; respectively) or d 61 to 90 (0.99 and 1.00 kg/d for DW and CON; respectively). Calves that were dewormed returned $5.15 per hd in Trial 1 and $2.77 per hd in Trial 2 more than the CON calves when valued at $1.00 per 0.45 kg of BW at weaning. Cost of the dewormer would be approximately $1.60 per calf, excluding the cost of labor. Deworming nursing calves in early June (90 days prior to weaning) increased calf weaning weight in Trial 1 and increased the value of the calf at weaning in both trials.

Key Words: Calves, Deworming

Breeding and Genetics - Livestock and Poultry

T51   Joint analysis of egg and production traits in broilers. R. L. Sapp[1], T. Wing[2], and R. Rekaya*[3], [1]*USDA-ARS, Miles City, MT,* [2]*Cobb-Vantress, Inc., Siloam Springs, AR,* [3]*University of Georgia, Athens.*

The objective of the study was to investigate the relationship between egg and production traits in chickens. The data were obtained from a closed, fully pedigreed, commercial broiler line. Records included measurements of body weight (BW), residual feed intake (RFI), percent breast meat (PBM), egg production (EP) and egg weight (EW) from 13,836 birds. A total of five analyses were conducted: 1) joint analysis of BW, RFI, PBM, EP, and EW in parent data (PA); 2) joint analysis of BW, RFI, and PBM in progeny data (PR1); 3) PR1 with EP and EW covariates (PR2); 4) PR1 with covariates of EP and EW grouped into 6 classes; and 5) joint analysis of BW, RFI, PBM, EP, and EW in both progeny and parent data (PR4). The mixed model included

fixed effects of contemporary group (flock-week of hatch-parent's flock) and sex; and random additive effects of bird, maternal effects of hen, maternal permanent environment and residual. For PA and PR4, random effect of permanent environment was also included in the analysis. The structure of the data was such that if birds had RFI, then they would not have PBM and vice versa. Heritability estimates obtained from PA for BW, PBM, RFI, EP, EW, and maternal BW were 0.16, 0.53, 0.26, 0.22, 0.47, and 0.16. For progeny data, heritability estimates of PBM and RFI were consistent across PR1 — PR4. In contrast, estimates for BW and maternal BW varied across PR1 — PR4 with PR2 and PR3 having higher estimates. Heritability estimates of the six traits using PR4 were similar to those obtained from PA. However, BW estimates obtained from PR2 and PR3 were significantly different from the estimates obtained using PA; thus indicating that methods including EP and EW as covariates overestimated BW heritability. Genetic and residual correlations ranged in magnitude and direction depending on the type of analysis. In conclusion, heritability estimates for the egg and production traits suggest that genetic improvement could be made. However, the relationship between these traits varies with the type of data and method used in the analysis. The fluctuation in these relationships could be due to the large number of missing records for PBM and RFI.

Key Words: Breast Meat, Egg Weight, Feed Conversion

T52   Cow/calf pre-weaning efficiency of Nellore, British × Nellore and Continental × Nellore crosses[1]. Liana Calegare*[1], Maurício Mello de Alencar[2], Irineu Umberto Packer[1], and Dante Pazzanese Duarte Lanna[1], [1]*ESALQ, Piracicaba, SP, Brazil*, [2]*Embrapa, Sao Carlos, SP, Brazil*.

In Brazil, purebred Nellore and its crosses represent around 75% of the total beef cattle herd. Crossbreeding programs have introduced different breed types with higher growth potential. However, knowledge of nutritional requirements and biological efficiency is vital to match maternal breed types to the environment. The objective of this study was to determine cow/calf efficiency. Data from fifty-eight cows from three breed types Nellore (NL), Angus × Nellore (AN), and Simmental × Nellore (SN) were used. Cows were randomized in blocks by calving date during two separate years (2002 and 2006). Crossbred cows were bred to Canchim (5/8 Charolais) bulls and NL cows to Nellore bulls. Cows and respective calves were individually fed from postpartum to weaning (20-190 d). The estimated ME and CP content of the diet were 2.2 Mcal and 16% CP for 2002 and 1.9 Mcal and 12% CP/kg DM for 2006. Calves received the same diet of their dams *ad libitum* beginning at 35 d of age. Milk yield was estimated by weighting calves before and after suckling. ME intakes by cow/calf pairs were different (P<0.01); 4212±66.9 for SN, 3895±67.3 for AN and 3433±70.7 Mcal for NL. The energy intake was parallel to milk yield and calf's growth rate. At birth the ¼S calves were heavier (P<0.05; 43.2±1.4) than ¼A (38.8±1.4) and Nellore (32.5±1.5 kg). This group had lower BW at weaning (P<0.01; 171±7.2) than ¼A (231±6.9) and ¼S calves (241±6.8 kg). NL pairs had lower (P<0.05) cow/calf efficiency (grams of calf BW gain/Mcal of MEI by cow/calf pair); 40.9±1.6 vs. 47.4±1.5 for SN and 49.5±1.6 g/Mcal for AN. The lower efficiency of purebred Nellore is confounded by the fact that there is no heterosis in this group. The higher MEI by crossbred pairs was more than compensated by the higher BW gain. There was high individual variability of efficiency (between and within-breed). Crossbred cows had 15% greater energy

requirements than Nellore cows and may not be adapted to certain environments.

Key Words: Biological Efficiency, Breed Type, Weaning Weight

T53   Morphologic evaluation of Murrah water buffalo through regression and principal component analysis. J. R. B. Sereno*[1], M. V. Snel-Oliveira[2], S. M. Vasconcelos[2], A. A. Egito[3], M. S. M. Albuquerque[3], C. McManus[4], and J. C. Souza[5,6], [1]*Embrapa Cerrados, Planaltina, DF Brazil*, [2]*UPIS-Faculdades Integradas, Brasilia, DF Brazil*, [3]*Embrapa Recursos Geneticos e Biotecnologia, Brasilia, DF Brazil*, [4]*Universidade de Brasilia, Brasilia, DF Brazil*, [5]*Universidade Federal do Parana, Campus Palotina, PR Brazil*, [6]*University of Missouri-Columbia Scholarship of CNPq, Brazil, Columbia, Mo USA*.

This study aimed to analyze morphometric data of the Murrah water buffalo using principal component and regression analysis. Traits included ear length and width, horn length and width, back diameter, head length and width, body length, hip height, thoracic and cannon bone perimeter, height and length of croup, distances observed between pelvic bones, width of haunches, head profile and body score. Two hundred and twenty seven females were used, divided in four categories (suckling, weaned, intermediate and adults). These were measured using a tape measure and a measuring stick. The first two principal components explained 78% of all variation between traits. Correlations between traits were in general high (>0.60), except for diameter at the ribs. The first component showed that as a one trait increased in size the other traits also increased in size, as expected. The second component separated the animals into those that were long and thin from those that were short and stocky. Two different groupings were observed, those represented by suckling and weaned heifers and another by intermediate and adult cows. Within group variation for the traits was low (CV<10%). Among the traits analyzed those related to head conformation were the most heterogeneous. The regression analysis showed that these animals increase in size up to 80 months of age, when there is a tendency for a plateau. These data serve as a basis for comparison with a larger number of animals, with the objective of confirming these tendencies for the Murrah breed.

Key Words: Management, Phenotypical Evaluation, Animal Breeding

T54   Genetic parameters for weaning weight by age of dam for Brazilian Nellore. L. O. Campos da Silva*[1], J. C. Souza[2,3], A. Gondo[3], C. H. M. Malhado[4], J. A. Freitas[2], I. W. Santos[2], J. R. B. Sereno[6], R. Weaber[8], L. D. Van Vleck[7], and W. R. Lamberson[8], [1]*Embrapa-GNPGC, Brazil*, [2]*Scholarship of CNPq, Brazil*, [3]*Parana Federal Univeristy, Palotina, PR Brazil*, [4]*Bahia State University, Brazil*, [5]*Mato Grosso do Sul Federal University, Brazil*, [6]*Embrapa-CPAC, Brazil*, [7]*University of Nebraska, Lincoln*, [8]*Univeristy of Missouri, Columbia*.

The objective was to estimate genetic parameters by age of dam subclass for weaning weight of Nellore cattle raised on pasture in two regions of São Paulo State, Brazil, between 1975 at 2001. The data were from ABCZ / EMBRAPA and included 51,664 weights at 205

d (W205) from progeny of 24,996 cows. Records were grouped on the basis of age and number of calves of dams. Seven groups were established: G1 included all dams; G2 had dams with a minimum of 2 calvings, age of first calving greater than 60 mo, and calving between 280 and 1095 d; G3 had dams with one parturition (first) between 22 and 84 mo; G4 to G7 included dams calving between 35 and 60; 61 and 84; 85 and 120; 121 and 240 mo of age, respectively and all had at least two parturitions with no restriction for calving interval. Estimates of variances and covariates were obtained from single trait analyses using the MTDFREML set of programs. Fixed effects were contemporary group [season (dry or wet), year, sex and farm combination] with age of dam as linear and quadratic covariates. Random effects were direct and maternal genetic effects with covariance, and the uncorrelated maternal permanent environmental effect. Estimates of direct heritabilities ranged from $0.14 \pm .02$ to 0.19 ± 0.02 for all groups except G5 which had an estimate of 0.26 ± 0.06. Maternal heritabilities ranged from 0.02 ± 0.09 to 0.11 ± 0.11. Estimates of the direct-maternal genetic correlation were negative and increased from $-0.14 \pm .66$ for G4 to -0.87 ± 0.20 for G6, although the estimate was near zero with a large standard error for G7. These results suggest that heritabilities remain relatively constant across age of dam groups for Nellore, but that the direct-maternal genetic correlation may become more negative for older dams.

Key Words: Age of Dam, Heritability, Weaning Weight

T55   Dairy cattle mortality trends in southeastern states. G. W. Rogers*[1], J. B. Cooper[1], and J. S. Clay[2], [1]*University of Tennessee, Knoxville*, [2]*Dairy Records Management Systems, Raleigh, NC.*

Lactation records from dairy herds in 9 Southeastern states processed through the Dairy Records Management Systems were utilized to determine rates of dairy cow mortality between 1982 and 2005. Over 1.1 million cows in 2038 herds born on or after January 1, 1980 were used for calculating the frequency for died code (termination code of 6) by calving year, lactation number and breed (Holstein or Jersey). Herds were required to have 10 or more years of continuously collected Dairy Herd Improvement data and 5 or more first calvings per year. These edits resulted in 1768 Holstein herds and 270 Jersey herds averaging over 1500 calvings. The percentage of cows that died during first lactation increased from the early 1980s to early 2000s; Jersey death losses in first lactaton increased from 1.4% to 2.6% and Holstein death losses in first lactation increased from 1.7% to 4%. Actual mortality rates in this age group may be higher as cows that calve and die before their first test date often are not included in records. Frequencies for mortality in lactation 2 and lactations 3 or greater are conditional on survival during the previous lactation. The percentage of cows that died during second lactation also increased from the early 1980s to early 2000s; Jersey death losses in second lactation increased from 2.2% to 4% and Holstein death losses in second lactation increased from 2.3% to 5.7%. The percentage of cows that died in third and later lactations increased from the mid 1980s to early 2000s; Jersey death losses in this group increased from 4.4% to 9% and Holstein death losses increased from 3.8% to 10.1%. Average death losses in the 24-year period for Jersey herds was less than that for the Holstein herds: 4.4% versus 4.8% for all lactations, 1.9% versus 2.9% for first lactations, 3.0% versus 3.8% for second lactations and 7.0% versus 7.2% for lactations 3 or greater. Cow mortality

has increased approximately 2.5 fold over the past 2 decades in Southeastern dairy herds.

Key Words: Dairy Cow Mortality, Death Losses, Southeastern US

T56   Weaning weight and wool traits in a grade-up program of Rambouillet sheep with Australian Merino genetics. W. M. Rauw*[1], H. A. Glimp[1], T. Wuliji[1], M. Teglas[1], W. Jesko[2], and L. Gomez-Raya[1], [1]*University of Nevada, Reno*, [2]*Rafter 7 Ranch, Yerington, NV.*

The aim of the present study was to evaluate the influence of inclusion of Merino genetics on weaning weight (WW), greasy fleece weight (FW), staple length (SL) and fiber diameter (FD) and to calculate heritabilities, and phenotypic (rp) and genetic correlations (rg) for the wool traits. Records were available on 4408 to 9597 animals between 1992 and 2005. The Rafter 7 flock was initiated in Nevada in 1990 with the purchase of 500 purebred Rambouillet (R) ewes. A grade-up program (1/2, 3/4, 7/8, purebred) was initiated using Australian Merino semen (M) with the aim of developing a purebred Merino flock. The Rafter 7 line (approximately 5/8 M and 3/8 R), was created in 1999 and has been a closed line since. The percentage of M in the flock increased during this time interval. Least squares means of WW were estimated from a model that included the effects of sex, breed, year of birth, birth-rearing type, age of the dam and age at weaning. Least squares means of wool traits were analyzed with the same model but including age at shearing instead. Phenotypic correlations were estimated after adjustments were made for the traits included in the model. Heritabilities and genetic correlations were estimated with a multi-trait animal model. Heritabilities were 0.20 for SL ($\pm$ 0.018), 0.39 for FD ($\pm$ 0.013), and 0.27 for FW ($\pm$ 0.019). Animals with higher SL had higher FD (rp = 0.22, P<0.0001; rg = 0.26 $\pm$ 0.053) and higher FW (rp = 0.31, P<0.0001; rg = 0.52 $\pm$ 0.055). Animals with higher FD had higher FW (rp = 0.32, P<0.0001; rg = 0.38 $\pm$ 0.042). Results indicate that in general, within year of birth, the inclusion of Merino genetics resulted in decreased WW (P<0.05), increased FW (P<0.05), and decreased FD (P<0.05). Clear effects on SL were not apparent. This indicates that the grade-up program had a somewhat negative effect on WW, but resulted in improved wool quantity and quality.

Key Words: Merino Sheep, Weaning Weight, Wool Traits

T57   An evaluation of SNP associations with calpastatin enzyme activity and shear force measures in Brahman steers. D. E. Franke*[1], M. G. Thomas[2], A. J. Garrett[2], and T. D. Bidner[1], [1]*Louisiana State University Agricultural Center, Baton Rouge*, [2]*New Mexico State University, Las Cruces.*

Objectives were to associate SNPs in the GeneSTAR tenderness panel of genetic markers (www.bovigen.com) with calpastatin (CAST) enzyme level and Warner-Bratzler shear force of steaks aged for 7 (SF7) and 14 (SF14) d from purebred Brahman steers (n=382). Steers were fed postweaning and harvested when they reached 10 to 15 mm fat thickness and acceptable market weight. Samples of DNA were collected from each steer prior to slaughter. Genotypic frequencies at a CAST locus in the 3′ untranslated region were 0.107 for C/C, 0.469 for C/T, and 0.424 for T/T nucleotides, respectively. Allelic frequencies were 0.342 for C and 0.658 for T nucleotides. Genotypic frequencies

at the calpain (CALP316) locus were 0.063 for C/G and 0.937 for G/G nucleotides, resulting in allelic frequencies of 0.031 and 0.969 for C and G, respectively. Similarly, genotypic frequencies at the CALP4751 locus were 0.099 and 0.901 for C/T and T/T nucleotides, respectively. Allelic frequencies were 0.050 and 0.950, respectively, for C and T nucleotides. No C/C nucleotide pairings at the CALP316 locus or C/C nucleotide pairings at the CALP4751 locus were observed. Genetic markers at the CAST locus significantly influenced variation in calpastatin enzyme activity but not in SF7 or SF14. Regression of calpastatin enzyme activity on number of favorable marker alleles at the CAST locus was -0.343 ± 0.071 ($P \leq 0.01$). Genetic markers at the CALP316 or the CALP4751 locus did not influence variation in shear force. However, regression on combinations of CALP316 and CALP4751 favorable markers predicted variation in SF7 ($-.226 \pm 0.110$) and SF14 (-0.240 ± 0.091), respectively. Eight haplotypes were identified among the three loci with C-G-T and T-G-T having the highest frequencies at 0.314 and 0.606, respectively. Haplotype T-G-C had a frequency of 0.032 and all other haplotypes had frequencies less than 0.02. Results suggest that combinations of SNP genetic markers in the GeneSTAR tenderness panel will significantly reduce SF7 and SF14 in Brahman steers. Most importantly, a SNP within CAST influenced the activity of this protein.

T58   Gene polymorphisms associated with mastitis and reproduction traits in Holstein cows. G. M. Pighetti*, C. J. Kojima, and A. M. Saxton, *University of Tennessee, Knoxville.*

Genetically identifying cattle less susceptible to mastitis and more fertile will be a key factor in producing healthier cattle populations. Because mastitis and fertility are influenced by a variety of factors, several markers most likely will be needed to identify an animals genetic potential. As a step towards this goal, we evaluated the association of a series of single nucleotide polymorphisms (SNP) in two immune related genes (CXCR1 and NRAMP1) on BTA2 with mastitis and reproductive traits in 96 Holstein cows. Of the >40 SNP identified, 5 were chosen that best represented the genetic variation in that region of BTA2. Of the SNP evaluated, 3 were associated ($P<0.10$) with disease and/or reproductive traits, 4-226 and 5-577 in CXCR1 and K1-245 in NRAMP1. The 4-226 SNP tended to be associated ($P<0.10$) with clinical mastitis, subclinical mastitis, and days open. In our sample population, cows with an AA or AG genotype were twice as likely to develop subclinical and clinical mastitis as cows with the GG genotype. Interestingly, the AA genotype tended to have fewer days open then the other two genotypes. A second SNP in CXCR1, 5-577, introduces an early stop codon in the receptor which has a strong potential to influence immune function. This SNP tended to be associated with subclinical mastitis. The NRAMP SNP was significantly associated ($P<0.05$) with clinical mastitis: heterozygous cows experienced twice as many infections as cows homozygous for the C allele. No significant associations with were observed with somatic cell score, however this may be related to low SCS observed in the herd (<3.0). Nor were any significant associations observed with days to first service. Based upon these findings and our prior research indicating a significant association between mastitis and immune function with another SNP in the CXCR1 gene, we believe this region of BTA2 is a relevant mastitis resistance locus and potentially reproductive trait locus. To further define a desirable genetic background, the next step is to evaluate these 3-5 SNP in a larger, well-defined Holstein population.

T59   The genomic architecture of a major QTL region on chicken chromosome 4: CpG islands, gene density and repetitive elements. G. A. Ankra-Badu and S. E. Aggrey*, *University of Georgia, Athens.*

This study was conducted to characterize the genomic landscape of a major QTL region and to identify novel candidate genes by CpG island detection and comparative mapping. One hundred and nine genes and 179 CpG islands were detected at this locus and thirty four percent of these genes contained CpG islands. The region spanning 68-70 Mb had the highest CpG island density and the second highest number of genes. Analysis of the distribution of repetitive elements showed that LINE, low complexity and simple repeats constituted the majority of repetitive DNA in the QTL region. Generally regions with a high GC content and gene and CpG island density had a relatively low percentage of repeats. Seventy three genes from a match with twenty species which are involved in protein synthesis, transcriptional regulation and other functions were identified by comparative mapping. Six probable novel genes were identified on GGA4 by blasting a selection of these genes against the chicken genome. Three of these genes are housekeeping genes which are either involved in protein transport or signal transduction. A putative ortholog of rhotekin, which is a housekeeping gene with nucleotide binding and apoptosis functions, was detected in the region orthologous to the Fugu (puffer fish).

T60   Modeling social competition assuming a single dominant animal per pen. J. M. Achi*, I. Misztal, and R. Rekaya, *University of Georgia, Athens.*

The model of social competition by Muir and Schinckel (MS) assumes continuous expression of social dominance. The purpose of this study was to examine a model where such an expression is binary. The simulated data set included 18,000 animals across three generations. A pen effect was included with six animals per class. Two additive values were assigned per animal, direct and social dominance; both effects were assumed correlated. Liability of social dominance was calculated as a sum of the social dominance effect plus a residual term. For each pen, the animal with the highest liability was declared dominant. The simulated growth phenotype was calculated as a sum of effects of pen, generation, direct, dominance advantage, and the residual. The effect of dominance advantage was only present in records of dominant animals. It was fixed to a constant value in model 1 (M1) or equal to the effect of social dominance in model 2 (M2). A bivariate linear-threshold was used for analysis where the second trait was the dominance status assumed known. Initial analyses assumed M1. When the second trait was ignored, the estimate of the dominance advantage was unbiased when the covariance was 0, was biased upwards when the covariance was positive, and downwards if negative. There was no bias when the second trait was considered in the analysis.

Variance components were estimated for a scenario with a positive correlation. There was an upward bias for the direct variance and downward for the competitive variance and the covariance. The biases were traced in part to the fixed threshold used for all records. A variable threshold is required so that exactly one animal per pen is selected as dominant. Variance components were estimated and animal effects predicted with the MS model. The correlations between the competitive effects from the two models were close to 0. When M2 was used, the same correlation was -0.1. It seems that modeling social dominance with different models may result in drastically different rankings.

Key Words: Social Dominance, Competitive Effects, Simulation

T61   Obtaining multiple QTL solutions without inverting the IBD matrix. M. Jafarikia*, J. A. B. Robinson, and L. R. Schaeffer, *University of Guelph*, *Guelph, Ontario, Canada*.

The inverse of an Identity By Descent (IBD) probability matrix is required for most Quantitative Trait Loci (QTL) studies. Although different methods are available for the calculation of an IBD matrix, direct inversion of that matrix can be computationally very demanding for large data sets. In order to obtain the QTL solutions without inversion, an average gametic relationship IBD matrix was used so polygenic and QTL incidence matrices were equal. A subset of the mixed model equations consisting of fixed and polygenic effects was created and after obtaining the solutions for this subset, the following formula was used to obtain the QTL solutions: $\hat{u}_n = (\sigma_{un}^2 G_n A^{-1} \hat{a})/\sigma_a^2$ where $\hat{u}_n$ is the vector of solutions for qtl n and σ_{un}^2 is the variance of QTL n and G_n is the IBD matrix of haplotype n, A^{-1} is the inverse of additive relationship matrix, $\hat{a}$ is the vector of polygenic solutions and σ_a^2 is the additive genetic variance. Using an iteration procedure, the predicted QTLs effects were subtracted from observations and the fixed/polygenic subset of equations were re-solved with the adjusted observations. Then the QTL effects were solved as above and the cycle repeated until convergence was reached. The proposed methodology was applied to a simulated chromosome with 20 markers and four QTLs located in the middle of four haplotypes. The number of markers on each haplotype was four, ten, two and four respectively. A half-sib population with five grand sires, 50 sons per grandsire and 50 daughters per son was simulated. The model included fixed contemporary groups, random polygenic, QTL and residual terms with variances of 22.08% for polygenic, 1.92%, 1.92%, 4.48%, 9.6% for the four QTLs and 60% for the residual. The example converged after 39 iterations and there were no significant differences between the solutions of the full equations and proposed shortcut method. Both the Pearson and Spearman rank correlations were 1.00.

Key Words: IBD, QTL, Inverse

T62   A Microsatellite Repeat Search (MRS) tool for eukaryotic genomes. L. Klein*[1,2], S. Puri[1,2], G. Blachut[3], and E. Smith[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*Blacksburg High School*, *Blacksburg, VA*, [3]*Hinsdale South High School*, *Hinsdale, IL*.

There continues to be significant interest in microsatellites because of their implication in neurological diseases and their utility as DNA markers for common disorders. Their distribution in the genomes of model, human and agriculturally important species therefore remains of interest to scientists. Previous studies, supported by annotation results of the recently released chicken genomic DNA sequence, suggest that microchromsomes have a higher gene density and by inference lower repetitive sequences than macrochromosomes. Here, we developed a bioinformatics tool, Microsatellite Repeat Searcher (MRS), that was used to evaluate the relative distribution of microsatellites on micro- and macrochrosmosomes in the chicken, Gallus gallus. A total of 9,138 repetitive elements were identified within a total of 1,133,629,576 bp of sequence scanned. Though inconsistent, an inverse correlation was observed between chromosomal length and microsatellite frequency. The tool described here should be useful for searching whole genomes of other vertebrates for repetitive elements. Our data appears to support the hypothesis that the gene-rich microchromosomes also have a lower percentage of repetitive elements.

Key Words: Microsatellites, Bioinformatics Tool, Chicken

T63   Analysis of protein in pig blood serum at growing stages. H. Y. Chung*, S. H. Yoon, B. H. Choi, K. T. Lee, and G. W. Jang, *National Livestock Research Institute*, *Suwon, KY, Korea*.

The purpose of this study was to detect differentially expressed proteins in pig blood serum at growing stages, which were constructed with birth, 6, 12, 18, 24 and 30 weeks of age. A total of 16 spots from 2D gels were observed for differential expression at each growing stage. Mass spectrometric (MS/MS) analysis of the spots identified Ig kappa light chain, Ig lambda chain C, haptoglobin alpha 1S, gamma fibrinogen, Ig gamma 1 chain, Retinol-Binding Protein, albumin, apolipoprotein A-IV, antithrombin protein, alpha-1-antitrypsin and fibrinogen A-alpha-chain. Most of the proteins were gradually expressed from birth to 30 weeks, but a few proteins were not expressed at birth. SNPs from the identified loci were genotyped across 300 pigs from a commercial population. Three loci for the Ig lambda chain C and haptoglobin alpha 1S gene were significantly associated with birth and weaning weights (P<0.01). Therefore, genes identified in this study may account for some of the genetic variation and differential protein expression in animal growth.

Key Words: Growing Stages, 2D Analysis, Polymorphism

T64   Construction of SNP maps in the region of the swine SLA class I for miniature pig. H. Y. Chung*, S. H. Yoon, B. H. Choi, K. T. Lee, and G. W. Jang, *National Livestock Research Institute*, *Suwon, KY, Korea*.

In order to construct SNP maps focusing on the swine leukocyte antigen region, the SLA class I region was screened by PCR using miniature pig BAC clones. The swine leukocyte antigen (SLA) class I region containing MHC class Ia, Ib, related genes, and pseudogenes, was analyzed to provide genetic information for transplantation research in pig. A total of 990 primers were designed and covered 1,500,000 bp locating on pig chromosome 7q11-16. Miniature pigs were used to infer haplotypes and SNP maps, with a total of 4,000 SNPs discovered. The sequence information from miniature pigs was compared with 5 pig breeds (Landrace, Hampshire, Yorkshire, Duroc,

and Berkshire). The SNPs discovered in this study may provide useful genetic information for organ transplantation research.

Key Words: SNP, Swine Leukocyte Antigen (SLA), Haplotype

T65   Impact of inbreeding on IBD probabilities and estimates of QTL variance. G. Freyer[2] and N. Vukasinovic*[1], [1]*Monsanto Animal Genomics and Breeding*, *Saint Louis, MO*, [2]*Research Institute for the Biology of Farm Animals (FBN)*, *Dummerstorf, Germany*.

QTL mapping in complex pedigrees using a variance component approach has become popular as increasing numbers of animals are routinely genotyped in dairy populations. In this approach, the QTL effect is modeled as a function of the probabilities that two alleles in the same or in different animals at a particular position in the genome are identical by descent (IBD probabilities). Proper calculation of IBD probabilities and therefore, modeling and estimation of QTL variances depend on many factors such as the number of markers, their information content, and the level of relatedness of the animals in the pedigree. In this simulation study, we investigated how the level of inbreeding, coupled with varying marker information content, influenced IBD probabilities and the estimates of QTL variances. Four multi-generational pedigrees with 850 individuals each were simulated. The final offspring of 9 sires originated from two founder (great-grand) sires. Four family structures (FS) with different levels of inbreeding were considered: FS0 was non-inbred; FS1 contained an inbred sire originating from an aunt-nephew mating; FS2 contained a 25% inbred sire, originating from a half-sib mating. FS4 in addition contained a grand sire originating from a father- daughter- mating, where one of the two resulting sires was mated to his dam to further increase the level of inbreeding. All animals were assumed genotyped for 11 unevenly spaced markers within a 55cM long putative QTL region, containing a QTL within the 7th marker bracket. The number of marker alleles was 2, 4, or 6. Complete marker information and 20% randomly missing marker genotypes were considered. IBD probabilities for each cM in the segment were calculated using the nearest informative marker bracket. Means and variances of IBD probabilities increased with both increasing level of inbreeding and increased marker information. Estimates of the QTL variances at the true QTL position obtained from data sets with 2 marker alleles and without missing genotypes were closest to the simulated values, regardless of the inbreeding level.

Key Words: Inbreeding, Pedigree, QTL

T66   Relationship of herd-heritability with sire misidentification and entry into a proven sire lineup. C. D. Dechow[1], H. D. Norman*[2], and N. R. Zwald[3], [1]*The Pennsylvania State University*, *University Park*, [2]*Animal Improvement Programs Laboratory*, *Beltsville, MD*, [3]*Alta Genetics, Inc.*, *Watertown, WI*.

The objectives of this study were to estimate the relationship of individual herd heritability with sire misidentification rate and the likelihood of a sire entering an active sire lineup after progeny testing. Milk, fat and protein yield and somatic cell score (SCS) were provided by the Animal Improvement Programs Laboratory at USDA. Paternity verification results from DNA marker analysis were provided by Alta Genetics, Inc. for 145 herds. The number of cows tested per herd ranged from 5 to 274. Herd heritability was calculated with daughter-dam regression and daughter-sire predicted transmitting ability (PTA) regression using 6,848,885 records from 17,608 herds. Herd heritabilities were estimated with regression models in AS-Reml that included fixed breed, age within parity, herd-year-season of calving, dam records nested within state, and sire PTA within state; random regression coefficients were dam records and sire PTA within herd. Average daughter-dam herd heritability estimates ranged from 0.26 (SCS) to 0.41 (fat yield), whereas daughter-sire herd heritability ranged from 0.11 for SCS to 0.20 for fat yield. Correlations between herd heritability and sire misidentification rate ranged from -0.23 to -0.43. The correlation between a principal component for all measures of herd heritability and sire misidentification rate was -0.45. Sires that were proven in low heritability herds were less likely to enter a proven sire lineup than sires proven in average to high heritability herds. Individual herd heritabilities can be generated with simple regression techniques for several thousand herds simultaneously. The herd heritability estimates could be used to identify herds that might provide inaccurate data for progeny testing, and could be used to identify sires with potentially underestimated genetic evaluations.

Key Words: Herd Heritability, Sire Misidentification, Daughter-Dam Regression

T67   Heritability estimates for producer recorded clinical mastitis events. C. D. Dechow[1], J. Vallimont*[1], C. G. Sattler[2], and J. S. Clay[3], [1]*The Pennsylvania State University*, *University Park*, [2]*Select Sires, Inc.*, *Plain City, OH*, [3]*Dairy Records Management System*, *Raleigh, NC*.

The objective of this study was to estimate heritability for producer-recorded clinical mastitis events. Cow health events were provided by Dairy Records Management Systems (Raleigh, NC) for progeny test herds that use PCDART. First through fifth lactation data from cows calving between 20 and 120 months of age and that calved in a herd-year with at least 1% of cows with a clinical mastitis event were retained. The edited dataset contained 105,527 records. Mastitis (1 = at least one mastitis event during lactation, 0 = no mastitis events) was analyzed with two single trait animal models in AS-Reml with fixed effects for age within parity and herd-year-season of calving; random effects were animal, permanent environment and error. Mastitis was treated as a linear response variable in the first analysis and as a binary response variable in the second analysis. The incidence of clinical mastitis was 14%. When data was restricted to herds with a minimum of 5% clinical mastitis, the average lactation incidence rate was 19%. Heritability estimates were 0.02 when mastitis was treated as a linear response variable and 0.15 when treated as a binary response variable. Repeatability estimates were 0.07 and 0.16 for the linear and binary response variables, respectively. The correlation between PTA from the linear and binary models was 0.98. Significant genetic variation exists for clinical mastitis and health events recorded by producers could be used to generate genetic evaluations for cow health. While heritability estimates varied between linear and binary models, sires ranked similarly for daughter mastitis susceptibility with both methods.

Key Words: Mastitis, Heritability, Repeatability

T68 Different UBX domain D Gene from subtraction cDNA isolated from Korean native chicken. S. S. Sun*, K. Kuk, and K. H. Myung, *Chonnam National University, Gwangju, Korea.*

The objectives of this study are to identify specific functional genes which related with growth and structure of pectoral muscle in Korean native chicken. Pectoral muscle was isolated from the Korean native chickens (KNC, red brown, 12 months old, 2.41kg±0.24) and Cornish chickens (16 month old, 2.76±3.04kg). The subtraction cDNA library was prepared in PCR4 Blunt-TOPO vector and the insert was sequenced. The DNA sequence homology was compared with other breeds and species in GenBank. A clone NDS-10 was unique for the DNA sequence homology with UBX family. NDS-10 has 612 nucleotides. This partial sequence has high homology (98%) with chicken UBX domain D. The expression of DNS-10 could change three-dimensional structure of skeletal muscle and could modify texture of breast muscle. Several regions were mutated from T in chicken to C or G in NDS-10. It may have severe structural modification due to not making H-bond between T and A. They are going to make G-C linkage for their three-dimensional structure. The late regions were point deleted and then can not be translated or expressed to different protein. Chicken UBX domain containing 4 (UBXD4) and mRNA for hypothetical protein from clone 10c14 ND were compared. They are 98% (571/579nt) homology of nucleotide sequence. Chicken UBX domain has chicken (93%), cattle (68%), dog (67%), and mouse (64%), human (63%) nucleotide sequence homology. We conclude that the clone NDS-10 could be a new candidate gene for UBX family gene.

Key Words: UBX Domain D, cDNA, Korean Native Chicken

T69 Efficiency of Brown Swiss, Holstein and their crosses estimated with data envelopment analysis. C. D. Dechow[1], M. I. Phelps*[1], S. Roth[1], G. W. Rogers[2], and J. B. Cooper[2], [1]*The Pennsylvania State University, University Park*, [2]*The University of Tennessee, Knoxville.*

The objective of this study was to compare the efficiency of Brown Swiss (BS), Holstein (HO) and crosses among BS and HO using data envelopment analysis (DEA). A multi-dimensional efficiency frontier that is derived from of the most efficient production units (cows) is generated by DEA. Cows that do not reside along the frontier must reduce inputs relative to their level of output to become efficient. The output variables were first lactation total milk, fat and protein yield obtained from six herds. Input variables were days in milk, age at calving, days open and estimated body weight. BS and HO were assumed to have equivalent body weights and heterosis for body weight was assumed to be 3%. The analysis was performed with the DEA Excel Solver for each herd individually. A solution was successfully attained for three herds totaling 334 cows of the following breed combinations: 184 HO, 89 BS, 27 first generation crosses (F1) and 34 backcrosses (F2). Resulting efficiency values were analyzed with the GLM procedure of SAS. Breed combination and herd-year-season of calving were independent factors and least squares means for efficiency were estimated for breed combination. Least squares means for efficiency were 0.79, 0.86, 0.91 and 0.83 for BS, HO, F1 and F2, respectively. The heterosis estimate for efficiency in the first generation of crossbreeding was 10.3%, and F1 were significantly more efficient than BS or HO. Relative to F1, BS were required to reduce all inputs and increase milk production to become more efficient.

HO were generally required to reduce days open and increase fat and protein yield when compared to F1. To raise efficiency of F1 further, milk production needed to increase when compared to HO and protein yield needed to increase relative to BS. An efficiency value that does not require assumptions about the economic value of inputs or outputs can be obtained with DEA in order to compare cows of different breeds. However, more advanced software was required to handle large datasets. There was evidence that crossbreeding with BS increased the efficiency of production when compared to pure HO.

Key Words: Data Envelopment Analysis, Crossbreeding, Efficiency

T70 Estimation of genetic and phenotypic parameters for days open and test day milk yields in Japanese Holsteins. Y. Masuda*, H. Abe, and M. Suzuki, *Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Japan.*

The objective of this study was to estimate genetic and phenotypic parameters for days open and test day milk yield in the first two lactations of Holstein cattle in Japan. Monthly test day yields and insemination data were provided by the Hokkaido Dairy Milk Recording and Testing Association. Cows with first test day yields recorded after 35 days in milk and with days open less than 22 d or greater than 300 d within lactation were excluded. The first five test day records for each cow were extracted and treated as a separate trait. All data were split along lactation numbers into two data sets; days open and test day records from 158,994 and 73,290 cows calving between 1990 and 2002 for first and second parities, respectively. (Co)variance components within lactation were estimated using a bivariate animal model and the AI-REML procedure. The model included herd-year of calving, age at calving and month-year of calving as fixed effects, and random animal and residual effects. Heritability estimates for days open were 3.0% and 2.6% for first and second parities, respectively. Genetic correlations between days open and 1st to 5th test day milk yields were 0.42, 0.48, 0.52, 0.54 and 0.48 (0.27, 0.36, 0.34, 0.38 and 0.30) for the first (second) lactation, respectively. These results indicate that genetically high milk production during early lactation may lead to increase days open especially in first parity. Phenotypic correlations between days open and test day yield ranged from 0.04 to 0.07 and 0.03 to 0.05 for first and second parities, respectively. In another analysis, averages and standard deviations for days open decreased as the production level of the herd increased. Although there is an undesirable genetic relationship between days open and milk yields in early lactation, phenotypic correlation is close to zero due to an effort to improve reproductive efficiency in the individual herd.

Key Words: Days Open, Test Day Milk Yield, Genetic and Phenotypic Correlations

T71 Residual feed intake and temperament breed differences among Florida heifers. D. G. Riley*[1], G. R. Hansen[2], S. W. Coleman[1], and C. C. Chase[1], [1]*USDA, ARS, Brooksville, FL*, [2]*University of Florida, Marianna.*

The objective of this work was to evaluate residual feed intake, average daily gain, chute temperament score, and exit velocity of Brahman (B), Angus (A), and Romosinuano (R) (n = 40, 19, and 26, respectively)

and F_1 (n = 7, 8, and 12 for BA, RA, and RB, respectively) heifers. One month after weaning in September 2006, heifers were transported 485 km to the Florida panhandle. Heifers were placed in feeding pens and acclimated to a corn-based diet for 3 wk. Subsequently, they completed a 70-d intake test. Body weight, chute temperament score (from 1 to 5; higher scores indicated more nervous behavior), and exit velocity (m/s) were recorded weekly. Body weight and feed consumption records were used to generate residual feed intake values (RFI). Average daily gain and feed conversion ratio (FCR) were calculated. Pen (n = 6), breed (n = 6; 3 purebred and 3 crossbred groups), and age of dam were fixed effects. Age in days at test start was included as a covariate. Body weight was a covariate in analyses of chute score and exit velocity. Records were placed in 3 RFI groups: high, medium (mean ± 0.5 SD), and low values, and this term was modeled as a fixed effect in additional analyses. Sire was a random effect. Brahman heifers had more favorable (P < 0.05) RFI (–1.08 ± 0.25 kg) than other groups which ranged from 0.06 ± 0.17 (R) to 0.46 ± 0.2 kg (A). Brahman ADG (0.84 ± 0.06 kg) was less than (P < 0.05) that of Angus heifers (1.06 ± 0.05 kg). Means for ADG of crossbred heifers were 0.86 ± 0.08 (RB), 1.08 ± 0.1 kg (BA), and 1.1 ± 0.09 kg (RA). No breed effect was detected for FCR (P = 0.31). Brahman and Brahman-cross heifers had the largest exit velocity means (range from 2.89 ± 0.15 for RB to 3.43 ± 0.19 m/s for BA); these were larger (P < 0.05) than Angus (2.22 ± 0.12 m/s) and Romosinuano (2.12 ± 0.1 m/s). Chute temperament score means for Angus (2.38 ± 0.1) and RA (1.9 ± 0.26) were lower (P < 0.05) than those of all other breed groups. Groups for RFI did not explain variation in analyses of temperament traits (P > 0.29).

Key Words: Brahman, Residual Feed Intake, Temperament

T72 **Organ weights and ulcer severity of 1980 vs. 2005 pigs when fed 1980 or 2005 feeding programs.** J. S. Fix, E. van Heugten, D. J. Hanson, J. P. Cassady, and M. T. See*, *North Carolina State University, Raleigh*.

The objective of this study was to assess changes over 25 years in pig organ weights and ulcer severity. Pigs (n=162) representative of current commercial industry were compared to pigs representative of commercial industry 25 years ago. The 1980 genetic line was produced from dams selected to minimize genetic improvement and frozen semen from boars available in 1980. Pigs within sex, farrowing group, and genetic line (GL) were randomly assigned to a feeding program (FP) and placed 3 per pen (n=54) at an initial wt of 7±0.4 kg. The 2005 FP included 7 pelleted diets (lysine from 1.51 to 0.73% and ME from 3428 to 3651 Kcal/kg) and current diet formulation. The 1980 FP consisted of 4 meal diets (lysine from 1.05 to 0.62% and ME from 3262 to 3317 Kcal/kg) based on formulations from 1978 PIH. Pigs were slaughtered and viscera were collected on a weekly basis when average pen wt exceeded 116 kg. Heart, lungs, liver, kidneys, pancreas and all non organ matter were separated and weighed. Stomach, small intestine and large intestine were separated, cleaned and weighed. Weights were adjusted to constant BW of 116 kg. Stomachs were scored for ulcer and keratinization severity on a scale of 1-7 (1=normal to 7= severe ulceration). The 2005 GL pigs had heavier small intestines (1599 vs. 1375 g; P < 0.01), large intestines (1548 vs. 1405 g; P < 0.05), hearts (392 vs. 374 g; P < 0.05) and livers (1614 vs. 1550 g; P = 0.05) than pigs from 1980 GL. Pigs fed 1980 FP had heavier large intestines (1582 vs. 1371 g; P < 0.01) and lungs (673 vs. 611 g; P < 0.05) than pigs fed 2005 FP. A GL x FP interaction (P < 0.01) was observed for kidney weight where 1980 GL pigs fed 1980 vs. 2005 FP had heavier kidneys while 2005 GL pigs fed 1980 vs. 2005 FP had lighter kidneys. Pigs fed 1980 FP had heavier stomachs (624 vs. 518 g; P < 0.01) and less ulcer severity (2.26 vs. 3.53; P < 0.01) than pigs fed 2005 FP. Changes in genetics led to heavier organ weights but did not affect stomach ulcer severity. Changes in feeding program resulted in lower organ weights and an increase in stomach ulcer severity.

Key Words: Pigs, Genetics, Stomach Ulcers

T73 **Genetic and environmental factors that affect gestation length.** H. D. Norman, J. R. Wright, M. T. Kuhn, S. M. Hubbard*, and J. B. Cole, *Agricultural Research Service, USDA, Beltsville, MD*.

Genetic and environmental factors that might affect gestation length (GL) were investigated so that more accurate predictions of calving dates could be provided to dairy producers. Data from >8 million calvings from 1999 through 2005 for 5 dairy breeds were assembled from lactation, reproduction, and dystocia records from across the United States. Effects examined were calving year, calving herd-year, calving month, age-parity, calf birth code (gender and multiple-birth status), lactation length, milk yield, service sire, sire, and cow. All effects were fixed except for service sire, sire, and cow. Mean GL for cows (parities 2 through 5) was 279.5 d for Holsteins, 280.1 d for Jerseys, 281.9 d for Ayrshires, 285.8 d for Guernseys, and 287.6 d for Brown Swiss. Mean GL for heifers (parity 1) was 277.9 d for Holsteins, 278.6 d for Jerseys, 281.8 d for Ayrshires, 285.0 d for Guernseys, and 287.0 d for Brown Swiss. Estimated standard deviation of GL was greatly affected by data restrictions but appeared to be near 6 d for all breeds. For Holstein cows, calving year differences in GL were small, but effect of calving month was large; mean GL was 278.2 d for July compared with 280.4 d for November. Mean GL for Holstein cows with twins was 274.9 d compared with 279.4 and 280.5 d for those with single-birth females and males, respectively. Holstein cows with lactations of ≤250 d had a mean GL of 280.1 d compared with 278.8 d for cows that were milked for >500 d. Holstein cows with standardized yield of ≤6,000 kg had a mean GL of 279.0 d compared with 279.8 d for cows with yield of >16,000 kg. Heritability estimates for GL derived from parities 2 to 5 were 24% for service sire and 8% for sire. Better prediction of time of parturition can help herd managers to fulfill the nutritional needs of pregnant cows and to administer better preventive health care so that metabolic diseases are minimized during high risk phases of cows' lives.

Key Words: Gestation Length, Calving Date

T74 **Construction of a cDNA library of the guinea fowl adipose tissue and evaluation for expressed sequence tags.** S. N. Nahashon*, G. Kelley, J. Johnson, J. Tyus II, and A. Amenyenu, *Institute of Agricultural and Environmental Research, Tennessee State University, Nashville*.

Fat accretion in poultry directly influences the efficiency of feed utilization and consumer acceptability of poultry and poultry products. Excessive fat deposition, which is undesirable to poultry processors and consumers alike, also reduces meat quality. Losses estimated at about US$250-300 million are incurred by consumers and processors annually in pollution control, fat extraction and in discarding excess

carcass fat. Understanding the mechanisms that lead to excessive fat deposition in birds will be an avenue to improving poultry carcass quality while minimizing production cost. The aim of the proposed project was to generate a cDNA library for the guinea fowl adipose tissue. The guinea fowl is genetically diverse from other avian species such as chickens and turkeys and its carcass and abdominal fat content is significantly lower than that of these other avian species. Therefore, genome sequence information realized from the cDNA library would provide a tool for comparative mapping of the avian species and an understanding of the factors associated with fat accretion in poultry. A partial sequence cDNA library of the guinea fowl adipose tissue was constructed using the Stratagene® cDNA library construction kit. DNA sequences were cloned into the pBluescript cloning vector and screened by the polymerase chain reaction. Two hundred clones were cycle-sequenced using the Dye Terminator® cycle sequencing kit and the ABI 3100 Genetic Analyzer. Similarity of DNA sequences was evaluated using the National Center for Biotechnology Information (NCBI) databases using the BLAST (http://www.ncbi.nlm.nih.gov/BLAST/). About 90% of the DNA sequences retrieved were unique to the guinea fowl and they range in size from 386 to 1,059 bases. About 15% of these sequences had less than 20% match with mammalian sequences, whereas 85% exhibited homology ranging from 55-96% with avian species and 44-75% with mouse and human DNA sequences. These sequences provide an invaluable tool for comparative mapping of the avian genome and an understanding of the mechanisms underlying excessive fat accretion in poultry.

Key Words: cDNA Library, Guinea Fowl Adipose Tissue, Poultry

T75   Optimising turkey parent stock selection for an integrated processing company and a non-integrated poult supply company. B. J. Wood* and N. Buddiger, *Hybrid Turkeys*, *Kitchener, Ontario, Canada.*

Mass selection on body weight is an effective method that can improve the commercial performance of progeny from selected parent stock (PS). Selection on body weight is a common procedure within the North American industry with the industry averaging 50% selection from the total number of PS tom poults placed. Increased selection pressure increases costs in two ways, first, increased numbers of PS are required, and second, facilities in to house additional PS. The aims were to economically model PS selection to determine the optimum selection intensity to maximise profit when either an independent poult supplier or integrated turkey processing company. Poult production costs increased slowly above non-selection to $0.01 per poult at 50% selection and then increased more rapidly to $0.04 and $0.12 at 20% and 10%, respectively, thereafter, at higher intensities the price increased exponentially. For a non-integrated company, returns are generated purely on the sale of poults with benefits accrued from increased market share or higher poult price and so must be determined on an individual company basis. For integrated companies return on investment comes in the form of improved live performance and processing. Body weight was assumed to have a heritability of 0.4 and genetic (r_g) and phenotypic (r_p) correlation between male and female bodyweight was assumed to be $r_g = 0.85$ and $r_p = 0.70$, respectively. Correlations between bodyweight and feed intake, BMY and mortality were assumed to be to be r_g = -0.15, -0.16, 0.2 and r_p = -0.15, -0.12 and 0.15, respectively. The optimal intensity was between 15% and 25% depending on breast meat and feed price which corresponded to the level where there was substantial increase in poult cost. Optimal selection age was always the same as slaughter age and hen selection was shown not to be profitable at any selection pressure level. It could be concluded that current PS tom selection intensities could be increased with substantial increases in profit compared with current industry levels.

Key Words: Economic Model, Parent Stock Selection, Genetics

T76   Defining the haplotype blocks in outbred livestock populations. M. Jafarikia*, J. A. B. Robinson, and D. Ashlock, *University of Guelph*, *Guelph, Ontario, Canada.*

Recent studies propose a block-like structure for genome haplotypes. There are two major methods for defining the haplotype blocks based on finding a region with limited diversity, and detecting regions with high levels of historical recombination. In order to develop a methodology to define the haplotype blocks in outbred livestock populations, maximum likelihood was used in a simulation study to detect the hotspot regions, using the information from the genotypes of grand sires and their sons in the following formula:

$$X^2 = -2\ln(\Pi[(p^{r_i}q^{(n_i-r_i)})/(p_i^{r_i}q_i^{(n_i-r_i)})]\Pi q^{n_i})$$

where X^2 was the LR value for every informative interval and p as a population measurement, was the probability of having recombination in an informative interval computed from the total number of recombinations divided by the total number of informative intervals in the population: $p=\Sigma r_i/\Sigma n_i$ where the number of grand sires (families) was from i=1 to GS. r_i and n_i denoted the number of recombinations in the progeny of every grand sire, and the total number of informative intervals in the progeny of every grandsire respectively. p_i was a family measurement which is the number of recombination in the progeny of a grandsire divided by the total informative intervals of that grand sire, $p_i=r_i/n_i$. q and q_i were the possibility of having no recombination in an informative interval in the population and family respectively. n_i-r_i was the number of progeny which did not show any recombination in meiosis. In order to test the method, a simulated ten cM chromosome having 30 SNPs in a population with five grand sires and 80 sires per grandsire and two blocks of haplotypes was developed. The possibility of recombination was 95% in hotspot region and 5% in coldspots region. The proposed method was able to successfully detect the hotspot regions (P<0.001).

Key Words: Haplotype Blocks, Recombination Hotspot, Maximum Likelihood