W28 Relationship of plasma immunoglobin G concentrations to temperament and growth performance. K. R. Parker*[1], S. T. Willard[2], R. D. Randel[3], T. H. Welsh, Jr.[4], and R. C. Vann[1], [1]*MAFES-Brown Loam Experiment Station*, *Raymond, MS*, [2]*Mississippi State University*, *Starkville*, [3]*Texas A&M University Agricultural Research & Extension Center*, *Overton*, [4]*Texas A&M University*, *College Station*.

This study was designed to assess the relationships between immune function, innate temperament and growth performance. Blood samples and BW were taken from spring born calves (n = 196) at 24h, 48h, 14d, and 84d post-calving. At birth calves were assigned a calf vigor score, calving ease score and dams were given a BCS according to Beef Improvement Federation guidelines (2002). Plasma was harvested via centrifugation and concentrations of immunoglobin G (IgG) were determined by ELISA. Temperament data were recorded in the form of pen scores (PS) and exit velocity (EV). These measures were taken along with BW at 28d pre-weaning, weaning, 28d post-weaning, 56d post-weaning and as yearlings. Overall temperament scores (TPS) were assigned to each animal by averaging PS and EV over the four time periods. Statistical analyses were performed using the Proc Mixed procedure of SAS and where appropriate repeated measures analyses were used. Calves were ranked based on their TPS as follows: calves 1 SD above the mean were considered temperamental (T, n=26), calves 1 SD below the mean were considered calm (C, n=36), all other calves were considered intermediate (I, n=127). Calves were classified based on their IgG concentration with calves 1 SD lower than the mean ranked low (L, n=3), calves 1 SD above the mean ranked high (H, n=27), and remaining calves ranked moderate (M, n=159). Heavier calves at birth ($P \leq 0.05$) had lower IgG at 24h and 48h. Calves with higher IgG at 48h exhibit greater ($P = 0.062$) ADG between weaning and 56d. Calves with higher IgG concentrations did not experience calving difficulties ($P \leq 0.001$). Scrotal circumference (SC) at weaning and 56d post-weaning were higher ($P \leq 0.03$) for calves with greater 48h IgG concentrations and were higher in calves classified as calm. Calves with higher immune classification had improved growth performance after weaning. These results suggest that IgG classification could be useful in predicting growth performance after weaning.

Key Words: Immunoglobin, Beef Calves, Temperament

W29 Impact of entomopathogenic fungus *Metarhizium anisopliae* on cattle naturally infested by adult *Haematobia irritans* in temperate Mexico. E. Maldonado-Simán[1], R. D. Améndola-Massiotti*[1], E. Galindo-Velasco[2], C. A. Angel-Sahagún[2], L. Bermúdez-Villanueva,[1], and R. Lezama-Gutiérrez[2], [1]*Universidad Autónoma Chapingo*, *Chapingo, México, México*, [2]*Universidad de Colima*, *Tecomán, Colima, México*.

Farmers tend to control horn fly (*Haematobia irritans* L.) with heavy pesticide applications which increase the risks of insecticide residues in products and the environment; therefore, biological pest control is considered to be ecologically safer. The University of Colima, Mexico recently developed a biopesticide based on the spores of the fungus *Metarhizium anisopliae* Ma34 as a natural pathogen. No studies have tested on the field the action of this entomopathogenic fungi on the control of *H. irritans*; therefore, the aim of this study was to asses the efficacy of *M. anisopliae* on the control of *H. irritans* in naturally infested cattle. The study took place in the Experimental Station of the University of Chapingo (temperate central area of the country). Twenty two grazing Holstein cows were randomly allocated into two groups of the same size, which grazed in different paddocks. Cows in the treated group were sprayed every seven days with a conidial suspension of *M. anisopliae* (strain Ma34) at a concentration of 1×10^8 conidia/ml. Eight applications took place during the experimental period. The other group remained as untreated control. The horn fly burdens were recorded on days 0, 1, 2, 3, 4, 5, 6 and 7 post-treatment. Cows sprayed with *M. anisopliae* showed fly counts 28% lower than the untreated control ($P<0.05$). Since the experiment took place during the second half of the fall, horn fly counts became lower through time (from week one to week eight) in both treatments, being reduced from 156 to 24 flies per cow in the sprayed cows and from 216 to 37 flies per cow in the untreated cows; the reduction due to the application remained fairly constant. This result shows that *M. anisopliae* (strain Ma34) was effective in the control of adult *H. irritans* and might be a promising substitute of chemical pesticides.

Key Words: Hyphomycetes, Biological Control, Horn Fly

Breeding and Genetics - Livestock and Poultry III

W30 The genes commonly expressed at early embryonic stages in mammals. C. Y. Lien*, E.-C. Lin, C. C. Hsu, S. T. Ding, and W. T. K. Cheng, *National Taiwan University*, *Taipei, Taiwan*.

The early stages of embryogenesis are critical for mammalian embryo development. Several key developmental events occurred in these stages, such as cell growth, migration, differentiation, and morphogenesis. In spite of the importance occurring in the early embryogenesis, limited information has been provided by previous studies. The UniGene database in the National Center for Biotechnology Information (NCBI) was designed to collect sequences of expressed sequences tags (ESTs) and mRNA to provide many sets of transcript sequences from the same transcription locus.The purpose of this study is to utilize the UniGene database to screen those commonly expressed genes with related functions at early embryonic stages in mammals. Those unigene entries of embryos before implantation collected from *Bos taurus*(Bt), *Mus musculus* (Mm) and *Sus scrofa* (Ssc) were 1,727, 13,923 and 3,982, respectively. The unigene sequences of Mm (13,923) were used to search against (blastn) the unigene sequence sets of Bt (1,727) and Ssc (3,982) to obtain 972 and 2,039 commonly expressed genes (bit score ≥ 200), respectively. However, there were 417 unigene entries commonly expressed in all these three species. The 417 commonly expressed genes annotated to have certain gene identity in public databases for Bt, Mm and Ssc were 339, 361 and 151, respectively. Furthermore, those commonly expressed unigenes of Mm were annotated their functional classification using Gene Ontology terms into three categories: biological process (P), molecular function (F) and cellular component (C). The results showed the number of commonly expressed genes with functional annotation were 160 (P), 169 (F) and 153 (C), respectively. The commonly expressed genes and their related functions might be annotated using alignment tool among sequence databases of different species. The analytical procedure in this study would assist animal scientists to screen the commonly expressed genes with fundamental roles and functions.

Key Words: Early Embryonic Stages, Commonly Expressed Genes, Mammals

W31 Environmental and genetic effects on growth traits of farmed red deer. R. Ramírez-Valverde*, A. Sánchez-Cervantes, J. G. García-Muñiz, and R. Núñez-Domínguez, *Universidad Autónoma Chapingo*, *Chapingo, México, México*.

Currently, there are in Mexico only a handful of farms with farmed red deer; however, in recent times their number has increased, therefore, it is important to characterize this species under main production systems. The objective of this study was to identify environmental and genetic effects on growth traits, in a herd of farmed red deer in Mexico. The animals were raised on an intensive rotational grazing system of grass-legume mixed temperate pastures. Evaluated traits (n=270 to 428) were weights at birth (BW), weaning adjusted to 100 d (WW) and yearling (YW), for males and females born from 1996 to 2003. Analyses were performed using the MTDFREML program. Final univariate animal models considered the fixed effect of sex-year (contemporary group), age of dam at calving as a covariate for BW and WW, and the direct (BW, WW and YW) and maternal (WW) random genetic effects. Contrasts were performed to determine statistical differences within fixed and covariates effects. Genetic evaluation was carried out in the total of the pedigree (n=528). Means and standard deviations for BW, WW and YW, were 8.7±1.2, 42.4±5.6 and 80.8±13.3 kg, respectively. Means for BW, WW and YW of males were higher ($P<0.05$) than those of females (4.6, 9.9 and 21.9%, respectively). There were differences between contemporary groups ($P<0.05$). Linear and quadratic age of the dam affected ($P<0.05$) both BW and WW. For BW, the heaviest weights were predicted for dams with an age of 36.9 months, while for WW a maximum was achieved at 108.7 months of age. Estimators of direct heritability were 0.00, 0.41 and 0.17, for BW, WW and YW, respectively. Maternal heritability for WW was 0.22. Standard deviations of direct breeding values were 1.4 and 1.3 for WW and YW, and 1.0 for maternal WW. As expected (no selection for growth traits), genetic trends for WW and YW were not different from zero ($P>0.05$). Based on the genetic variability of WW and YW, the results suggest the possibility of genetic improvement of those traits through selection in this herd.

Key Words: Heritability, Grazing, Animal model

W32 Effects of selected weather factors on feed intake of Angus, Polled Hereford, and Simmental beef bulls during feedlot performance tests. G. T. Tabler, A. H. Brown, Jr.*, E. E. Gbur, I. L. Berry, Z. B. Johnson, D. W. Kellogg, and K. C. Thompson, *University of Arkansas*, *Fayetteville*.

Selected weather data were analyzed to more closely define the relationship between climate and feed intake of three breeds of beef bulls during feedlot performance tests. Intake data originated from Angus (n = 282), Polled Hereford (n = 440) and Simmental (n = 372) bulls in University of Arkansas Cooperative Bull Tests from 1978 to 1990. Bulls were given a 21-d adjustment period, then individually full-fed a total mixed ration twice daily in the same stall for 140 d. Initial age and weight were recorded at start of each test with weights taken at 28-d intervals. Data were pooled, divided into five 28-d periods beginning with start of each test, with data from each period and breed analyzed separately. Initial age and weight were included in principal components regression as independent variables to adjust for initial animal differences. Principal component (PC) analysis was utilized to reduce number of independent variables in the regression and overcome collinearity concerns associated with numerous climatic variables. Initial weight and initial age had positive regression coefficients throughout the trial for each breed. Regression coefficients for effects of weather variables ranged from positive to negative depending on period and breed. No weather variable had a consistent effect throughout all five periods across all three breeds; although, effect of barometric pressure was positive in all periods for Polled Hereford and Simmental bulls. Results indicated rainfall, relative humidity, barometric pressure, day length, and wind speed have individual effects on feed intake. Additional evidence is provided indicating that temperature alone is inadequate to represent effects of weather on feed intake of various beef cattle breeds used in production systems today.

Key Words: Beef Cattle, Breed, Climate

W33 Promoter region of the bovine growth hormone receptor (GHR) gene: Resequencing, SNP detection, and association with performance traits in Brangus bulls. A. J. Garrett*[1], G. Rincon[2], J. F. Medrano[2], G. A. Silver[1], and M. G. Thomas[1], [1]*New Mexico State University*, *Las Cruces, New Mexico, United States*, [2]*University of California*, *Davis*.

Expression of the growth hormone receptor (GHR) gene and its binding with growth hormone is essential for growth. A TG microsatellite exists in the 5′ untranslated region (UTR) of bovine GHR segregating a short (11 bp) and a long (14-16 bp) allele. Favorable associations with carcass characteristics have been found with the longer allele in Angus cattle. Herein, a 1000 bp region flanking the TG microsatellite was resequenced to detect SNPs and completed an association study of genotype/haplotype to phenotype in performance tested Brangus (3/8 Brahman x 5/8 Angus; n = 340 from 80 sires) bulls. Target region was resequenced in twenty four familialy unrelated beef animals including Simmental, Angus, Brahman, and Brangus. Nine sequence variations were identified and 5 were genotyped via Taqman® assays. Haplotype analysis indicated polymorphisms were in phase ($r^2 = 0.84$; $D' = 0.92$) and an A/G tag SNP (125634) was identified. Mendelian segregation was verified using three generation families. The A allele was derived from Brahman and the G allele was derived from Angus. The AA genotype of the SNP was found to be a predictor of yearling weight with AA genotype being heavier ($P < 0.05$) than the AG or GG genotypes. Least squared means for intramuscular fat percentage (IMF) for genotypes of the SNP were 3.55, 3.60, 3.73 ± 0.08 for AA, AG, and GG genotypes respectively, suggesting an inverse relationship between yearling weight and IMF. Regression on the number of favorable alleles summed across markers appeared additive with a slope coefficient of 0.10 ($P < 0.03$). Prediction analysis involving haplotypes suggested animals possessing Angus alleles had greater (0.69 > 0.64 ± 0.03 cm, $P < 0.05$) rib fat than those possessing Brahman alleles. A GHR SNP in the 5′ UTR was associated with growth and carcass traits. The favorable allele segregated from Angus and appears additive for IMF in Brangus bulls. The A/G tag SNP may offer an alternative method of genotyping to the TG microsatellite in association studies involving body fat traits and yearling weight in Brangus cattle.

Key Words: Cattle, SNP, Growth Hormone Receptor

W34 Animal model analyses of additive and non-additive genetic effects for 205-day weight in a Nellore x Hereford multibreed population in Brazil.

A. de los Reyes[1], M. A. Elzo*[2], V. M. Roso[3], R. Carvalheiro[3], L. A. Fries[3], and J. L. Ferreira[1], [1]*Federal University of Goias*, *Goiania, GO, Brazil*, [2]*University of Florida*, *Gainesville*, [3]*GenSys Associated Consultants*, *Porto Alegre, RS, Brazil*.

Choosing an appropriate model to obtain reliable estimates of additive and nonadditive genetic effects is essential for the implementation of a sound crossbreeding program. The objective of this study was to assess the importance of direct and maternal breed additive, dominance, and epistatic recombination group effects for 205-d weaning weight (W205) in a large Nellore x Hereford multibreed population using 11 homoscedastic animal models. Four epistatic recombination expressions were evaluated: 1 (Dickerson) = NsHs + NdHd; 2 (Fries) = 0.5(HETs + HETd); 3 (Kinghorn) = 2NaHa; and 4 (Elzo) = 1 - NsNsNdNd - HsHsHdHd; N = Nellore fraction, H = Hereford fraction, HET = heterozygosity, a = animal, s = sire, and d = dam. The data file had 124,638 W205, 3,768 contemporary groups (CG = herd-year-season-management group-sex of calf), 1,078 sires, and 88,750 dams. The pedigree file included 202,475 animals. Fixed effects were CG, cow age at calving (fourth degree polynomial), weaning age as a deviation from 205 d (third degree polynomial), direct and maternal breed additive effects (models 2 to 11), direct and maternal heterosis (models 3 to 11), and direct and maternal epistatic recombination effects (direct: models 4 to 11; maternal: models 5, 7, 9, 11). Random effects were direct and maternal additive genetic effects, maternal permanent environmental effects, and residual effects. Additive relationships were accounted for. The Akaike (AIC) and Bayesian (BIC) information criteria were used to compare models. Inclusion of direct and maternal heterosis, and direct and maternal epistatic recombination (all definitions) showed an improvement in model fitting according to AIC and BIC (except for maternal epistatic recombination in models 9 and 11). Thus, both heterosis and epistasis need to be accounted for in genetic evaluation models for this multibreed population.

Key Words: Cattle, Multibreed, Recombination

W35 Growth and pubertal development of F_1 bulls from Hereford, Angus, Norwegian Red, Swedish Red and White, Friesian, and Wagyu sires.

E. Casas*, D. D. Lunstra, L. V. Cundiff, and J. J. Ford, *USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE*.

The objective of the study was to characterize growth, testicular development and puberty between 9 and 14 mo of age in bulls (n = 120) produced by mating sires from Hereford (H), Angus (A), Norwegian Red (N), Swedish Red and White (S), Friesian (F), and Wagyu (W), to MARC III (¼ Hereford, ¼ Angus, ¼ Red Poll, ¼ Pinzgauer) cows. Traits evaluated were birth weight, weight at 200 d, weaning weight (at 215 d), yearling weight, average daily gain from 8 to 14 mo of age, paired testis volume growth from 8 to 14 mo of age, age at puberty (determined by production of 50 x 10^6 sperm with 10% motility), age at freezable semen (determined by production of 500 x 10^6 sperm with 50% motility), paired testis weight, and daily sperm production per testis pair at 15 mo. At birth; animals with H and F inheritance were heavier (43 kg and 41 kg, respectively, $P = 0.04$), when compared to those with N, S, and W inheritance (39 kg, 38 kg, and 38 kg, respectively). Differences in weight were also observed at one year of age ($P = 0.004$), where the heaviest animals were those with A inheritance (450 kg), while the lightest animals were those with W inheritance (403 kg). Bulls with W inheritance had the lowest ($P = 0.0003$) average daily gain (1.13 kg/d) when compared to bulls with inheritance from H (1.23 kg/d), A (1.29 kg/d), N (1.27 kg/d), S (1.24 kg/d), and F (1.27 kg/d). No differences ($P = 0.14$) were observed for paired testis volume growth rate. They ranged from 1.95 in A sired to 1.66 cm^3/d in W sired bulls. There was a tendency ($P = 0.06$) of sire breed for age at puberty. The range was from 268 to 302 d. There were no differences ($P > 0.05$) for paired testis weight and daily sperm production. Growth of animals with W inheritance is slower than animals with N, S, F, H, or A inheritance. At 15 mo of age testicular development was similar for all breeds despite predicted differences in mature body weight.

Key Words: Beef Cattle, Bulls, Puberty

W36 Evaluation of post-weaning phenotypic residual feed intake in an Angus-Brahman multibreed herd of beef cattle.

M. A. Elzo*[1], G. R. Hansen[2], J. G. Wasdin[1], J. D. Driver[1], and J. L. Jones[1], [1]*University of Florida*, *Gainesville*, [2]*North Florida Research and Education Center*, *Marianna, FL*.

Residual feed intake (RFI) has become ubiquitous for evaluating feed efficiency in cattle. The objective here was to evaluate phenotypic RFI in a group of 200 bull, heifer, and steer calves of breed compositions ranging from 100% Angus (A) to 100% Brahman (B). Calves were born in Gainesville, Florida, from December 2005 to March 2006, and moved to a GrowSafe automated feeding facility in Marianna, Florida, in September 2006. Calves were randomly allocated to 10 pens of 20 calves each by sire group (1 = A, 2 = ¾ A ¼ B, 3 = Brangus, 4 = ½ A ½ B, 5 = ¼ A ¾ B, and 6 = B) and sex (bull, heifer, and steer). Calves were fed a concentrate diet composed of whole corn, soybean hulls, corn gluten feed, cottonseed hulls, and a protein, vitamin, and mineral supplement (DM = 91.2%, CP = 17.3%, DIP = 11.3%, NEm = 1.7 mcal/kg, and NEg = 1.2 mcal/kg). There was a pre-trial adjustment period of 21 d. Individual daily feed intake and weekly weights were obtained during a 70-d feeding trial. Phenotypic RFI was computed as the difference between the actual feed intake and the expected feed intake (function of average daily gain and metabolic mid-weight). Phenotypic RFI was analyzed using a homoscedastic mixed linear model. Fixed effects were pen, age of dam, sex of calf, initial age, initial weight, Brahman fraction of calf, and probability of A and B alleles at 1 locus in the calf. Random effects were sire and residual. Important effects were sex ($P < 0.002$; Males had lower RFI than females), initial weight ($P < 0.02$), and Brahman fraction ($P < 0.02$; Brahman had lower RFI than Angus). Subsequently, calves were assigned to 3 RFI groups: high (calf RFI > mean + 0.5 SD), low (calf RFI < mean - 0.5 SD), and medium (calf RFI between mean ± 0.5 SD; SD = 2.1 kg). High and medium RFI group estimates were higher ($P < 0.001$) for daily feed intake and feed conversion ratio, and lower ($P < 0.001$) for average daily gain and final weight than those of the low RFI group.

Key Words: Cattle, Feed Intake, Multibreed

W37 Regression of feed intake on selected environmental factors for beef bulls during postweaning feedlot performance tests.

G. T. Tabler*, A. H. Brown, Jr., E. E. Gbur, Jr., I. L. Berry, Z. B. Johnson, D. W. Kellogg, and K. C. Thompson, *University of Arkansas*, *Fayetteville*.

Selected weather data were analyzed to identify and quantify effects on feed intake of performance-tested beef bulls. Feed intake data originated from bulls (n = 1,874) in University of Arkansas Cooperative Bull Tests during 52 trials from 1978 to 1990. Bulls were given a 21-d adjustment period then individually full-fed a total mixed ration twice daily in the same stall for 140 d. Initial weight and age were recorded at start of each test with weights taken at 28-d intervals. Selected environmental variables used in the final analysis included maximum temperature, relative humidity, barometric pressure, rainfall, day length and wind speed. Data were pooled, divided into five 28-d periods with each period analyzed separately using all animals over all tests. Principal component analysis was used to reduce number of independent variables in the regression and overcome collinearity associated with numerous weather-related variables. Initial age and weight were included in principal components (PCs) regression as independent variables to adjust for initial animal differences. Feed intake was influenced by five PCs representing initial weight, initial age, maximum temperature, day length, rainfall, relative humidity, barometric pressure and wind speed throughout the study. Regression coefficients for initial weight and initial age were positive for each period on trial. Coefficients for environmental factors on feed intake ranged from positive to negative during various periods throughout the study. No single environmental variable had a consistent effect throughout all five periods. Results indicated numerous environmental factors influence feed intake throughout a feeding period and effects may vary as feeding period progresses, increasing the difficulty of accurate feed intake predictions.

Key Words: Beef Cattle, Day Length, Feed Intake

W38 Genetic parameters for growth traits and their relationships with yearling wool weight in Baluchi sheep breed of Iran.

A. Kamali*[1], H. R. Mirzaee[1], H. Naeemipour[2], A. Delghandi[3], and H. Farhangfar[2], [1]*Zabol University*, *Zabol, Iran*, [2]*Birjand University*, *Birjand, Iran*, [3]*Jihade Agriculture*, *Mashhad, Iran*.

In this study heritabilities of and genetic correlations among birth weight (BWT), weaning weight (WWT), pre-weaning average daily gain (ADG0-3) and yearling wool weight in Baluchi sheep breed of Iran were estimated. Data were a total of 4099 records collected from a flock of Baluchi sheep breed in Abbas Abad breeding center located in northeast of Mashhad. Analyses were carried out applying restricted maximum likelihood statistical method using univariate and bivariate animal models. Heritability estimates for BWT, WWT, ADG0-3 and yearling wool weight in the univariate analyses were found to be 0.074, 0.03, 0.172 and 0.075 respectively. In the univariate analyses, direct and maternal additive genetic and environmental random effects as well as fixed effects of year, season of lambing, sex, birth type and age of dam (linear and quadratic covariates) were included. Based on bivariate analyses, genetic correlations among growth traits were 0.069 between BWT and WWT, 0.995 between WWT and ADG 0-3. Wool weight had high positive genetic correlations with BWT (0.899), WWT (0.647) and ADG 0-3 (0.737) suggesting that a correlated response would be expected for yearling wool weight as the direct genetic selection is practiced based upon weight traits.

Key Words: Baluchi Sheep, Growth Traits, Wool

W39 Estimation of genetic parameters for pre and post weaning average daily gains in a flock of Iran-black sheep breed of Iran.

H. Farhangfar*[1], M. H. Molaee[2], and H. Naeemipour[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Zabol University*, *Zabol, Iran*.

In this study a total of 1068 growth records obtained from Iran-black sheep breed (a synthetic breed resulted from crossing between Baluchi and Chios breeds) covering the period from 1988 to 2002 was used to estimate direct and maternal heritabilities for pre and post weaning average daily gains as well as genetic and environmental correlations between the traits under consideration. The number of lambs, sires, dams and total animals in the pedigree file were 1068, 56, 526 and 1496 respectively. The average daily gains for pre (0-3 months) and post weaning (3-6 months) ages were 188 g and 87 g respectively. AI-REML algorithm in a bivariate animal model was used to estimate genetic, permanent and temporary environmental variance and covariance components utilizing DMU package. In the model, systematic environmental factors of year and month of birth, sex, birth type, covariate of dam age, covariate of lamb age at weighing, and random effects of direct and maternal additive genetic as well as maternal permanent environment were included. For both traits, the covariance between direct and maternal genetic effects was assumed to be nonzero in the bivariate animal model. Direct and maternal heritability estimates for pre weaning average daily gain were 0.037 and 0.132 respectively and the corresponding figures for post weaning average daily gain were 0.007 and 0.017 respectively. Direct additive genetic correlation between pre and post weaning daily gains was -0.253. The results showed that for pre and post weaning daily gains, direct and maternal genetic effects were positively correlated (0.992 and 0.126 respectively). Permanent and temporary environmental correlations between pre and post weaning daily gains were found to be 0.579 and -0.231 respectively.

Key Words: Iran-Black Breed, Average Daily Gain, Genetic Parameters

W40 Genetic analysis of birth and weaning weights in a flock of Iran-black sheep breed of Iran.

H. Farhangfar*[1], M. H. Molaee[2], and H. Naeemipour[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Zabol University*, *Zabol, Iran*.

To estimate genetic parameters and genetic trends for birth and weaning weights in a flock of Iran-black (a synthetic breed resulted from crossing between Baluchi and Chios breeds) sheep breed of Iran, a total of 1362 weight records collected during 1988-2002 was used. The number of lambs, sires, dams and total animals in the pedigree file were 1362, 56, 612 and 1876 respectively. The average birth and weaning weights were 3.63 Kg and 19.91 Kg respectively. Genetic, permanent and temporary environmental variance and covariance components were estimated using AI-REML algorithm in a bivariate animal model consisted of the environmental factors of year and month of birth, sex, birth type, covariates of dam age (for both traits) and lamb age at weaning (for weaning weight only), and random effects of direct and maternal additive genetic as well as maternal permanent environment. The covariance between direct and maternal genetic effects was assumed to be nonzero in the animal model. The analysis was undertaken by DMU package. Direct and maternal heritability estimates for birth weight were 0.072 and 0.097 respectively and the corresponding figures for weaning weight were 0.067 and 0.094 respectively. The additive genetic correlation between birth and weaning weights was found to be 0.936. The results showed that direct and maternal genetic effects for birth weight were negatively correlated (-0.032) while there were positively correlated (0.908) for weaning weight. Regression analysis of average predicted breeding value of lambs on year of birth indicated that there were no statistically significant annual increases at genetic level for both traits over the period of study.

Key Words: Iran-Black Breed, Heritability, Genetic Trend

W41 **Estimation of genetic parameters for early growth traits in the Mehraban sheep using different models.**

P. Zamani*[1] and H. Mohammadi[2], [1]*Bu-Ali Sina University*, *Hamedan, Iran*, [2]*Agricultural-Jahad Organization*, *Hamedan, Iran*.

Genetic parameters for birth weight (BW), weaning weight (WW) and pre-weaning daily gain (PWDG) in Iranian Mehraban sheep were estimated using Restricted Maximum Likelihood (REML) procedure. Six different animal models were fitted, differentiated by including or excluding maternal effects and with and without covariance between maternal and direct genetic effects. The direct heritability estimates (h^2) ranged from 0.26 to 0.53, 0.18 to 0.32 and 0.15 to 0.33 for BW, WW and PWDG, respectively. The estimates were substantially higher when maternal effects, either genetic or environmental, were ignored from the model. The maternal heritability (h^2m) for BW was 0.25 when only maternal genetic effect was fitted in the model as second random effect. It was decreased to 0.14 when the maternal permanent environmental effect was added to model. More complete models resulted in more accurate estimations.

Key Words: Mehraban Sheep, Early Growth Traits, Genetic Parameters

W42 **Application of logistic regression model to estimate phenotypic trend for twining trait of Baluchi sheep in Abbasabad breeding station of Mashhad.**

H. Farhangfar*[1], M. Molaee[2], and H. Naeemipour[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Zabol University*, *Zabol, Iran*.

Twining, as a trait associated with prolificacy in sheep, has long been recognised of economic importance which is usually expressed in a binary mode and discrete phenotypic distribution. For analysis of twining in a given population, usual statistical methods which are based upon normality distribution of the variable cannot be used but instead generalized linear models should be applied. In the present research, in order to study some environmental factors (year of lambing, dam age and lamb birth weight) affecting on twining and to estimate phenotypic trend a total of 5100 birth records belonging to 1681 ewes lambing from 1984 to 2003 in a large flock of Baluchi sheep breed in Abbasabad breeding station of Mashhad was used. Only the records of singles and twins were used in this study. The average ewe age and birth weight of lambs were 2.79 years and 4.25 Kg respectively. Twining information was analyzed by a logistic regression using GENMOD procedure of SAS programme. The results obtained showed that year of lambing, dam age at lambing and lamb birth weight had statistical significant effect on the probability of twining. The probability of twining had a positive correlation with dam age while it was negatively correlated with lamb birth weight suggesting that birth weight of individual lambs born from twin-lambing ewes is expected to be lower as compared to lambs born from single-lambing ewes. The results also revealed a positive significant phenotypic trend for the probability of twining over the period of 20 years which was estimated to be 0.01 per year of lambing.

Key Words: Baluchi Sheep, Twining, Logistic Regression

W43 **Genetic parameters estimation of Cashmere production for an indigenous goat in southern Khorasan province of Iran by using a repeatability model.**

H. Naeemipour*, H. Farhangfar, M. R. Asghari, and M. Bashtani, *Birjand University*, *Birjand,Iran*.

A total of 1490 Cashmere production records obtained from 567 indigenous goats in southern Khorasan province of Iran was used to estimate genetic parameters. Data were collected between 2000 and 2003. A single trait repeatability animal model in which fixed effects of sex, birth type, year of shearing and lamb age (linear and quadratic covariates) as well as additive genetic and environmental random effects were included. (Co) variance components were estimated by restricted maximum likelihood procedure using Powel algorithm applied in DFREML software. The results revealed that the estimates of heritability and repeatability of Cashmere production were 0.16 and 0.53 respectively indicating that a large proportion of total phenotypic variance is contributed by temporary environmental variation.

Key Words: Goat, Cashmere, Genetic Parameters

W44 **Effect of genotype on characteristics of porcine aortic valves and bovine pericard as substitute heart valves.**

S. De Smet*[1], W. Deklerck[1], E. Claeys[1], G. Van Nooten[2], and K. Narine[2], [1]*Laboratory for Animal Nutrition and Animal Product Quality, Department of Animal Production, Ghent University*, *Melle, Belgium*, [2]*Department of Cardiac Surgery, University Hospital Ghent*, *Ghent, Belgium*.

Porcine aortic valves and bovine pericardium are frequently used as bioprosthetic heart valves. However, the life span of these valves is limited due to calcification and structural failure. Characteristics of the original fresh tissue in relation to the animal genotype may be involved in this life span variability. The aim of this study was therefore to measure some compositional and structural (stress test) characteristics of porcine aortic valves and bovine pericardium in genotypes widely differing in morphology and muscle physiology. Slaughter pigs of different sex, stress genotype and IGF2 genotype were sampled. Pericardium was taken from double-muscled Belgian Blue young bulls and culled cows, and from dairy cows. Bovine pericardium contained more total collagen ($P<0.001$), soluble collagen ($P<0.05$) and less uronic acid ($P<0.001$) compared with porcine valve leaflets.

The maximum load, extension and stiffness of bovine pericardium were more than twice as high ($P<0.001$). There were few differences between slaughter pig genotypes. Valve leaflets from stress positive pigs had a higher soluble collagen content and a lower uronic acid content compared to those from stress negative pigs ($P<0.05$). The uronic acid content was slightly higher in barrows compared to gilts ($P<0.01$). There were no differences in the pericardium characteristics of different cow types. However, soluble collagen content, extension and maximum load were all higher ($P<0.001$) in young slaughter bulls compared to culled cows. Consideration of the animal genotype might be warranted in studying the relationship between properties of fresh tissue and the durability of a bioprosthesis.

Key Words: Heart Valve, Pig, Cattle

W45 Response to genetic selection for *longissimus*color in Landrace swine: Status following two generations of selection.

A. C. Naber*, K. M. Brueggemeier, S. J. Moeller, H. N. Zerby, and K. M. Irvin, *The Ohio State University*, *Columbus*.

The objective of the study was to measure response to selection for decreased longissimus Minolta L* (L) color in a population of Landrace swine. The population was established in 2002 from females obtained from 13 herds and males from 17 different genetic lines. Populations were established in two seasons (January and July farrowing) within a year. Two generations of random mating preceded separation of the populations, within season, in the year 2004 into Select (S; selected for darker loin L) and Control (C, Average EBV for loin L) based on an estimated breeding value (EBV) for L in candidate males. Available female litter mates were split into S and C randomly. After initial designation, the S and C populations were closed within a season and generations did not overlap. Selection in subsequent generations was focused on the male, and based on EBV for L. Matings within S and C were assigned randomly, while attempting to minimize full- and half-sib matings. Animal model EBVs were calculated based on sibling date within a replicate and using MTDFREML for L. Average EBVs of parent males, across seasons, for S and C in 2004 were -1.50 and 0.52 units, and in 2005 were -1.59 and 0.17 units, respectively. Responses, following two generations of selection, were evaluated using a mixed model with a fixed effect of treatment (S or C) and random harvest group within season for quality measures and season for measures of growth and carcass traits. Results indicate that S and C populations were not different for L ($P = 0.18$), although numerically, L was 1.0 unit less (darker) in the S population. After two generations of selection, S pigs had less ($P < 0.01$) loin area and greater days to 113 kg, with a trend for fatter 10th rib backfat ($P < 0.08$) than C pigs. No differences were observed between C and S pigs for visual loin color, marbling or loin shear force following two generations of selection. Heritability of L was estimated to be 0.36, providing a strong genetic basis for differentiation of the S and C lines if selection is effective in forthcoming generations.

Key Words: Swine, Selection, Pork Quality

W46 Genetic parameters for different measures of feed efficiency and their relationships with its component traits in Duroc pigs.

M. A. Hoque*[1], K. Suzuki[1], H. Kadowaki[2], and T. Shibata[2], [1]*Tohoku University*, *Miyagi, Japan*, [2]*Miyagi Prefecture Animal Industry Experiment Station*, *Japan*.

Genetic parameters for feed efficiency traits on 380 boars and their component traits on 1642 pigs (380 boar, 868 gilts, and 394 barrows) in 7 generations of Duroc population were estimated with REML. Feed efficiency traits were included feed conversion ratio (FCR) and residual feed intake (RFI), and their component traits were daily gain (DG), metabolic body weight (MWT), and daily feed intake (FI). Three measures of RFI were calculated as the difference between actual and expected feed intake. They were calculated by the residual of phenotypic (RFI_p) and genetic (RFI_g) regressions from the multivariate analysis of FI on MWT and DG, and by the difference between actual feed intake and predicted nutritional requirement (RFI_n). The mean values for RFI_p and RFI_g were close to zero (-0.05 and -0.03 kg/day, respectively), and for RFI_n was negative (-0.11 kg/day). Most of the traits studied were moderately heritable (ranging from 0.34 to 0.53), except for FCR, which was low (0.27). The genetic and phenotypic correlations between DG and FI were high (0.77 and 0.51, respectively), while between MWT and FI were low (0.26 and 0.14, respectively). The corresponding correlations between RFI_p and RFI_g were above 0.95 implying that they might be regarded as the same trait. The genetic and phenotypic correlations of FCR with different measures of RFI were high but lower than unity. RFI_p was phenotypically independent of its component traits, MWT ($r_p = 0.01$) and DG ($r_p = 0.03$). RFI_g was genetically independent of MWT ($r_g = -0.04$), whereas there was a weak genetic relationship ($r_g = 0.15$) between RFI_g and DG. RFI was more heritable than FCR, and the genetic and phenotypic correlations of RFI_p and RFI_g with FI were positive and stronger than of FCR with FI. These results provide evidence that RFI_p or RFI_g should be included for genetic improvement of feed efficiency in Duroc pigs breeding program.

Key Words: Duroc Pigs, Feed Efficiency, Genetic Parameters

W47 Genetic parameters for carcass traits and their genetic relationships with feed efficiency traits in Duroc pigs.

M. A. Hoque*[1], K. Suzuki[1], and T. Oikawa[2], [1]*Tohoku University*, *Miyagi, Japan*, [2]*Okayama University*, *Japan*.

Genetic parameters for carcass traits on 1642 pigs (380 boar, 868 gilts, and 394 barrows) and their genetic relationships with feed efficiency traits on 380 boars in 7 generations of Duroc population were estimated. Carcass traits were backfat thickness (BFT), loin eye muscle area (EMA), intra-muscular fat (IMF), and meat tenderness (MTR). Feed efficiency traits included feed conversion ratio (FCR) and residual feed intake (RFI). Three different measures of RFI, i.e., phenotypic (RFI_p), genetic (RFI_g), and nutritional (RFI_n) RFI were calculated by the difference between actual and predicted feed intake. The RFI_p and RFI_g were estimated, respectively, by the residual of phenotypic and genetic regressions of FI on MWT and daily gain. The RFI_n was estimated by the difference between actual and expected feed intake that predicted by the nutritional requirement. The heritability estimates for all the carcass traits were moderate (ranged from 0.38-0.46), except for BFT, which was high (0.72). Measures of RFI were positively correlated with IMF (r_g=0.14, 0.17, and 0.18 for RFI_n, RFI_p, and RFI_g, respectively), and negatively correlated with EMA (r_g=-0.61, -0.57, and -0.56 for RFI_n, RFI_p, and RFI_g, respectively). The genetic correlations of feed efficiency traits (FCR and all the measures

of RFI) with BFT were favorable (positive). BFT was more strongly correlated with RFI ($r_g \geq 0.76$) than with FCR ($r_g = 0.58$). Selection responses in feed efficiency traits through selection for daily gain, EMA, BFT, and IMF were small but in the desired direction, i.e. breeding values for feed efficiency traits decreased as selection generation progressed. Large responses in IMF and weak responses in EMA, BFT and MTR would be expected. This study provides evidence that selection against either RFI_p or RFI_g would give similar correlated response in carcass traits.

Key Words: Carcass Traits, Feed Efficiency, Genetic Relationships

W48 Prediction of number born alive and weaning weight of litter in first parity using performance test traits in four breeds of swine.

Z. B. Johnson*, *University of Arkansas*, *Fayetteville*.

The objective of this study was to examine relationships between performance test traits and subsequent reproductive performance in first parity females in four breeds of swine. Performance test records were collected in a commercial swine operation from 1992 to 1999. All females were grown to 100 d of age. At this time pigs were weighed (WT100) and selected for performance testing based on a combination of maternal and performance indexes which were different for each breed. Pigs were weighed at the end of the 77-d performance test and ADG calculated. Backfat (BF), loin eye area (LEA), and body length (LEN) were measured. Number of live born pigs (NBA) and weight of litter at weaning (WWL) were recorded. Regression analyses were used to determine if NBA and WWL could be predicted using previous performance test records of the dam. Regression models included effects for contemporary group of the dam, maternal grandsire, and sire of the litter, and WT100, ADG, LEA, BF, and LEN as covariates. In Landrace, ADG was a significant covariate ($P = 0.02$) for NBA. For Yorkshire, LEN was a significant ($P < 0.01$) covariate for NBA; ADG ($P = 0.06$) and LEA ($P < 0.01$) were significant covariates for WWL. In Duroc, WT100 ($P < 0.01$) and LEN ($P = 0.02$) were both significant covariates for NBA, while LEN ($P = 0.03$) was a significant covariate for WWL. In Hampshire ADG was a significant ($P = 0.05$) covariate for NBA, and WT100 ($P < 0.01$), ADG ($P = 0.01$) and BF ($P = 0.03$) were significant covariates for WWL. Regression models accounted for 37 to 59 % of the variation in NBA and WWL; however, the majority of this variation was due to contemporary group, maternal grandsire and sire of the litter. No covariate alone contributed more than 1% to the total variation in NBA or WWL, implying that while significant ($P < 0.05$) relationships did exist these covariates would probably not be useful in predicting these litter traits.

Key Words: Litter Size, Weaning Weight, Performance Test Traits

W49 Estimation of the additive and dominance variances in SA Landrace pigs.

D. Norris*[1], L. Varona[2], D. P. Visser[3], H. E. Theron[3], and S. F. Voordewind[3], [1]*University of Limpopo*, *Polokwane, South Africa*, [2]*Center UDL-IRTA*, *Lleida, Spain*, [3]*ARC-Animal Improvement Institute*, *Irene, South Africa*.

The objective of this study was to estimate dominance variance for number born alive (NBA), interval between parities (FI) and 21- day litter weight (LWT21) in South African Landrace pigs. A total of 26223 NBA, 16370 FI and 21335 LWT21 records were analysed. Bayesian analysis via Gibbs sampling was used to estimate variance components and genetic parameters were calculated from posterior distributions. Estimates of additive genetic variance were 0.669, 43.46 $d^2$and 9.02 kg^2 for NBA, FI and LWT21, respectively. Corresponding estimates of dominance variance were 0.439, 123.68 d^2 and 2.52 kg^2, respectively. Dominance effects were important for NBA and FI. Permanent environmental effects were significant for FI and LWT21 It may be beneficial to evaluate non-additive genetic merit of individuals and families in addition to their transmitting abilities. A breeding program that capitalizes on non-additive genetic merit may be desirable.

Key Words: Non-Additive Genetic Effects, Bayesian Analysis, Genetic Parameters

W50 EpiSNP: A computer package for genome-wide analysis of SNP epistasis and single-locus effects of quantitative traits.

L. Ma*, D. Dvokin, J. R. Garbe, and Y. Da, *University of Minnesota*, *St. Paul*.

The EpiSNP computer package is designed for genome-wide analysis of SNP epistasis and single-locus effects on quantitative traits and is applicable to all bi-allelic candidate genes. The statistical tests were based on an extended Kempthorne model that allows Hardy-Weinberg disequilibrium and linkage disequilibrium for genome-wide single-locus testing and pairwise epistasis testing of potentially large numbers of SNPs. The package currently has four individual programs. The main program, EPISNP, offers tests of three single-locus effects, SNP marker effect, additive and dominance effects, and tests of five pairwise effects, two-locus interaction, additive x additive, additive x dominance, dominance x additive, and dominance x dominance epistasis effects. The CPUHD program estimates the CPU time and disk space required to execute the EPISNP program, the EPISNPPLOT program produces graphical views of single-locus significant results and sample sizes for each chromosome, and the EPINET program draws figures of epistasis networks. The EpiSNP computer package including the user manual is freely available at http://animalgene.umn.edu.

Key Words: SNP, Genome-Wide Association, Epistasis

W51 SPSSQTL: A computer program for calculating statistical power and sample size for QTL and candidate gene detection.

J. R. Garbe*, L. Ma, and Y. Da, *University of Minnesota*, *St. Paul*.

The SPSSQTL computer program offers calculations of statistical power and sample size for detecting two single-locus effects (additive and dominance) and four epistasis effects (additive x additive, additive x dominance, dominance x additive, and dominance x dominance) of a QTL or a candidate gene. The program consists of one dialog box with fields for the user to enter parameter values for calculating statistical power or sample size. For detecting additive and dominance QTL effects, the user has a choice of F-2 or reciprocal backcross (RBC) design. For detecting epistasis QTL effects, the F-2 design is assumed. To calculate statistical power, the user needs to enter parameter values of QTL heritabilities (measures of QTL effect size), type-I error, recombination frequency between the marker and QTL, and sample size. To calculate sample size, the user needs to enter

statistical power in addition to all the above parameter values except sample size. Changing any field in the dialog box will cause the calculated power or sample size to be updated. For candidate gene testing, power and sample size are calculated by setting the marker-QTL recombination frequency to zero. The program including the user manual is freely available at http://animalgene.umn.edu.

Key Words: Statistical Power, Sample Size, QTL

W52 The effect of two freezing rates and two equilibration times on semen post-thaw motility of bad freezer bulls.

G. Rocha-Chavez[1], J. M. Tapia-Gonzalez[1], J. G Michel-Parra[1], M. A. Pinto-Jacobo[2], and G. Gonzalez-Guerra*[1], [1]*CUSUR Univ de Guadalajara*, *Cd Guzman, Jalisco, Mexico*, [2]*URPJ*, *Guadalajara, Jalisco, Mexico*.

It is a well known fact that beef cattle living in tropical areas tend to have low freezability on their semen intended for artificial insemination. The objective of this study was to determine the effect of two freezing rates and two equilibration times on post thaw motility of low freezability semen. Each ejaculate from six bulls known as bad freezers was diluted 1:1 with Andromed® extender, split in four parts and allocated in a 2x2 factorial arrangement into one of the following experimental groups: (1) semen equilibrated for 4 hr and slow freezing rate (FR); (2) semen equilibrated for 4 hour and fast FR; (3) Semen equilibrated for 24 hr and slow FR; (4) semen equilibrated for 24 hr and fast FR. Each of the six bulls (3 simmental and 3 brahaman) was collected 10 times and semen was frozen on 0.5 cc straws using a standard protocol. Equilibration was made at 4°C and freezing rates were 0.5°C/min and 4°C/min for low and fast respectively. Motility readings were made on thawed semen after being frozen for at least a 24 hr period. All readings were made in duplicate using video recording technology and descriptive statistics was used for initial arrangement of data. The chi squared procedure was used for finding differences between treatments. Readings on post-thaw motility of 47 ± 7.7, 52 ± 5.6, 58 ± 3.2 and 49 ± 6.3 % were found for treatments 1, 2, 3, and 4 respectively with no statistical differences between treatments except for group 3 ($P<0.05$). No interaction between breeds and treatment was found. It was concluded that, under conditions of this study, longer equilibration periods and slower freezing rates are beneficial for semen of low freezability.

Key Words: Semen, Freezability, Bulls

W53 Effect of selection for increased egg production, age, and sex on turkey breast muscle development.

C. S. Coy*, K. E. Nestor, and S. G. Velleman, *Ohio Agricultural Research and Development Center, The Ohio State University*, *Wooster*.

Genetic selection plays an important role in breast muscle development in turkeys. Previous studies have shown a correlation between growth selection and altered breast muscle morphology leading to muscle fiber damage. In a recent study, genetic selection for increased egg production showed no significant changes in breast muscle morphology from 8 to 16 wk of age between a line (E) selected for increased egg production and its randombred control line (RBC1). However, there was a significant interaction between line and age suggesting that the E and RBC1 line may develop differently. Morphological structure of the breast muscle was better in males than females. The purpose of this study was to examine breast muscle morphology changes in the E and RBC1 lines during key stages of muscle development. Breast muscle morphology was observed at embryonic d 25, and 1, 4, 8, 16, and 20 wk posthatch in the E and RBC1 lines. Breast muscle samples from 10 birds per age-line-sex subgroup were collected, fixed, processed, embedded in paraffin, sectioned, and stained with hematoxylin and eosin. Representative muscle sections from each bird were scored by 4 individuals based on breast muscle morphology. Scores ranged from 1 (little extracellular space and indistinct muscle fibers) to 5 (large extracellular space and distinct muscle fibers). Posthatch breast muscle morphology scores did not differ between the E and RBC1 lines, but age and sex differences were significant. The morphological scores were best at embryonic d 25 but declined significantly at 1 wk posthatch. Scores improved significantly from 1 to 4 wk posthatch and remained constant through 20 wk posthatch. Males had higher scores than females. The results of this and previous studies suggest that selection for increased egg production may be associated with a slight reduction in breast muscle morphology scores at 16 wk of age.

Key Words: Turkey, Genetic Selection, Muscle

W54 Sequence homology comparison between goose and chicken liver cDNA libraries.

Y. H. Wang*[1], E.-C. Lin[1], M. C. Hsu[2], C. Y. Lien[1], B. T. Tsai[1], C. F. Yen[1], H. W. Lin[1], S. T. Ding[1], W. T. K. Cheng[1], K. T. Yang[3], M. C. Huang[3], Y.-H. Fan[3], S.-H. Chiou[3], C. F. Chen[3], Y. P. Lee[3], [1]*National Taiwan University*, *Taipei, Taiwan*, [2]*National Taitung Junior College*, *Taitung, Taiwan*, [3]*National Chung Hsing University*, *Taichung, Taiwan*.

The DNA sequence information of goose is very limited in the public databases. In this study, we utilized expressed sequence tags (ESTs) of goose and chicken liver cDNA libraries for sequence homology comparison. The goose and chicken cDNA libraries were constructed by using livers from 4 Taiwanese native chickens and 6 White Roman geese. There were totally 2,400 and 6,686 clones sequenced in the goose and chicken liver cDNA libraries, respectively. After excluding sequences with low quality, short and low complexity, 8,403 high quality sequences (2,075 of goose; 6,328 of chicken) were clustered and assembled using tgicl package (from TIGR website) with minimum requirements of 65 base pairs overlapping and 95% similarity. Totally 605 clusters (≥2 sequences per cluster reaching the requirements, averaging 9.3 sequences per cluster) were found with 636 contigs assembled in those clusters. The number of clusters with sequences from both of goose and chicken was 29, which are highly similar in the cDNA sequences between the two species. There were 14 clusters which have different contigs per cluster assembled from either goose or chicken sequences only. Such clusters might represent certain differences happened in the same gene between goose and chicken. To assist the comparison of sequence homology, the remaining clusters were searched against NCBI NT database using blastn. There were 76 clusters annotated to be 35 gene identities, which indicated more variation of sequence in such clusters than the previous two categories. However, the other 486 clusters could not be classified that might result from the lack of enough sequence information from goose. This comparison might provide more information for the further genomic studies of goose.

Key Words: Goose, Chicken, Sequence Homology

W55 Combining ability of characteristics of egg quality of quail for analyze system of diallel crossbreds.

A. Piccinin, J. N. Gimenez, C. H. M. Malhado, C. Móri, C. Andrighetto, R. M. S. Emediato*, S. A. Maestá, A. A. Ramos, H. C. Gonçalves, and E. N. Martins, *São Paulo State University*, *Botucatu, São Paulo, Brazil*.

The goal of this trial was to indicate crossbreds to improve quality of eggs of quail. It was used a system of diallelic crossbreds between three ancestries. Effect of general capacity of combination, specific capacity of combination and reciprocal effect have been estimated. It was studied characteristics as specific gravity, height of albumen, Haugh unit, egg yolk percentages, shell and albumen. Ancestries 1 and 2 have improved the indices of specific gravity, and ancestry 3 improved the percentage of egg shell and consequently shelf-life, when the general capacity of combination is considered. lineages of crossbred 1x2 was more efficient for Haugh unit and albumen height, indicating bigger shelf-life of these eggs. Lineages of the crossbred 1x3 and 2x3 have shown to be the best option for specific gravity and percentage of egg shell, respectively, which resulted in better egg quality. The reciprocal effect have shown significant in the majority of the characteristics, in the partial periods. Crossbreds between males of ancestry 2 with females of ancestry 1 have provided lineages with bigger height of albumen, Haugh unit and percentage of egg shell, and males of ancestry 3 with females of ancestry 2 have provided lineages with bigger specific gravity, percentage of egg yolk and egg shell. Both crossbreds can be used in programs of genetic improvement aiming get better internal quality of eggs.

Key Words: Diallelic Crossbreds, Egg Quality, Quail

W56 Long-term effects on the expression of the intestinal Na-P type IIb cotransporter in broilers fed phosphorus deficient diets early in life.

C. M. Ashwell*[1] and R. Angel[2], [1]*North Carolina State University*, *Raleigh, NC*, [2]*University of Maryland*, *College Park, MD*.

To determine the effects of dietary P on the expression of the chicken intestinal Na/Pi type IIb cotransporter (NaPcoT) experimental diets were formulated to be deficient in P. Male Ross 308 chicks were fed either a control (C) consisting of 1.11% Ca and 0.50% available P or a low (L) diet containing 0.59% Ca and 0.25% available P from hatch to 4 d of age (90hr). All birds were then fed a C diet consisting of NRC recommended levels of Ca and P until d 22. From d 22 to d 38 the birds were either maintained on a C (0.7%Ca and 0.3%P) or an L diet (0.4% Ca and 0.12% P). The three dietary treatments, C-C-C, C-C-L, and L-C-L met all other NRC (1994) nutrient recommendations. Performance data were collected for each dietary phase including weight gain, feed conversion, bone ash, and specific nutrient retention. RNA extracted from each of the regions of the small intestine were reverse transcribed to produce cDNA and analyzed by real-time PCR for the levels of both the NaPcoT mRNA and 18s rRNA. The effect of dietary treatment was determined by analyzing the resulting Ct values for each amplification and determining the ΔΔCt using the level of 18s rRNA as an internal standard for normalizing the amount of RNA in each reaction. The reduction of P in the post hatch diet had a significant effect on the expression of the NaPcoT by stimulating an average 2.8-fold increase in the mRNA levels in the small intestine. The most interesting aspect of this effect of diet on expression of NaPcoT in the intestine is the increase in expression levels later in life (d38) of the birds that experienced the low P diet for the first 90 hr post-hatch in comparison to the controls. This data correlates well with the apparent increase in efficiency of nutrient uptake measured in these birds. This clearly establishes that ‘imprinting’ or permanent modifications are occurring in the animal post-hatch that are long term and allow for significant increases in NaPcoT expression and improved P utilization when P deficient diets are fed in the grower/finisher phases.

Key Words: Gene Expression, Conditioning, Imprinting

W57 Analysis of expressed sequenced tags from abdominal muscle cDNA library of the pacific white shrimp *Litopenaeus vannamei*.

J. Cesar, B. Zhao, and J. Yang*, *University of Hawaii*, *Honolulu*.

As the shrimp industry expand rapidly worldwide, the pacific white shrimp, *Litopenaeus* vannamei, is becoming an economically important species in aquaculture. Along with culture technology and disease resistance, genetic enhancement of growth rate is an important aspect of shrimp aquaculture. Although abdominal muscle accounts for 90% of shrimp meat, little is known about the shrimp muscle genes, particularly the muscle regulatory genes. To identify the critical genes responsible for shrimp muscle growth and metabolism, we established a cDNA library based on juvenile abdominal muscle by a PCR-based SMART^{TM} cDNA technology. Library size was 5.0×10^6 pfu independent clones per microgram of starting DNA vector with the percentage of recombinant clones >95%. Single pass sequence analysis of 311 randomly picked positive clones revealed 197 expressed sequence tags with average insert size of 745 nucleotides. BLASTn searches using the sequences identified 161 unique clones, including 45 high (>98%) identity matches to previously identified genes; 36 medium (80% to 98%) identity matches (>100 bits hit score and $<2 \times 10^{-19}$ E-value); 76 unknown sequences; 2 sequences matching hypothetical protein sequences, 2 sequences matching DNA microsatellite markers with short TG, GA and CAA repeats in the database. Among the 45 high identity-matched ESTs, 12S ribosomal RNA, actin 1, actin 2 and arginine kinase and beta-actin were most abundant with 5 to 13 clones each. Primary hit sequences originate from shrimp, insects, mammal, lobsters, crabs, crayfish, and barnacle. According to the inferred or known functions of the gene products, genes were categorized as muscle structural proteins (28%), followed by unknowns (24%), protein synthesis (18%), enzymes (14%), carrier protein (6%), ion channel (2%), DNA replication (2%). In summary, more than 25% of the ESTs identified a new gene from the cDNA library supports full-scale EST strategy for discovery of the transcripts or genes that regulate abdominal muscle biology. A further analysis and identifications of the full-length cDNA sequences will significantly facilitate shrimp genomic program.

Key Words: cDNA Library, Expressed Sequence Tag, Shrimp