

Breeding and Genetics II

W28 Analysis of some environmental factors for growth parameters obtained from Gompertz nonlinear model in Kurdi sheep breed of Iran. H. Farhangfar^{*1}, D. A. Saghi², and M. H. Fathi Nasri¹, ¹*Birjand University, Birjand, Iran*, ²*Agricultural Research Centre, Mashhad, Iran*.

The main objective of the present research was to analyse some environmental factors for growth parameters in Kurdi sheep breed of Iran. The data consisted of 16949 weights recorded at different ages (0, 3, 6, 9 and 12 months) belonging to 4353 Kurdi sheep breed. The data were obtained from a large-size flock of Kurdi sheep (located at northern Khorasan province) during 1990-2005. All lambs were born in winter. Gompertz nonlinear model defined as $W = (z/b) \cdot \exp(-\exp(g_0 - b \cdot t))$ was initially fit to individual lambs to estimate corresponding parameters (z , b and g_0). Moreover, estimated parameters z/e ($e=2.71828$) and A (z/b) were also calculated for individual lambs. The estimated parameters z/e and A are associated with maximum daily growth rate and mature weight respectively. All estimated parameters were subsequently analysed by a general linear statistical model. In the model, fixed environmental factors of birth year, birth type, lamb sex, ewe lambing order, two way interactions between lamb sex and birth type, between lamb sex and ewe lambing, between birth type and ewe lambing and between birth year and lamb sex. The sire random effect was not considered in the analysis due to lack of sire identification in the data file. The analyses were carried out by SAS programme using nonlinear procedure. The results indicated that for all estimated parameters (z , b , g_0 , z/e and A) were significantly ($p < 0.05$) affected by year of birth, lamb sex and birth type. Ewe lambing had only a significant affect ($p < 0.05$) on estimated parameters z and z/e . The interaction between birth year and lamb sex was found to significantly ($p < 0.01$) affect on all estimated parameters. The results also revealed that the interactions between ewe lambing and birth type, between ewe lambing and lamb sex as well as between lamb sex and birth type had no significant ($p > 0.05$) influence on the estimated parameters.

Key Words: Kurdi Sheep, Growth, Gompertz

W29 Response surface regression analysis to locate optimal minimum age at sexual maturity based on body weights at weeks 8 and 12 for indigenous chicken in Khorasan province of Iran. H. Farhangfar^{*}, M. E. Hosseini, and S. M. Navidzadeh, *Birjand University, Birjand, Iran*.

An analysis using response surface regression statistical methods was carried out to locate optimal minimum age at sexual maturity (ASM) based on weight at weeks 8 (W8) and 12 (W12) for indigenous chicken in Khorasan province of Iran. The data used in this study consisted of 1617 weight and ASM records collected from 1617 indigenous chicken belonging to the same generation and sex (female) during year 2006. The arithmetic means W8, W12 and ASM were 513, 865 g and 162 days ($SD=10.45$ days) respectively. In the data file, the ASM ranged from 138 to 209 days. A response surface regression in which ASM was dependent and W8 and W12 were independent variables was fitted to the data set. In the model, linear, quadratic terms of the independent variables as well as interaction between W8 and W12 were included. The model was fitted using RSREG procedure of SAS programme. The results obtained in the present research indicated that except the intercept

term fitted in the model, all the independent variables (linear, quadratic and interaction terms) had no statistical significant ($p > 0.05$) effects on ASM variation suggesting that other possible environmental factors could affect sexual maturity age of the indigenous chicken studied in this research. However, the predicted value of the minimum ASM was found to be approximately 161 days (close to the simple average of ASM in the data set) as the chicken weight at W8 and W12 were 504 and 997 g respectively.

Key Words: Age at Sexual Maturity, Weight, Indigenous Chicken

W30 Estimates of genetic parameters for direct and maternal effects on growth traits and fleece weight of Angora goat (Markhoz) in Iran. M. B. Zandi^{*1}, S. R. Miraei Ashtiani¹, M. Moradi Shahrabak¹, and A. Rashidi², ¹*Tehran University, Karaj, Tehran, Iran*, ²*Kurdistan University, Sanandaj, Iran*.

The aim of the current study was to estimate additive and non-additive parameters for birth weight (BW), weaning weight (WW), 6-month weight (W6), 9-month weight (W9), yearling weight (YW), and fleece weight at first shearing (FW), which are essential to design a selection programme for Kurdish Angora goat (Markhoz). Data and pedigree information which were used in this study were collected at the Sanandaj and Saqez Animal Breeding Research Institute during 1993 to 2007. Data contains of 2950 to 4008 records for this traits and total number of sires and dams in the study was 364 and 1391 respectively. Genetic parameters were estimated using univariate and multivariate traits animal model analyses with restricted maximum likelihood (REML) method by ASREML software. Estimates of direct heritability were 0.25 for BW, 0.26 for WW, 0.30 for W6, 0.21 for W9, 0.14 for YW and 0.12 for FW. Estimates of maternal heritability were 0.120, 0.110, 0.034, 0.030, 0.036 and 0.046 for BW, WW, W6, W9, YW and FW, respectively. Estimates of direct genetic correlations among growth traits were positive and ranged from 0.28 to 0.89. FW had a moderate to high positive direct genetic correlation with BW, WW and YW but had a negative direct genetic correlation with W6 (-0.22) and W9 (-0.202). The results of this study showed that maternal heritability was higher for pre-weaning than for post-weaning traits and the magnitude of the heritability estimates for those traits indicate possibility of an effective selection.

Key Words: Markhoz Goat, Heritability, REML

W31 Comparison and estimation factors affected body weight traits in the Markhoz breed of goats. M. B. Zandi^{*1}, M. A. Syed Reza¹, M. Moradi Shahrabak¹, and R. Amir², ¹*Tehran University, Karaj, Tehran, Iran*, ²*Kurdistan University, Sanandaj, Iran*.

Data from 4008 Kids of the Markhoz breed were used to estimate genetic parameters. Traits analyzed were weights at birth (BW), 90 days (Ww), 6-month weight (W6), 9-month weight (W9), yearling weight (YW), and fleece weight at first shearing (FW). REML estimates of variance and covariance components were obtained assuming animal models that included the fixed effects of sex, age of dam, effect of year of birth and types of birth or rearing, and the animal random effects for the direct, maternal genetic and permanent environmental

effects. Results showed that an important direct additive and maternal genetic effects were observed. Estimates of the direct heritability, maternal and permanent environmental heritability with standard errors were respectively 0.32(0.046), 0.085(0.036), 0.085(0.028) for BW; .30(0.044), 0.15(0.034), 0.024(0.013) for WW; 0.35(0.046), 0.12(0.033), 0.014(0.012) for W6, 0.37(0.043), 0.12(0.026) 0.00(0.00) for W9, and 0.43(0.043), 0.10(0.024) 0.00(0.00) for YW. Estimates of additive direct-maternal correlations were important and negative ranged from -0.57 to -0.80 for pre-weaning weights, and from -0.80 to -0.89 for post- weaning weights. Results suggest that estimates of additive and maternal heritability were important but permanent environmental maternal effect had some influence on body weights at pre-weaning that we must selection goats for this trait. These results indicate that goats have maternal ability for single, twins and triple kids (litter size) and we must considering these traits in the selection programs.

Key Words: Markhoz Goats, Maternal Ability, Heritability

W32 Weaning results of Simmental beef calves. F. Szabó* and S. Bene, *University of Pannonia, Keszthely, Hungary.*

Weaning weight, preweaning daily gain and 205-day weight of Simmental calves (n = 8929, male = 4539, female = 4390) born from 232 sires between 1980-2003 were examined. Farm, age of cows, year of birth, season of birth and sex of calves as fixed, while sire as a random effect was treated. Data were analysed with Harvey (1990) Least Square Maximum Likelihood Computer Program, moreover two animal models were used for breeding value estimation. Variance, covariance components and heritability values and correlation coefficients and the effect of the maternal permanent environment on genetic parameters and breeding values were examined.

The overall mean value and standard error of weaning weight, preweaning daily gain and 205-day weight were 217±4.5 kg, 1009±19.8 g/day and 242±4.1 kg, respectively. Calving year and season, sire, age of dam and herd had significant (P<0.05) effect on the evaluated traits.

The direct heritability (h²_d) of weaning weight, preweaning daily gain and 205-day weight was between 0.37 and 0.42. The maternal heritability (h²_m) of these traits was 0.06 and 0.07. The direct-maternal correlations (rdm) were medium and negative -0.52 and -0.74. Contribution of the maternal heritability and maternal permanent environment to phenotype is smaller than that of direct heritabilities (h²_m + c² < h²_d). The proportion of the variance of maternal permanent environment in the phenotypic variance (c²) changed from 3 to 6 %. Estimated breeding values changed whether the permanent environmental effect of dam was not taken into consideration but the rank of the animals was not modified. The genetic value for weaning results of Simmental population has increased since 1997.

Key Words: Breeding Value, Heritability, Weaning Weight

W33 Genotype and environment interaction of weaning results of Simmental calves. A. Fördös and F. Szabó*, *University of Pannonia, Keszthely, Hungary.*

The interaction of sire and population in the Simmental breed of cattle was examined on data from the Hungarian Simmental Breeders Association. Data of 2345 progeny (1260 male and 1085 female), born between 1992-2003, of thirty five sires from two populations were

evaluated. Preweaning daily gain (PDG) and 205-day weight (205dW) were analysed. Population, age of cows, year of birth, season of birth and sex of calves were treated as fixed, while sire and sire x population were treated as random effects. Genetic (rg) and rank (rrank) correlations were calculated for sires represented in the two populations (A,B). Data were analysed according to Harvey (1990) Least Square Maximum Likelihood Computer Program and SPSS 9.0 for Windows. Results were as follows: rg= PDGA -PDGB: 0.31(P<0.01); 205dWA-205dWB: 0.22(P<0.01) and rrank= PDG: -0.04 (P>0.05); 205dW: 0.078 (P>0.05). According to the result of examination important and significant (P<0.001) sire x population interaction were found in case of the two traits in Simmental population.

Key Words: 205-Day Weight, Genetic Correlation, Rank Correlation

W34 Genetic association between age and litter traits at first farrowing in a commercial Pietrain-Large White population raised in an open-house system in Thailand. P. Pholsing¹, S. Koonawootrittriron¹, T. Suwanasopee¹, and M. A. Elzo*², ¹*Kasetsart University, Bangkok, Thailand,* ²*University of Florida, Gainesville.*

The Thai swine industry is becoming an increasingly competitive business. Producers are striving to increase productivity and decrease costs. A trait of interest is age at first farrowing. The goal is to reduce costs by lowering age at first farrowing without detrimental effects to economically relevant litter traits. The objective here was to evaluate genetic associations between age at first farrowing (AFF) and 3 litter traits: total born alive (TBA), still born and mummy (LOST), and total birth weight of live piglets (TBW), in a negative halothane gene swine commercial population composed of Pietrain (PT) and Large White (LW) pigs. Data consisted of pedigree, and first-farrowing traits (AFF, TBA, LOST, and TBW) from 1,777 PT and 450 LW sows gathered from 1999 to 2006. Pigs were raised in an open-house system and received the same nutrition, management, and health care. Restricted maximum likelihood estimates of variance and covariance components for AFF, TBA, LOST, and TBW were used to calculate heritabilities and genetic correlations. A 4-trait animal model (AFF-TBA-LOST-TBW) that accounted for contemporary group (year-month) and breed as fixed effects, and animal and residual as random effects was used. Computations were performed with the ASREML program. Large White had shorter AFF (10.00 ± 2.34 d; P < 0.01), higher TBA (1.20 ± 0.22 piglets; P < 0.01), lower LOST (0.20 ± 0.11 piglets; P < 0.01), and smaller TBW (1.11 ± 0.30 kg; P < 0.01) than PT. Heritability estimates were 0.07 ± 0.03 for AFF, 0.11 ± 0.04 for TBA, 0.08 ± 0.04 for LOST and 0.08 ± 0.03 for TBW. Genetic correlations between AFF and TBA (0.19 ± 0.26), LOST (-0.12 ± 0.33), and TBW (0.14 ± 0.32) were low and had high standard errors. These low correlation estimates indicate that selection for AFF may be carried out in this commercial swine population without severe undesirable effects on litter traits.

Key Words: Farrowing, Pig, Tropical

W35 Factors affecting plasma cholesterol, lipoproteins, and triglycerides in growing pigs of various breed compositions raised under Thai tropical conditions. S. Koonawootrittriron¹, T. Suwanasopee¹, and M. A. Elzo*², ¹*Kasetsart University, Bangkok, Thailand,* ²*University of Florida, Gainesville.*

Concentration of plasma cholesterol (CHOL), high density lipoproteins (HDL), low density lipoproteins (LDL), and triglycerides (TRIG) may vary in pigs of different breed composition under tropical conditions. Selection of pigs for low plasma CHOL, LDL, and TRIG, and high HDL could be beneficial for their health and for human consumption. The objective was to evaluate factors that may affect plasma CHOL, HDL, LDL, and TRIG in growing pigs from 5 breed groups: Pietrain (P), Large White (W), WP, Landrace-Pietrain (LP), and WLP, under tropical conditions in Western Thailand. Ten hogs and 10 gilts of the same age (85 d) and similar weight (30.03 ± 7.07 kg) from each breed group were assigned randomly to each cell of a 5×2 factorial design (5 breed groups \times 2 sexes). Pigs in each factorial group were kept in a 4.5 m by 7.5 m pen throughout the 90-d trial. All pigs were raised in an open barn, and received the same nutrition, management, and health care. Weights, ultrasound backfat thickness and lean percent were measured at 3 ages (89 d, 136 d and 178 d). Blood samples were drawn from the 3 fastest and the 3 slowest growing pigs within each factorial group at each age. Plasma was analyzed for concentration of CHOL, HDL, LDL, and TRIG by an enzymatic-colorimetric method. The statistical model considered breed group, sex, and age, the interactions breed group \times sex, breed group \times age, and sex \times age, and the covariates backfat thickness and lean percent, and residual. Computations were performed using the mixed procedure of SAS. Breed group was important for CHOL, HDL, and LDL ($P < 0.001$), but not for TRIG. Pietrain had the lowest least squares means (LSM) for CHOL (71.21 ± 3.04 mg/dL) and LDL (40.61 ± 2.45 mg/dL), WLP had the lowest LSM for TRIG (45.18 ± 4.24 mg/dL), and LP had the largest LSM for HDL (40.78 ± 1.29 mg/dL). Ultrasound lean percent was negatively associated with LDL ($P < 0.01$).

Key Words: Cholesterol, Lipoprotein, Pig

W36 Multibreed beef cattle breeding value estimation based on weaning results. Sz. Bene¹, I. Komlósi², Zs. Fekete¹, Z. Lengyel¹, and F. Szabó^{*1}, ¹University of Pannonia, Keszthely, Hungary, ²University of Debrecen, Debrecen, Hungary.

Weaning results of 603 calves (297 male and 306 female; 388 purebreed and 215 crossbreed) born from 9 dam breeds (Hungarian Fleckvieh, Hereford, Aberdeen Angus, Red Angus, Lincoln Red, Limousin, Charolais, Blonde d'Aquitaine, Shaver), kept among the same condition on peat-bog soil pasture at Keszthely were evaluated between 1997 - 2006. Variance, covariance components, heritability values and correlation coefficients were estimated. Three different animal model were used for the estimation.

Different models had different fixed effects of genotype: model 1 genotype of calf; model 2 genotype of calf and dam; model 3 genotype of sire and dam

The direct heritability of weaning weight, preweaning daily gain and 205-day weight was between 0.30 and 0.51, the maternal heritability of these traits was 0.07 and 0.15. The direct-maternal correlations in weaning weight and preweaning daily gain were -0.12 and -0.27. Contribution of the maternal heritability and maternal permanent environment to phenotype is smaller than that of direct heritabilities. The total heritability was between 0.37 and 0.47.

The results obtained with three different animal models were similar with very small difference. The rank-correlation between the three models was strong and positive ($r = 0.93 - 0.99$; $P < 0.01$), accordingly the simpler models adaptable successfully.

Key Words: Beef Cattle, Multibreed, Breeding Value

W37 Effect of breed composition, temperament, and ELISA scores for paratuberculosis on phenotypic residual feed intake and growth in an Angus-Brahman multibreed herd. M. A. Elzo^{*1}, D. G. Riley², G. R. Hansen³, D. D. Johnson¹, R. O. Myer⁴, D. O. Rae¹, J. G. Wasdin¹, and J. D. Driver¹, ¹University of Florida, Gainesville, ²USDA-ARS STARS, Brooksville, FL, ³North Carolina State University, Plymouth, ⁴North Florida Research and Education Center, Marianna, FL.

Breed composition, temperament, and subclinical paratuberculosis in dams are factors that may have an effect on growth and feed efficiency in beef cattle. The objective of this research was to assess the effect of breed group (Angus (A), Brahman (B), Brangus, 3/4 A 1/4 B, 1/2 A 1/2 B, and 1/4 A 3/4 B), chute score (CS), exit velocity (EV), and ELISA scores for paratuberculosis in dams of calves (ES) on 5 feed intake and growth traits in bulls, heifers, and steers ($n = 461$) ranging from 100% Angus to 100% Brahman. Traits were post-weaning phenotypic residual feed intake (RFI), daily feed intake (DFI), feed conversion ratio (FCR), average daily gain (ADG), and weight gain (WG). Calves were assigned to pens in a GrowSafe automated feeding facility by sire group and sex, and fed a concentrate diet (cottonseed hulls, corn, molasses, and a protein, vitamin, and mineral supplement). The pre-trial adjustment period lasted 21 d. Individual daily feed intake was collected during the 70 d feeding trial. Weights and temperament traits were recorded every 2 weeks. Phenotypic RFI was computed as the difference between actual and expected feed intakes. Traits were analyzed using mixed models. Fixed effects were contemporary group (year-pen), RFI group (except when trait was RFI), age of dam, sex of calf, age of calf, B fraction of calf, heterozygosity of calf, mean CS, mean EV, ES, and residual. The RFI groups were high (RFI $>$ mean + 0.5 SD), medium (RFI between mean \pm 0.5 SD), and low (RFI $<$ mean - 0.5 SD; SD = 5.4 kg). Random effects were sire and residual. Brahman had lower ($P < 0.01$) RFI, DFI, and WG than Angus. Calves with higher mean EV had lower ($P < 0.04$) DFI and ADG than calves with lower mean EV. Neither mean CS nor ES were important for RFI, DFI, FC, ADG, and WG.

Key Words: Cattle, Feed Intake, Temperament

W38 Association between breed composition, phenotypic residual feed intake, temperament, ELISA scores for paratuberculosis, and ultrasound carcass traits in an Angus-Brahman multibreed herd. M. A. Elzo^{*1}, D. G. Riley², G. R. Hansen³, D. D. Johnson¹, R. O. Myer⁴, D. O. Rae¹, J. G. Wasdin¹, and J. D. Driver¹, ¹University of Florida, Gainesville, ²USDA-ARS STARS, Brooksville, FL, ³North Carolina State University, Plymouth, ⁴North Florida Research and Education Center, Marianna, FL.

Ultrasound carcass measurements are an important tool for preliminary assessment of carcass worth in beef cattle. Breed composition, phenotypic residual feed intake (RFI), temperament, and subclinical paratuberculosis in dams may affect calf ultrasound traits. The objective was to evaluate the association between breed group (Angus (A), Brahman (B), Brangus, 3/4 A 1/4 B, 1/2 A 1/2 B, and 1/4 A 3/4 B), RFI, chute score (CS), exit velocity (EV), ELISA score for paratuberculosis (ES), and ultrasound longissimus muscle area (ULMA), subcutaneous fat thickness (UFT), percent intramuscular fat (UPIF), and tenderness score (UTS) in calves ($n = 461$) ranging from 100% Angus (A) to 100% Brahman (B). Calves were allotted to pens (by sire group and sex) in a GrowSafe automated feeding facility (adjustment period = 21 d; feeding trial = 70 d), and fed a ration of corn, cottonseed hulls, molasses, and

a protein, vitamin, and mineral supplement. Individual feed intake was recorded daily, CS and EV biweekly, and ultrasound measurements at the end of the feeding trial. Phenotypic RFI was estimated as actual minus expected feed intake. Statistical analyses used homoscedastic mixed models. Fixed effects were contemporary group (year-pen), age of dam, RFI group (high: RFI > mean + 0.5 SD; medium: RFI between mean \pm 0.5 SD; low: RFI < mean - 0.5 SD; SD = 5.4 kg), sex of calf, age of calf, B fraction of calf, calf heterozygosity, mean CS, mean EV, and ES. Sire and residual were random effects. Brahman had lower ($P < 0.001$) ULMA, UFT, UPIF, and higher ($P < 0.001$) UTS values than Angus. Low RFI calves had lower UPIF ($P < 0.001$) than high and medium RFI calves. High ULMA was associated with low mean EV ($P < 0.015$). Mean CS and ES were non-significant for all ultrasound traits.

Key Words: Cattle, Feed Intake, Ultrasound

W39 Relationship between carcass traits and phenotypic residual feed intake, breed composition, temperament, and ELISA scores for paratuberculosis in an Angus-Brahman multibreed herd. M. A. Elzo*¹, D. D. Johnson¹, D. G. Riley², G. R. Hansen³, R. O. Myer⁴, D. O. Rae¹, J. G. Wasdin¹, and J. D. Driver¹, ¹University of Florida, Gainesville, ²USDA-ARS STARS, Brooksville, FL, ³North Carolina State University, Plymouth, ⁴North Florida Research and Education Center, Marianna, FL.

Identification of factors that permit animals to grow quickly and efficiently, and have desirable carcass characteristics remains a primary goal in beef production. The objective was to evaluate the relationship between 7 carcass traits and breed group (Angus (A), Brahman (B), Brangus, 3/4 A 1/4 B, 1/2 A 1/2 B, and 1/4 A 3/4 B), residual feed intake (RFI) group (high: RFI > mean + 0.5 SD; medium: RFI between mean \pm 0.5 SD; low: RFI < mean - 0.5 SD), chute temperament score (CS), exit velocity (EV), and dam ELISA score for paratuberculosis (ES) in 84 steers ranging from 100% A to 100% B. Carcass traits were hot carcass weight (HCW), longissimus muscle area (LMA), fat thickness (FT), kidney, pelvic, and heart fat (KPH), marbling score (MS), Warner-Bratzler shear force (SF), and tenderness score (TS). Records of ES were taken preweaning, and CS, EV, and RFI (actual minus expected feed intake) were obtained post-weaning during a 70-d feeding trial at a GrowSafe automated feeding facility. Subsequently, animals were sent to a South Texas feedlot, and commercially slaughtered at approximately 14 mm of FT. Carcass traits were collected at the slaughter facility, and SF and TS were obtained at the Florida Meat Processing Lab. Traits were analyzed using mixed models. Fixed effects were pen, RFI group, age of dam, age of calf, B fraction of calf, calf heterozygosity, mean CS, mean EV, and ES. Random effects were sire and residual. Brahman had lighter HCW ($P < 0.05$), smaller LMA ($P < 0.001$), lower MS ($P < 0.02$), higher SF ($P < 0.03$), and lower TS ($P < 0.001$) than Angus. High KPH was associated with high mean EV ($P < 0.03$). Mean CS, RFI group, and ES were non-significant for all carcass traits.

Key Words: Carcass, Feed Intake, Multibreed

W40 Genotype x environmental interaction to Nelore cattle raised in two Brazilian regions. J. C. DeSouza*¹, L. O. C. DaSilva², J. A. DeFreitas¹, C. H. M. Malhado³, A. Gondo², P. B. Ferraz Filho⁴, R. L. Weaber⁵, and W. R. Lamberson⁵, ¹Parana Federal University, Palotina Campus, PR, Brazil, ²Embrapa Beef Cattle Research Company, CNPqC,

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The objective this paper was to estimate genotype \times environment interaction between progeny of Nelore bulls in two different regions and estimate correlations of traits. Records were from calves raised in two Brazilian regions, Pará State (Region one) in North of Brazil and Bolsão (Region two) in Mato Grosso do Sul State. The regions were characterized by ARRUDA and SUGAI (1994) and differed by one or more of the following: production system, technology level, and natural resources such as climate, rain, topography and quality of the soil. The data were provided by the Brazilian Zebu Breeders Association (ABCZ) and by the National Beef Cattle Research Center (CNPqC) of the Brazilian Agricultural Research Corporation (Embrapa). The traits analyzed were: gain between birth and 120 d (GBWT_WT120, kg); weight at 120 days of age (W120, kg); gain between 120 d and 205 d (GWT120_WT205, kg); weight at 205 d (WT205, kg); gain from birth to weaning (GBWWT205, kg); weight at 365 d (WY, kg); and gain between 205 d and 365 d (GWT205WY, kg). The G \times E interaction was calculated using an animal model in the MTDFREML program. The variation accounted for by G \times E was between 0.42 (GWT205WY) and 0.93 (GW120_205, WT205, GBWWT205). The change in environment calculated using MME solutions of fixed effects (contemporary group) were 17.4 kg, and 20.7 kg; 37.3 kg, 26.9 kg; 59.1 kg and 25.5 kg, respectively, for weight 120 d, WT205 and WT365, for Pará and Bolsão. For WT120 the better trend was in Bolsão, but for others weights, in Pará. The genotype \times environment interaction (co)variance components resulted in an improved fit of the model for all traits. However, the large genetic correlations between regions or management systems (greater than 0.80) provides evidence for combining the production data of Nelore cattle from different regions and management systems across Brazil. In this case, specifically using sires in both regions should yield similar results. The result of evaluation of the environments showed a positive trend.

Key Words: Gain, Weight, Zebu

W41 Comparison of different nonlinear functions to describe beef cattle growth. L. G. Albuquerque*^{1,7}, S. Forni¹, M. Piles², A. Blasco³, L. Varona⁴, H. N. Oliveira^{5,7}, and R. B. Lobo⁶, ¹Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil, ²IRTA, Unidad de Cunicultura, Caldes de Montbui, Spain, ³Universidad Politécnica de Valencia, Valencia, Spain, ⁴Centre UdL-IRTA, Lleida, Spain, ⁵Universidade Estadual Paulista, Botucatu, Sao Paulo, Brazil, ⁶Universidade de Sao Paulo, Ribeirao Preto, Sao Paulo, Brazil, ⁷National Counsel of Technological and Scientific Development - CNPq, Brasilia, DF, Brazil.

The aim of the present work was to compare different nonlinear models for the prediction of adult weight of Nelore females. The growth curve parameters, their (co)variance components and environmental and genetic effects acting on these parameters were estimated jointly in a Bayesian hierarchical model. In the first stage of the hierarchy, four nonlinear equations were employed: Brody, Von Bertalanffy, Gompertz and Logistic. The analyses were carried out using three different data files to determine the consequences of having animals with few records. Three approaches were considered to describe the fitting errors standard deviations: constancy throughout the trajectory, linear increasing until 3 years of age and constancy thereafter, and nonlinear variation following the same function applied in the first stage of hierarchy. Models were

compared using Akaike's Information Criterion, Bayesian Information Criterion and Deviance Information Criterion. The fit at different points of the growth curve were compared applying the Gelfand's check function. The mean estimates of adult weight ranged from 531.78 to 586.89 kg. The Brody model provided higher estimates of asymptotic weight than the other models. Considering the same growth function, higher adult weight mean estimates were obtained when the fitting error variance was constant along the trajectory. None of the models was suitable to describe the fitting errors standard deviations at the beginning of the growth curves. All functions provided less accurate predictions at the beginning and predictions were more accurate after 48 mo of age. An increase in the number of animals that did not reach maturity did not impair the prediction of adult weights since growth curve parameters and their (co)variance components were estimated jointly. The Gompertz, Von Bertalanffy and Brody models were adequate to establish mean growth patterns and to predict the adult weight of Nelore females. The Brody model was more accurate in predicting the birth weight of these animals and presented the best overall goodness of fit.

Key Words: Bayesian Analysis, Longitudinal Data, Model Choice

W42 Principal component analysis of body measurements of Hanwoo. J. J Lee* and N. S Kim, *Chungbuk National University, Republic of Korea.*

Unlike carcass traits, body size measurements are composed of more than ten traits that are highly phenotypically correlated. The technique of principal component analysis was used to reduce a large number of variables to a smaller number of new variables (PCs) and characterizing cattle according to body shape. The objective of this study was to estimate and identify the combination values of principal components calculated using body measurements of Hanwoo (Korean Cattle). During 2004 to 2007, ten body measurements were collected by Korean Animal Improvement Association using 744 cattle records at yearling (12 months of age) and 411 cattle records at the end of test (30 months of age). These measurements included wither height (WH), rump height (RH), body length (BL), chest depth, chest width, rump length, hip width, thurl width, pin bone width and chest girth (CG). Phenotypic correlations among body measurements were estimated ranging from 0.23 to 0.97 at 1 year of age and from 0.25 to 0.93 at the end of test. The first principal component (PC1) indicated a weighted average of overall body measurements, accounting for 71.3% and 55.7% of the total variation for yearling and end of test, respectively. The two first PC had positive coefficients for all body measurements. The major sources of PC1, such as CG, BL, RH and WH, were similar for both periods of test. The second principal component (PC2) included withers height, rump height and body length with chest girth for both periods of test. PC2 accounted for slightly less than 20% of total variation for both periods of test. Further studies are needed to estimate genetic principal components through the simple reparametrization for animal breeding purposes.

Key Words: Hanwoo, Principal Component Analysis, Body Measurement

W43 Analysis of growth trait in Brazilian Simmental. M. G. Dib*¹, F. R. Araujo Neto², L. F. A. Marques³, and H. N. de Oliveira¹, ¹*Faculdade de Medicina Veterinária e Zootecnia - UNESP, Botucatu,*

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Estimates of variance components were obtained from a sample of 22,000 records of weaning weight (WW) and weight gains from weaning to yearling (GWY), yearling to 550-day (GY5), and 550 to 730-day (G57) of Simmental cattle raised in Brazilian farms. Data were collected by Brazilian Simmental Breeders Association. The pedigree data included information from 60000 animals. Variance components were estimated within a Bayesian context considering a multiple trait animal model with the fixed effects of contemporaries groups and age of dam and random direct and maternal genetic effects of animal, and maternal permanent environmental effect. Maternal (genetic and permanent) effects were included in the model only for WW. Analysis was performed using GIBBS2F90 (Misztal, 2006). Flat priors were assumed for variance components and fixed effects. Marginal densities of the variance components and other genetic parameters were estimated from the Gibbs output. Graphical inspection and the Gibanal program (Van-Kaam, 1998) were used for assessing convergence to the equilibrium distribution, the joint posterior. A burn-in period of 20,000 iterations was adopted, followed by 550,000 iterations with a thinning interval of 100 iterations. Hence, nominal sample size for post-Gibbs analyses was 5,500. Posterior means of heritability estimates were low: 0,16 (WW); 0,12 (GWY); 0,11 (GY5) and 0,16 (G57) for the direct effects and 0,05 for maternal effect (WW). For the environmental correlations the posterior means were near to zero, except for the between GY5 and G57 (0.20). For the genetic correlations values were high and positive ranging from 0,39 (between GWY and GY5) to 0,72 (GWY and G57). For yearling, 550 days and 730 days heritabilities calculated from the estimates were, respectively, 0,21; 0,26 and 0,34. Results confirm that under Brazilian conditions, selection for growth on Simmental cattle should be effective. Although Simmental cattle are recognized among beef breeds by their good maternal ability, genetic variation among cows plays minor role on purebred calf growth in Brazil.

Key Words: Heritability, Correlations, Variance Components

W44 Relationship between ultrasonically-measured beef cow carcass traits and lifetime productivity. L. A. Pacheco*, J. R. Jaeger, D. W. Moser, and K. C. Olson, *Kansas State University, Manhattan.*

The objective of our study was to determine if ultrasonically-measured intramuscular fat (IMF) and longissimus muscle depth (LMD) of replacement heifers was related to lifetime cow productivity, cow longevity and progeny performance. Angus heifers (n=160) were managed as a contemporary group and developed in a dry lot until breeding at 14 months of age. Heifer IMF and LMD were measured at approximately 205 d of age. Each year females were mass-mated following estrus synchronization and exposed to bulls 10 days later for the remainder of the 45 d breeding season. Following first breeding, heifers were managed in a spring-calving, native range-based production system with a 12-mo calving interval for the duration of the study (2004-2007). Animals were examined for pregnancy during August each year. Following pregnancy determination, non-pregnant females were removed from the herd. Calves were weighed at birth; weaning weights were adjusted for age of calf, age of dam, and sex of calf. Pregnancy rate as heifers was not related to IMF or LMD (P=0.12 and P=0.18, respectively) measured at 205 d of age. As mature cows pregnancy rate was not related to IMF or LMD (P=0.12 and P=0.18, respectively). Similarly, calf birth weights

were not related to dam IMF; however, calf birth weights increased ($P < 0.06$) as dam LMD increased. A 1 mm increase in dam LMD was associated with an increase of 0.15 kg in calf birth weight. Calf adjusted weaning weights were not related ($P = 0.13$) to dam IMF. Conversely, calf adjusted weaning weights increased ($P < 0.04$) as dam LMD increased. A 1 mm increase in dam LMD was associated with an increase of 0.78 kg in calf adjusted weaning weight. Calving date was not related to dam IMF or LMD ($P = 0.3$ and $P = 0.08$, respectively). These data were interpreted to suggest that increases in cow LMD were associated with greater birth weights and weaning weights of progeny. In contrast, cow IMF measured at 205 d of age was not related to pregnancy rate, calf birth weights, calf weaning weights, or calving dates.

Key Words: Intramuscular Fat, Longissimus Muscle, Beef Cows

W45 Estimates of genetic parameters for reproductive traits in Nelore cattle females. M. J. Yokoo^{*1}, L. G. Albuquerque¹, C. U. Magnabosco², J. F. H. Rodrigues¹, R. B. Lobo³, L. A. F. Bezerra³, and G. J. M. Rosa⁴, ¹São Paulo State University, Jaboticabal, São Paulo, Brazil, ²Embrapa Cerrados, Planaltina-DF, Brazil, ³University of São Paulo, Ribeirão-Preto-SP, Brazil, ⁴University of Wisconsin, Madison.

This study aimed to estimate genetic parameters of female reproductive traits (RTs) in Nelore cattle, including age at first calving (AFC), first calving interval (FCI), average calving interval (ACI), gestation length (GL), and days to conception (DC). Data on 3,203 females were analyzed using univariate animal models, and Bayesian inference was utilized for inferring variance components (VC). The models included the fixed effect of contemporary groups and the random effect of animals. Permanent environment was also included in the models as a random effect, except for the traits AFC and FCI. The table below shows the means of the posterior distributions of VC and heritability. Heritability estimates were relatively low, indicating that these RTs will respond slowly to individual selection. Therefore, considering that these traits are highly influenced by environmental factors, improvements on females' management will probably enhance reproductive indices more effectively. In Zebu breeds selection has been made primarily for growth traits and the only RT widely used in the selection indexes is scrotal circumference. Female RTs are also highly influenced by the producer management decisions and, consequently, are difficult to select. However, these RTs present a significant impact in the production system profitability. As the gains obtained by selection are permanent, selection indexes including one or some of these female RTs could be developed. For that, further studies considering the genetic correlation between these RTs and other economic important traits are necessary.

Table 1. Posterior distributions of variance components and heritability for reproductive traits in Nelore cattle females

VC \ Trait	DC	GL	AFC	FCI	ACI
Direct additive genetic	657.4	2.1	372.8	691.0	555.3
Permanent environment	748.4	3.8	—	—	307.2
Residual	4749.8	56.9	3681.7	8410.2	7870.3
Heritability (SEM)	.11 (.02)	.03 (.02)	.09 (.05)	.08 (.02)	.08 (.02)

SEM = standard error of the mean

Key Words: Bayesian, Heritability, Zebu

W46 An approach for considering genotype × environment interaction in the genetic evaluations of Zebu beef cattle in Brazil. L. O. C. Silva^{*2,3}, S. Tsuruta¹, J. K. Bertrand¹, A. Gondo², P. R. C. Nobre⁴, R. A. A. Torres, Jr.³, and C. H. C. Machado⁵, ¹University of Georgia, Athens, GA, ²EMBRAPA Beef Cattle, Campo Grande, Brazil, ³National Council for Scientific and Technological Development, Brasilia, Brazil, ⁴Foundation for Agric. and Environment Research, Campo Grande, Brazil, ⁵Brazilian Association of Zebu Breeders, Uberaba, Brazil.

The objective of this study was to evaluate the importance of genetic × environment interaction when doing genetic evaluations of Zebu beef breeds in Brazil. The data set of Tabapua breed included 72,331 actual weights at weaning (WW) and 43,567 at yearling (YW) from 94,612 animals in the pedigree file. These data were collected between 1979 and 2007 by the Brazilian Association of Zebu Breeders and sent to National Center for Research on Beef Cattle from EMBRAPA. The observed weights (WW and YW) were analyzed using AIREMLF90 under an animal model. Fixed effects included contemporary group (CG); difference of ages within the CG (linear covariable), performance group (PG), age group of cows (AGC: young and mature), age of cow at calving within AGC (fit as linear and quadratic), and the actual age of the animals at weighing were included in the model. CG, included a minimum of five animals, was defined by sex, farm, year, season, and feeding management. Random effects in the model were direct, maternal, maternal permanent environment, and sire × performance group interaction (SxPG). PG was created based on the average of CG for adjusted WW and YW. The population was divided in three performance groups (1-low; 2-medium; 3-high performance), each including 33% of the CG numbers. Preliminary results showed values of variance components for SxPG of 2.48 ± 0.66 (0.84% of residual variance-RV) for WW and 6.79 ± 1.84 (1.27% of RV) for YW. Correlations direct effect for sires with at least 20 progeny in high and low PG were 0.992 for WW and 0.978 for YW. Results are indication of no substantial reranking of sires in environments with different level of production.

Key Words: Zebu Beef Cattle, Growth Weight, GxE Interaction

W47 Phenotypic correlations between the ratio of body measurements and economic traits in Korean native beef cattle. S.-H. Oh^{*1}, T. White¹, and S.-D Kim², ¹North Carolina A&T State University, Greensboro, ²National Institute of Animal Science, South Korea.

The objective of this study is to investigate if there are any correlations between the ratio of body measurements and economic traits in the population of Korean native beef cattle. The data has been collected at the National Institute of Animal Science in South Korea. The body was measured every six months from 6 months of age to 24 months of age. The number of animals measured was 183 at 6, 12, and 24 months, and 663 at 18 months. The collected data included height at wither(BH), height at rump(RH), horizontal distance between top of shoulder and pins(BL), depth at chest(CHD), width of chest(CHW), horizontal distance between top of hips(HW), horizontal distance between projecting part of pelvises(TW), horizontal distance between pins(PW), distance in straight line between front of hipbone to pinbone(RL), and girth of chest(CHG) as body measurements. In the meantime, the number of animals having the economic traits was 2706. The economic traits consisted of body weight(BW), backfat(BF), carcass weight(CW), index of yield(YGI), and the percentage of dressing(DP), which were measured at slaughter. Pearson correlations in SAS 9.1.3 were used to analyze the data. Some of the ratio of body measurements showed

30-40% of phenotypic correlation with economic traits. The ratio of BH/CHD had negative correlations with BW, BF, CW, and DP, which were -0.29, 0.24, -0.31, and -0.20, respectively. The ratio of RH/CHD also showed negative correlations with BW, BF, CW, and DP, which were -0.35, -0.27, -0.38, and -0.22, respectively. As a result, there were phenotypic correlations between the ratio of body measurements and economic traits, which means that producers may use the ratios as a selection tool for better individuals. Further study will be needed to investigate if there are genetic correlations among them.

Key Words: Correlation, Body Measurement, Economic Trait

W48 Polymorphism of IGF-I gene and its association with growth traits in chicken. B. W. Wang^{*1}, X. X. Wei¹, M. A. Zhang¹, B. Yue¹, L. Wang¹, Z. G. Yang^{1,2}, S. H. Yu¹, Y. C. Wang¹, L. Z. Jing¹, and G. L. Liu¹, ¹Qingdao Nongye University, Qingdao, Shandong Province, China, ²Feed Research Institute of Chinese Academy of Agricultural Sciences, Beijing, China.

In order to study the polymorphism of 5' region of the insulin like growth factor I (IGF-I) gene in chicken and the association with growth traits, the genetic polymorphism of IGF-I gene in 372 Luxi game chicken (12 weeks) and 423 Langya Chicken (12 weeks) was detected by PCR-RFLP, the relationships between genotypes and meat traits, egg traits, belligerence were analyzed with linear model. Frequencies of IGF-I genotypes (AA, AB, BB) were 0.3688, 0.4965, 0.1348 in Langya Chicken and 0.4516, 0.3710, 0.1774 in Luxi game chicken respectively after PCR products had been cut by Pst I enzyme. The A to G transition was detected at the 5' region of IGF-I gene by sequencing the homozygotes (GenBank accession number: EF198877, EF488284). The observed genotype distribution was not different from the expected distribution under the assumption of the Hardy-Weinberg equilibrium for the IGF-I allele of two kinds (Langya Chicken, $\chi^2 = 0.359$, $P > 0.05$; Luxi game chicken: $\chi^2 = 2.422$, $P > 0.05$). For Langya Chicken, AA genotype had the highest least square means of meat traits indexes such as body weight (1080±34 g), eviscerated weight with giblet (761.1±10.5g), leg muscle weight (126.1±7.6g) and chest muscle weight (104.1±6.0g); AB genotype had the highest least square means of egg traits indexes. For Luxi game chicken, AA genotype had the highest least square means of stronger belligerence indexes such as neck length (17.93±1.82cm) and shank length (9.01±0.69cm); BB genotype had the highest least square means of meat traits index such as body weight (2.41±0.06kg). The results showed that the genetic polymorphism of the 5' region of IGF-I gene had different genetic effects in different breeds. The experiment provided theoretical foundation for IGF-I gene's distribution state and further utilization of local chicken breeds in China.

Key Words: Chicken, IGF-I Gene Polymorphism, Growth Traits

W49 Genetic and non-genetic factors affecting broiler chick weight at hatch in South West Nigeria. O. T. F. Abanikannda¹, A. O. Leigh¹, O. N. Coker³, O. T. Adeseko^{*1}, O. Orunmuyi⁴, A. L. Dare², I. S. Okoya¹, and I. O. Ola-Gbadamosi¹, ¹Lagos State University, Ojo, Lagos State, Nigeria, ²Obasanjo Farms Nigeria Limited, Igboora, Oyo State, Nigeria, ³S & D Farms Nigeria Limited, Odeda, Ogun State, Nigeria, ⁴Ahmadu Bello University, Zaria, Kaduna State, Nigeria.

Measurable productivity traits of animals are influenced by both genetic and non-genetic components. Most performance traits of broilers like

other animals are also quantitative in nature. The broiler breeds investigated were Anak, Marshall and Ross, and the eggs were sourced from reputable parent stock farms. The effects of the following factors on chick weight were investigated; chick sex (X), breed (B), hen's age (A), egg weight (E), egg length (L), egg width (W), egg weight at candling (C). The statistical model describing this study is given as $Y_{ijklmno} = \mu + X_i + B_j + A_k + L_l + W_m + C_n + \epsilon_{ijklmno}$. With the exception of chick sex, egg length and egg width which were not significant ($P > 0.05$), all other factors were highly significant ($P < 0.001$) on chick weight. All the factors studied exhibited similar trend across the three breeds, with Anak breed having the least and Ross breed the highest. Breed alone accounted for 48.32 percent of total variation explained, while egg weight and hen's age contributed 32.40 and 16.53 percent respectively. The Ross breed significantly had the highest values for all the measurements taken, while the Marshall breed was intermediate between the Ross and the Anak breeds. Considering the direct relationship that exist between the chick's initial weight, average daily gain and final weight, the Ross breed promises to be a better breed in terms of meat yield.

Table 1. Effect of breed on some egg measurements[†]

Breed	N	Egg Weight (g)	Egg Length (mm)	Egg width (mm)	[‡] Weight at Candling (g)	Chick Weight (g)
Anak	361	58.66±0.28 ^c	57.38±0.14 ^b	42.93±0.08 ^c	50.60±0.27 ^c	39.19±0.24 ^c
Marshall	361	60.33±0.34 ^b	57.40±0.17 ^b	43.62±0.09 ^b	52.56±0.31 ^b	41.29±0.26 ^b
Ross	282	66.02±0.30 ^a	59.65±0.15 ^a	45.41±0.10 ^a	58.27±0.30 ^a	45.45±0.30 ^a
Combined	1004	61.33±0.21	58.02±0.09	43.87±0.86	53.46±0.20	41.71±0.17

[†]Means differs significantly ($P < 0.05$). [‡]Candling done at 18th day

Key Words: Egg Weight, Weight at Candling, Chick Weight

W50 Boar fertility and semen quality characteristics in lines of pigs selected for component traits of female reproduction. B. A. Freking^{*1}, P. Purdy², C. Welsh², S. Spiller², and H. Blackburn², ¹USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, ²National Animal Germplasm Program, Fort Collins, CO.

Selection for 11 generations for ovulation rate (OR) or uterine capacity (UC) resulted in significant changes in component traits of litter size. Our objective was to characterize male fertility as a correlated response to selection compared to an unselected control line (CO). Each boar (n=60) from two replicate seasons was collected twice. The sperm-rich fraction was obtained and volume and concentration of sperm cells was measured to estimate total sperm production. Each ejaculate was extended 1:3 v/v with Androhep Plus (Minitube, Verona, WI) and packed for shipping to the NAGP lab for processing into frozen straws. Semen quality was measured by computer assisted semen analysis at three time points: fresh (F), 24 h after extender added (E), and post-thaw (PT). A mixed model analysis of variance was applied to the data. Fixed effects of replicate, line and two-way interactions were fitted. The random effect of boar within line × replicate was used to test line differences. Sperm concentration was not different ($P = 0.18$) among the lines (0.594, 0.691, and 0.676 *10⁹ cells/ml) for CO, OR, UC lines, respectively. Significance ($P < 0.05$) was detected for volume of the sperm-rich fraction, greatest for OR (86.4 ml), intermediate for UC (75.6 ml), and lowest for CO (70.2 ml). Line differences were thus detected ($P < 0.02$) for total sperm production, greatest for OR (54.9 *10⁹), intermediate for UC (48.7 *10⁹) and lowest for CO (40.5 *10⁹). A higher percentage of progressively motile sperm and also higher estimates of sperm velocity only at time point E ($P < 0.01$) were detected in favor of CO. Estimates of motility,

velocity, and activity measured on F and E time points were moderately and positively correlated with estimates obtained PT. Selection for component traits of female reproduction has had a favorable effect on total sperm production of boars.

Key Words: Fertility, Pigs, Semen Quality

W51 Association analysis of candidate SNPs on reproductive traits in swine. L. A. Rempel*, J. W. Holl, and G. A. Rohrer, *USDA, ARS, US Meat Animal Research Center, Clay Center, NE.*

Being able to identify young females with superior reproduction traits would have a large financial impact on commercial swine producers. Previous studies have discovered SNPs associated with economically important traits such as litter size, growth rate, fat deposition, and feed intake. The objective of this study was to test candidate SNPs for sow prolificacy production traits, including: age at puberty (AGEP, n = 963), ovulation rate (OR, n = 1,122), weaning to estrus interval (WEI, n = 744), total pigs born (TB, n = 1,924), number born alive (NBA, n = 1,924), number born dead (NBD, n = 1,924), and number mummified (MUM, n = 1,924) and determine association of these traits in gilts and sows of a Landrace-Duroc-Yorkshire composite population. Candidate SNPs included estrogen receptors (ESR) 1 and 2; prolactin receptor (PRLR); alpha-D-mannosidase (MAN); leptin (LEP); and melanocortin 4 receptor (MC4R). Genotypes were verified using GenoProb. Association analyses regressed additive (A), dominant (D), and imprinting (I) SNP effects on each trait. ESR2 A949G was associated with AGEP (A = 2.18 d; P < 0.025). PRLR T1528A was associated with AGEP (I = 3.62 d; P < 0.001). PRLR C1217T was associated with TB (A = -0.31 piglets; P < 0.017). An association was identified between MUM and PRLR G1439A (A = -0.09 piglets; P < 0.003). Age of puberty was also associated with MAN A1426G (A = -2.47 d; P < 0.008 and I = 1.99 d; P < 0.06). MC4R A1426G was associated with WEI (A = 0.86 d; P < 0.003) as well as MUM (D = -0.130 piglets; P < 0.001 and I = -0.06 piglets; P < 0.046). No significant associations were detected for ESR1 or LEP SNPs. These results indicate that SNPs previously linked to more traditional production and growth traits may also serve in the capacity to assist with selection of young females for superior reproductive performance.

Key Words: Pig, SNP, Reproductive Traits

W52 Analysis of founder-specific inbreeding depression on Landrace sow longevity. J. Casellas*, L. Varona, N. Ibáñez-Escriche, and J. L. Noguera, *Genética i Millora Animal, IRTA-Lleida, Lleida, Spain.*

Inbreeding depression is a biological aspect mainly related to the recessive genetic load carried by a population. When this genetic load is unevenly distributed among founder genomes, heterogeneity of founder-specific inbreeding depression (FSID) could be anticipated, although this phenomenon has never been evaluated on sow longevity (SL). The objective of this study was to ascertain whether FSID impairs SL. Longevity data of 4,226 hyperprolific Landrace sows (13.28 ± 0.06 piglets per litter) were recorded in a selection herd registered in the Pig Spanish Data Bank (BDporc) between years 1988 and 2006. Sow longevity was measured as the time interval between the first mating

until culling or death (complete records), whereas records from sows still alive at the end of data collection were considered as censored. Full pedigree included 1,082 founders and 5,273 descendants, and only 35 founders contributed inbred descendants. Sow longevity was analyzed under a Weibull piecewise proportional hazard model solved through Bayesian inference. Prior distribution for FSID effects was modeled as asymmetric Gaussian to allow for skew patterns. Modal (and highest posterior density region at 95%) estimates for ρ and λ baseline parameters were 0.927 (0.881 to 0.973) and 0.00008 (0.00006 to 0.00011), with three cut points placed at 296 d (289 to 300), 492 d (477 to 499) and 1,012 d (1,008 to 1,017). Additive genetic variance for SL was 0.312 (0.248 to 0.384; $h^2 = 0.159$), whereas the variance component for the FSID effects was 0.005 (0.001 to 0.009), revealing a substantial degree of between-founders heterogeneity. Posterior distribution for FSID effects was asymmetric with an over-expressed right-tail, where founder-specific modal estimates for FSID effects ranged between -0.006 (-0.084 to 0.076) and 0.076 (0.005 to 0.148) for each 1% inbreeding. These results corroborated a wide and skew distribution of FSID effects, with null or negative effects on SL.

Key Words: Asymmetry, Inbreeding Depression, Sow Longevity

W53 SNPs of LEP and FABP4 genes in *Bos indicus* and crosses: Segregation and association with meat traits. M. G. Dib*¹, R. A. Curi¹, L. A. L. Chardulo², A. C. Silveira¹, M. D. B. Arrigoni¹, and H. N. de Oliveira¹, ¹Faculdade de Medicina Veterinária e Zootecnia - UNESP, Botucatu, SP, Brazil, ²Instituto de Biociências - UNESP, Botucatu, SP, Brazil.

Fat deposition is one of the most important factors affecting carcass and meat quality in beef cattle. Leptin and fatty acid binding protein 4 play important roles on fat metabolism. The objectives of this study were to estimate, in beef cattle of different genetic groups, the allele and genotype frequencies of SNPs located in the Leptin (LEP) and the fatty acid binding protein 4 (FABP4) genes and to evaluate associations between the polymorphisms and meat traits. One hundred and forty seven animals (46 Nellore (*Bos indicus*), 41 Canchim (5/8 *Bos taurus* + 3/8 *B. indicus*), 26 Rubia Gallega x Nellore crossbred (1/2 *B. taurus* + 1/2 *B. indicus*), 19 three-way cross Brangus (9/16 *B. taurus* + 7/16 *B. indicus*) and 15 three-way cross Braunvieh (3/4 *B. taurus* + 1/4 *B. indicus*)) were genotyped by PCR-RFLP and recorded for backfat thickness, total lipids, marbling score, ribeye area and shear force. Data analyses were performed with a linear model that included combined effect of contemporary and genetic group and genotypes effect. The A and G alleles of the LEP/BsaAI polymorphism (Y11369.1: G1620A) presented homogeneous distribution in all of the genetic groups but no association with the phenotypes were found. The FABP4/MspAII locus (AAFC01136716.1: G7516C) was found to be fixed for the C allele in *B. indicus* and in the crossbreed animals the C allele was found in very high frequency. Besides not being informative in *B. indicus* animals, the FABP4/MspAII polymorphism didn't show relevant association with the studied traits in the crossbreed animals. In spite of the importance of the studied genes in fat metabolism, it was not possible to find evidences supporting association between the studied polymorphisms and meat traits.

Financial support: Fapesp and CNPq

Key Words: Polymorphisms, Candidate Gene, Fat Deposition

W54 Markers on bovine chromosome 20 associated with fat related traits and incidence of contracting bovine respiratory disease. M. D. Garcia*¹, L. Matukumalli², T. L. Wheeler¹, S. D. Shackelford¹, M. Koohmaraie¹, T. P. L. Smith¹, and E. Casas¹, ¹USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE, ²USDA-ARS, Beltsville Animal Research Center, Beltsville, MD.

The objective of this study was to assess the association of single nucleotide polymorphism (SNP) markers with incidence of bovine respiratory disease (BRD) and fat related traits. Steers from the Cycle 7 of the Germplasm Evaluation Program (GPE7; n=565) were used. The GPE7 population comprises animals derived from 7 breeds: Angus, Charolais, Gelbvieh, Hereford, Limousin, Red Angus, and Simmental. Markers were located between centimorgan 14.5 and 20.3 on bovine chromosome 20 (BTA20). One SNP was associated with incidence of BRD and yield grade ($P < 0.008$). Animals inheriting the CT genotype had the lowest yield grade (2.82 ± 0.09), and the highest incidence of BRD (0.33 ± 0.04) when compared to those inheriting the CC genotype (3.12 ± 0.19 , and 0.17 ± 0.02 for yield grade and incidence of BRD, respectively). Animals inheriting the TT genotype were observed in low frequency (n=11) and were excluded from the analysis. A second SNP was associated ($P < 0.007$) with incidence of BRD, dressing percentage and estimated kidney, pelvic and heart fat percentage (KPH). Steers inheriting the AG genotype had the lowest incidence of BRD and KPH (0.15 ± 0.03 and 2.22 ± 0.05 , respectively) when compared to animals inheriting the AA genotype (0.28 ± 0.03 and 2.39 ± 0.05 , respectively). Animals inheriting the GG genotype had an intermediate incidence of BRD (0.21 ± 0.03), when compared to animals inheriting the AA and AG genotypes, and similar KPH as those inheriting the AA genotype (2.35 ± 0.05). Animals inheriting the AG and GG genotypes had lower dressing percentages (62.2 ± 0.13 and 62.2 ± 0.12 , respectively) when compared to animals inheriting the AA genotype (62.8 ± 0.13). Further evaluation of SNP markers in this region of BTA20 is needed to identify optimal marker combinations associated with BRD and fat related traits.

Key Words: Bovine Respiratory Disease, Carcass Traits, SNP

W55 Identification and comparison of a second stearoyl-CoA desaturase gene in pigs, sheep, and chickens. A. J. Lengi and B. A. Corl*, *Virginia Polytechnic Institute and State University, Blacksburg.*

Stearoyl-CoA desaturase (SCD) is an important enzyme of lipid metabolism controlling the ratio of monounsaturated to saturated fatty acids in body tissues. SCD catalyzes the addition of a *cis*-9 double bond to several saturated fatty acid substrates. Multiple isoforms have been described in some species, especially in mice which have four. Humans have two isoforms: SCD1 with homology to the SCD isoforms present in rodents, and SCD5 which appears to be a distinct gene not found in the mouse. We recently identified SCD5 in the cow. Here we report the identification of SCD5 in pigs, sheep, and chickens. We used 5' and 3' rapid amplification of cDNA ends to identify and sequence SCD5 transcripts. Sequencing revealed that the SCD5 gene has greater guanine and cytosine content than SCD1, especially in the 5' region. Aligning the amino acid sequences of human, cow, sheep, pig, and chicken SCD5 reveals high homology among the sequences, but less homology with SCD1 amino acid sequences. The amino acid sequence includes characteristic histidine motifs present in desaturase enzymes. Interestingly, the PEST-find algorithm showed that SCD5 lacks the PEST sequences present in the SCD1 protein that control its rapid degradation. We compared the

tissue specific mRNA expression of SCD1 and SCD5 by real-time PCR. Tissue expression of SCD1 was greatest in lipogenic tissues: adipose tissue of sheep and pigs and the liver of chickens. SCD5 had a different expression profile with consistently high expression in the brain of pigs, sheep, and chickens. This report expands the number of species known to have the SCD5 gene and is the first report of the SCD5 gene outside of mammals. These data tend to indicate that SCD1 and SCD5 are the result of a gene duplication event early in evolution.

Key Words: Stearoyl-CoA Desaturase, Brain, Fatty Acids

W56 Differential expression of cyclic AMP-responsive element modulator (CREM) transcription factor isoforms during boar spermatogenesis and in transcriptionally silent boar spermatozoa. S. Green* and B. L. Sartini, *University of Rhode Island, Kingston.*

Identifying the origins of male fertility variation can lead to greater reproductive efficiency in livestock. Recent studies have demonstrated that temporal regulation of functional isoform expression by alternative splicing and polyadenylation is necessary for development of the male germ cell. Specifically, differential expression of the CREM (cAMP-responsive element modulator) transcription factor isoforms occurs in spermatogonia, spermatocytes and spermatids. Aberrant CREM isoform expression has been correlated with subfertility and infertility in humans, mice, and horses. Although species variation in developmental CREM isoform expression has been reported, CREM gene expression during boar spermatogenesis has not been investigated. Using RT-PCR and 3' rapid amplification of cDNA ends (RACE) primers designed from the reported human CREM sequence, we amplified CREM in boar testis from different developmental stages. The predicted full-length mRNA transcript size of adult boar CREM is 1090 bp while prepubertal boar testis contains a predominant CREM mRNA transcript that is 690 bp in length. From these results, alternative isoforms of CREM are expressed in boar testis at different developmental ages. Additionally, we have amplified a 690 bp CREM transcript from the pool of mRNA in transcriptionally silent boar spermatozoa. The boar spermatozoa CREM transcript contains a poly(A) tail and further analysis will determine if the spermatozoa CREM transcript is a remnant from spermatogenesis or translated at a further stage. Understanding the regulation of gene expression during boar spermatogenesis will identify sources of male fertility variation in livestock.

Key Words: Boar, Spermatogenesis, mRNA

W57 Molecular analysis of the Mexican hairless pig in the Yucatan Peninsula. F. Cetz-Solis², A. Sierra-Vasquez*¹, A. Da Silva-Mariante⁴, S. Rezende-Paiva⁴, C. Cruz-Vazquez², and C. Lemus-Flores³, ¹Instituto Tecnológico de Conkal, Conkal, Yucatan, Mexico, ²Instituto Tecnológico el Llano, Aguascalientes, Mexico, ³Universidad Autónoma de Nayarit, Tepic, Nayarit, Mexico, ⁴Embrapa Cenargen, Brasília, DF, Brasil.

Mexican hairless pig (MHP) is a descendant of introduced breeds from Spain about 500 years ago, and it is in danger of extinction at the present time. The objective of this study was to characterize at molecular level the genetic variability of MHP in the Peninsula of Yucatan. Ten loci microsatellites were used in 52 unrelated pigs from ten location distrib-

uted in three states, Yucatan (n=31), Campeche (n=10) and Quintana Roo (n=11). Genetic diversity for animals in each state was estimated by the unbiased average heterozygosity values (H_o and H_e) and the allele number. Polymorphic information content (PIC) was estimated based on allelic frequencies. Nei's standard genetic distances were used to reveal the genetic relationship among state populations. Campeche pigs presented the highest H_o and H_e values (0.59 ± 0.05 and 0.64 ± 0.17), whereas Yucatan pigs had the lowest values (0.50 ± 0.03 y 0.52 ± 0.26). Eight microsatellites loci (considering all animals) were polymorphic, ranging from 0.42 to 0.88; SO355 and SO227 had low polymorphic

values (0.15 and 0.29, respectively). The average PIC for animals in the Peninsula of Yucatan was 0.54. A genetic relation among pigs from the three states was found, with pigs from Yucatan and Quintana Roo being more closely related. This evaluation found a lower genetic diversity than other related studies in México. This work should be considered in order to design conservation programs for MHP; especially for pigs from the Campeche and Quintana Roo regions.

Key Words: Microsatellites, Mexican Hairless Pig, Genetic Diversity