

ABSTRACTS
AMERICAN DAIRY SCIENCE ASSOCIATION
AMERICAN SOCIETY OF ANIMAL SCIENCE
POULTRY SCIENCE ASSOCIATION

July 24–29, 2004
St. Louis, MO
Monday July 26, 2004

POSTER PRESENTATIONS

* Author Presenting Paper

Breeding and Genetics

M1 The impact of herd opportunity and milk recording periods in estimating lifetime net income. E. Yook*, R. E. Pearson, and B. G. Cassell, *Virginia Tech, Blacksburg.*

The Purpose of this study was to determine how well estimators of lifetime net income based on 305 lactation yields and a ten year opportunity (RNI305.10) and based on complete lactation data but a five year opportunity (RNIc.5) predict the estimate based on complete lactations and a ten year opportunity (RNIc.10). Previous studies have used shorter (five year and seven year) opportunity periods and only production through 305-d to estimate a cow's lifetime net income. Records for 22,854 cows in Virginia herds born in 1988, 1990, and 1992 from the Dairy Records Management Systems (DRMS) in Raleigh, North Carolina were used. The relative net income (RNI) function included total milk, fat, and protein income - feed cost for production + net value of calves + net cull value - rearing cost - ((daily cost for labor, maintenance feed, supplies, and fixed expenses) × days in herd). Each RNI was calculated using milk-fat-protein pricing. A cow's RNIc.10 was calculated using all production initiated prior to her tenth birthday. All lactations initiated prior to her fifth birthday were used to calculate a cow's RNIc.5. We calculated an RNI305.10 using only milk produced during the first 305-d of every lactation initiated prior to tenth birthday. Total milk, fat, and protein based on c.5 were 20845kg, 737kg, and 666kg; those based on c.10 were 28539kg, 1009kg, and 905kg; finally, those based on 305.10 were 25304kg, 883kg, and 792kg. The means of RNIc.5, RNIc.10, and RNI305.10 were \$1445, \$2279, and \$1857, respectively. Regression analyses including herd and birth year in the model were used to estimate the regression of RNIc.10 on RNIc.5, and RNIc.10 on RNI305.10. The resulting regression coefficients were \$1.52 and \$1.14 explaining 68% and 96% of the variation of RNIc.10. Using RNIc.10 as the measure to estimate lifetime profit is strongly recommended over the two alternatives tested.

Key Words: Lifetime Net Income, Relative Net Income, Herdlife Opportunity

M2 Genotype by environment interactions in the association among milk yield, age and body weight at first calving in Holstein cows. R. Ruiz-Sánchez¹, H. Castro-Gómez², F. Sánchez y GF¹, and H. Castillo-Juarez*¹, ¹Universidad Autónoma Metropolitana, Unidad Xochimilco, ²Universidad Nacional Autónoma de México.

This study evaluated the effect of herd environment on the genetic and phenotypic relationships of milk yield (MEM) on age (AFC) and body weight at first calving (BW) in primiparous Holstein cows. Data analyzed were 248,230 first parity records of Holstein cows calving from 1987 to 1994, daughters of 588 sires in 3,042 herds in the US. Herds were classified into low and high environment classes. Genetic parameters were estimated with bivariate linear mixed models using the multiple trait derivative free software (MTDFREML). Heritability for AFC and BW were 0.33 ± 0.01 and 0.07 ± 0.01 in high environment herds and 0.20 ± 0.01 and 0.07 ± 0.01 in low environment herds respectively. Genetic correlations between MEM and AFC were -0.52 ± 0.02 and -0.31 ± 0.03 in high and low environment classes, whereas between MEM and BW in both classes were similar (-0.19 ± 0.06 and -0.21 ± 0.06 , respectively). Correlated responses estimated per 1000 kg of genetic gain in MEM for high and low herd environment classes were -22.1 and -19.3 days for AFC and -0.81 and -0.41 kg BW, respectively. BW information, as provided by AIPL (USDA) is inaccurate. Hence, results related to this trait are not conclusive. Different values of heritability for AFC, as well as changes in the genetic correlation between MEM and AFC across environments, indicated genotypic by environment interaction. Thus selection for MEM correlates with reduced AFC, but expected correlated response changes across environments.

Key Words: Genotype by Environment Interaction, Age at First Calving, Genetic Parameters

M3 Heritability of body weight at 130 days from hatching in the Pacific white shrimp (*Litopenaeus vannamei*) using an animal model. H. Castillo-Juarez*, *Universidad Autonoma Metropolitana, Unidad Xochimilco.*

To estimate the heritability of body weight (BW) in the Pacific white shrimp, *Litopenaeus vannamei*, an experiment was conducted using 101 families in two commercial units of a Mexican hatchery and two prawn

population densities (9.1/m² and 14.8/m²). These 101 families consisted of 17296 prawns, sibs from 51 sires and 101 dams. Prawns were injected with a colored, elastomer tag to identify families, which allowed mixing of families for performance evaluation. Prawns were individually weighted at an average of 130 days from hatching. Small differences in days from hatching were related to management practices. BW family phenotypic mean (s.d) was 18.2 g (2.3), ranging from 15.6 to 22.5 g. Females were 0.5 g heavier than males. Breeding values were calculated for all prawns using mixed model methodology with an animal model and MTDFREML software. The model included fixed effects of days from hatching and sex, plus commercial unit, population density and the animal additive genetic effect as random effects. BW heritability was 0.57. Since genetic selection in shrimp industry is based on family selection, families were ranked using BW phenotypic means, BW least square means and BW breeding value means. The rank correlation between family phenotypic means and family breeding value means was 0.64, and between least square means and breeding value means was 0.87. BW family breeding value means ranked from -1.921 to 3.527 g. Family breeding value means allow to better select families and apply different selection intensities within family to increase genetic gain in an optimal way.

Key Words: Shrimp, Genetic Parameters, Animal Model

M4 Merit of obtaining genetic evaluations of milk yield for each parity on Holstein bulls. H. D. Norman, J. R. Wright*, R. L. Powell, and P. M. VanRaden, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Modeling separate Predicted Transmitting Abilities (PTA) for each parity is becoming more frequent internationally. A concern when using a single trait genetic evaluation model is that changes in PTAs could be larger than expected for bulls whose daughters deviate considerably from the typical response due to aging. The objective of this research was to examine how difference in rate of maturity of bulls daughters impacts changes in bull evaluations across time. The 305-d milk records for Holsteins first calving between 1960 and 1998 were used to calculate 12 tailored PTAs for each bull. Tailored PTAs (controlled by parity combinations and run dates) were calculated for 1996 to 1999 run years using records of cows first calving prior to each January. Four annual evaluations included only first lactations on daughters and contemporaries (PTA₁). Four more included the first two lactations available (PTA₁₋₂), and the last four included the first three lactations (PTA₁₋₃). The three PTAs (different parities) for each year included cows first calving by the same cutoff date. Tailored PTAs had more uniformity across years in mean records/daughter than published PTAs. Stability (absolute differences, standard deviations (SD) of differences, and correlations between bull evaluations) across time was compared. Bulls born after 1984 having ≥ 500 daughters were examined because of their high precision and recent activity. SD of bull differences in PTA₁, PTA₁₋₂, and PTA₁₋₃ for milk between 1996 and 1997 were 28, 28, and 27 kg compared to 63 kg for the published evaluations. Similarly, SD between 1996 and 1999 were 36, 32, 32, and 79 kg, respectively. PTA₁₋₂ was usually intermediate to PTA₁ and PTA₁₋₃ for any bull having a large difference between PTA₁ and PTA₁₋₃. Results suggest that modification of the current evaluation model should reduce fluctuations in PTAs for individual bulls across time and should also improve the accuracy of evaluations.

Key Words: Milk Yield, Parity, Lactation Number

M5 Joint genetic evaluation of male and female fertility using longitudinal binary responses. R. Rekaya and T. Averill*, *Department of Animal and Dairy Science, University of Georgia, Athens.*

The improvement or at least the maintenance of herd fertility has become a major objective in several genetic improvement programs worldwide. Several types of responses are used in fertility evaluation including binary, count and continuous traits. Consequently, different models and methodologies used to analyze reproductive performances. Independently of the trait or methodology used not all sources of variation are accounted for making a joint evaluation of male and female fertility unfeasible. However, a longitudinal model that accounts for all breeding events makes a better use of available information and allows for joint

evaluation of males and females. Furthermore, as a by product of longitudinal analysis, several new selection criteria could be computed and used rather than the single breeding value. In this study, insemination records from dairy herds in California, generated between 2002 and 2003 and provided by AgriTech Analytics were used. After editing, the data consisted of a total of 369,353 insemination records with an average of 1.76 inseminations per cow. A random regression model at the liability scale was used to model the success (failure) of insemination events. The models included herd-year, technician and month of insemination as fixed effects and service sire, quadratic regression on days of milk, permanent environmental effects and residual terms as random effects. The heritability of success of insemination increased slightly with days in milk and ranged between 0.04 -0.055. The service sires and permanent effects variances were 0.01 and 0.012 respectively. Although small, these estimates are within the range of reported estimates for reproductive traits and indicate the possibility of improvement of male and female fertility through selection. Several new selection criteria such as the probability of conception after first insemination, after 3 insemination or the probability of no conception after a number of days were computed and can be used for selection decisions.

Key Words: Fertility, Male, Female

M6 Evaluation of net energy efficiency for lactation and economic performance as selection criteria in dairy cattle. P. Zamani*¹, S. R. Miraei Ashtiani¹, A. Naserian², A. Nik Khah¹, and M. Moradi Shahrabak¹, ¹*Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran,* ²*Department of Animal Science, Faculty of Agriculture, University of Ferdowsi, Mashhad, Iran.*

Improvement of feed efficiency and related economic performance is of great importance in dairy farming. This study was conducted to evaluate the net energy efficiency and economic performance of lactation as selection criteria for dairy cattle. 2589 monthly records collected from 723 lactating cows in 3 dairy farms were analyzed for the mentioned purpose. Different usages of energy were estimated, using National Research Council (NRC) models. A multivariate animal model including fix effects of herd-year-season, parity number and lactation stage, and random effects of animal genetic and permanent environment was adopted for estimation of genetic and phenotypic parameters, using Derivative Free approach of Restricted Maximum Likelihood (DFREML). Heritability estimates of milk yield, 3.2 percent fat corrected milk, net energy efficiency, gross income and variable profit, were 0.30, 0.31, 0.32, 0.34, 0.24 and 0.29 respectively. The results of this study showed that, the genetic factors considerably contribute to the feed efficiency and economic performance of lactating cows. However if measuring the feed efficiency is not feasible, considering 3.2 percent fat corrected milk in selection index may be an effective way for indirect selection and improvement of feed efficiency and economic performance in dairy cows.

Key Words: Dairy Cattle, Net Energy Efficiency, Fat Corrected Milk

M7 Estimates and relationships of growth curve parameters in NDama cattle. O. Mgbere^{1,2}, I. Imumorin*³, O. Olutogun¹, and A. R. Abdullah¹, ¹*Dept of Animal Science, University of Ibadan, Ibadan, Nigeria,* ²*Dept of Animal Science, Rivers State University of Science & Technology,* ³*Dept of Biology, Valdosta State University.*

Weight-age records of purebred NDama, a West African taurine beef cattle breed, were used to estimate growth curve parameters based on non-linear regression models of Brody, Von Bertalanffy and Richards and phenotypic relationships of the parameter estimates within each model. Records covered from birth to 69 months of age for 549 males and up to 84 months for 670 females accumulated over a 16-yr period at Fashola Cattle ranch in Oyo, Nigeria. Least squares estimates of asymptotic weight (A) from the models ranged from 386 \pm 9.8 kg and 254 \pm 4.6 kg in Von Bertalanffys function (model II) to 441 \pm 33.2 kg and 273 \pm 10.6 kg in Richards function (Model III) for NDama bulls and cows with a corresponding average maturing rate (K) of 0.032 and 0.044 kg.kg⁻¹.Mo⁻¹, respectively. Values of A and K for the breed average from the models were essentially intermediate between the two sexes. Estimates of integration constant (B) for the groups ranged from 0.46 \pm 0.03 to 0.98 \pm 0.02, while estimates of shape parameter (M) provided for only in Richards model were 0.91 \pm 0.16, 0.68 \pm 0.11 and 1.09 \pm 0.38 for

Ndama males, females and breed average, respectively. The phenotypic relationship between A and K in the models were highly negative ($r_p = -0.76$ to -0.98), indicating that genetic selection for early maturity would lead to small mature weights and vice versa in NDama cattle. With minor exceptions involving Richards model, the pattern of relationships followed similar trends indicating that growth curve parameters in the different models measured similar growth characteristics. We show that growth curve parameters, their relationships and biological implications can improve our understanding of the growth and development pattern of NDama cattle under various production environments in the tropics.

Key Words: Non-Linear Models, Growth Curves, Cattle

M8 Analysis of daughter pregnancy rates and estimated relative conception rates for a bimodal distribution. H. N. Schlessner^{*1}, R. D. Shanks¹, S. L. Rodriguez-Zas¹, J. S. Clay², P. M. VanRaden³, P. J. Berger⁴, and M. H. Healey⁴, ¹University of Illinois Urbana-Champaign, ²Dairy Records Management Systems, ³Animal Improvement Programs Laboratory, ⁴Iowa State University, Ames.

The objective of this research was to determine whether daughter pregnancy rates (DPR) and estimated relative conception rates (ERCR) have a bimodal distribution for certain bulls as seen with perinatal survival. Perinatal survival rates were computed for 12,034 sons at Iowa State University. AIPL calculated DPRs for 48,117 sons. One hundred and seventy six bulls with a minimum of 50 sons had DPRs. Dairy Records Management Systems computed ERCRs for 3,276 sons from breedings in 1988 through 1997. Seventeen bulls had at least 50 sons with ERCRs and were included in the analysis. A kernel density procedure estimated density of DPR and ERCR for each bull. Three different bandwidth multipliers were used (1,2,3). Densities that were bimodal at bandwidth multiplier one but fail to remain bimodal at bandwidth multiplier two were considered unimodal. None of the bulls were bimodal for DPR or ERCR. Of the 21 bulls that were bimodal for perinatal survival, all 21 had DPRs but only five had ERCRs. A significant ($P < 0.0001$) correlation of 0.134 between DPR and perinatal survival (8552 sons) was found. This positive correlation indicates that bulls with higher DPR tend to have higher perinatal survival. The correlations between DPR with ERCR for 1996 (1346 sons) and DPR with ERCR for 1997 (1611 sons) were not significant, nor were the correlations between perinatal survival with ERCR for 1996 (463 sons) and perinatal survival with ERCR for 1997 (414 sons). A significant ($P < 0.0001$) correlation of 0.361 between ERCR for 1996 and ERCR for 1997 (541 sons) was found. From this research we conclude that daughter pregnancy rates and estimated relative conception rates do not have a bimodal distribution like the ones seen with perinatal survival.

Key Words: Daughter Pregnancy Rate, Fertility, Dairy Bulls

M9 Genetic variation in residual energy intake and its association with body weight, milk yield, fat corrected milk yield and economic merit in dairy cattle. P. Zamani^{*1}, S. R. Miraei Ashtiani¹, A. Naserian², M. Moradi Shahrbabak¹, and A. Nik-Khah¹, ¹Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, ²Department of Animal Science, Faculty of Agriculture, University of Ferdowsi, Mashhad, Iran.

Residual energy intake is defined as the difference between actual energy intake and that predicted on basis of requirements for maintenance, lactation and body weight change. Residual energy intake is proposed as a measure of feed efficiency, because animal efficiency increases as the proportion of accountable energy intake increases or residual energy intake decreases. Variation in residual energy intake in relation to body weight, milk yield, fat corrected milk yield and economic merit (income over feed cost) was investigated using 2589 monthly records collected from 723 Holstein lactating cows in 3 herds. Energy requirements of each cow were estimated using NRC models. Genetic and phenotypic parameters were estimated using Derivative Free approach of Restricted Maximum Likelihood based on two-trait animal mixed model analyses. The model contained fixed effects of herd-year-season, parity number, stage of lactation (months after parturition) and random effects of animal genetic and permanent environment. Heritability estimation of residual energy intake was 0.17 ± 0.07 . Residual energy intake was negatively correlated to body weight, milk yield, fat corrected milk yield and economic merit, both phenotypically (-0.021 , -0.208 , -0.298 and -0.385 , respectively) and genetically (-0.031 , -0.363 , -0.465 and -0.618 ,

respectively). Fat corrected milk showed the most significant correlations with economic merit both phenotypically (0.635) and genetically (0.928). Because of its high correlations with residual energy intake and economic merit, more selection emphasis could be placed on fat corrected milk, when selecting indirectly for feed efficiency and economic performance.

Key Words: Dairy Cattle, Residual Energy Intake, Fat Corrected Milk

M10 Designer pork studies with small-scale farmers targeting niche markets. T. Barrios^{*1}, C. Talbott¹, T. See², and R. Pfortmiller³, ¹North Carolina Agricultural and Technical State University, Greensboro, ²North Carolina State University, Raleigh, ³National Swine Registry, West Lafayette, IN.

Small-scale producers may be able to secure a place at the pork industry table by producing a different type of pork than the the other white meat. By selecting for pork with higher levels of marbling, darker color and optimum pH levels, hog producers may be able to survive by marketing the other red meat through niche markets. Progeny sired from four different genetic populations of boars (not selected for lean conversion) were used to examine the potential to increase intramuscular fat in pork for niche-market application. Forty gilts were randomly assigned to one of four sire lines and bred artificially or by natural service. Upon detection of pregnancy, gilts were distributed to one of four participating farmers. Two castrates from each litter were identified with sire and sow lines and monitored through harvest. Carcass quality was assessed and IMF levels correlated with the presence or absence of the heart fatty acid binding protein (H-FABP) allele. Potential for conducting genetic studies with small-scale farmers are discussed.

Key Words: Designer Pork, Farmer Participatory Research, Niche Markets

M11 Contribution of inbreeding and recessive defects to early embryo loss. P. M. VanRaden and R. H. Miller^{*}, Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.

Lethal recessive genes that cause early embryo loss are difficult to detect because they may appear to be failed inseminations or missed heats. Nonreturn rate at 70 d after first insemination (NR70) was evaluated as a trait of the embryo from 1,739,055 first services using a nonadditive genetic model. Effects modeled included herd-year-season, parity of cow, sire of cow, service bull, interaction of service bull with sire of cow, and regression on inbreeding of embryo. Simultaneous solutions for all effects were not possible; thus, main effect variances were estimated using REML, and those effects were removed from the data. Interaction variance was estimated from the residuals using the tilde-hat approximation to REML. Service bull effects were assumed to be constant across time and unrelated. An additive relationship matrix was used for sire of cow and a dominance relationship matrix for the interaction term. Data included observations from January 1995 through January 2001 and represented 1,251 Holstein service bulls and sires of cows. For each 1% increase in inbreeding, NR70 declined by an estimated 0.096. A regression of this size could be explained by >20% of animals carrying defects that cause early embryo loss. Of the total variance, service bull contributed 0.36%; sire of cow, 0.24% (heritability of 1.0%); and interaction, 0.18% (dominance variance of 2.8%). Number of records per interaction averaged only 6 but with a maximum of 2,077, and 50 bull pairs had >500 records, which resulted in reliabilities of >50% for their interactions. Predicted interactions that included effects of inbreeding ranged from 3.6 to +2.9 as compared to the mean NR70 of 56%. The poorest interactions were not caused by known recessive defects. Complex vertebral malformation (CVM) generally causes loss of pregnancies later in gestation, and few current bulls carry the gene for deficiency of uridine monophosphate synthase (DUMPS). Further study of the families with poorest interactions could uncover new recessive defects.

Key Words: Fertility, Embryo Loss, Recessive Defects

M12 Relationships among measures of growth performance and plasma urea nitrogen (PUN) in barrows. J. Klindt*, USDA-ARS; U.S. Meat Animal Research Center, Clay Center, NE.

Our previous work [J. Anim. Sci. 81(Suppl. 2):36, 2003] showed that plasma concentrations of PUN are genetically regulated and moderately heritable, 0.35. Objective of the present study was to examine the relationships among measures of growth and PUN in grower/finisher pigs. Barrows, $n=96$, BW= 29.3 ± 0.5 kg, 3 to 4 per litter, 27 litters, were assigned at 69 ± 0.5 d of age. Pigs were placed in individual pens and fed standard grower/finisher diets until slaughter at 118 kg BW. At slaughter, chilled carcass wt (ClDwt) and wt of trimmed lean cuts (Tlncut) were recorded. At 2-wk intervals during the trial BW, average of ultrasonic backfat at three sites, and feed consumption were recorded. At each weighing a blood sample was collected for determination of plasma urea nitrogen (PUN). Within pig PUN was averaged to obtain mPUN. Two pigs were removed before the end of the trial. Data recorded at the end of the trial was adjusted to average slaughter wt, 117.2 ± 0.3 kg. Daily change in average of three backfat measures (ADCBF), ADG, days to slaughter (Tday), final average backfat thickness (FnBF), ClDwt, Tlncut, and mPUN were affected ($P < 0.05$) by litter. Litter affected ($P < 0.08$) total feed consumed (Tfeed). Feed/d and efficiency of BW gain (Eff) were not affected by litter ($P = 0.14$). For the subsequent examination of the relationship of mPUN with growth measures, pigs were classified as loPUN ($n=31$; mPUN, 26.1 to 36.1, mean= 32.1 mg/dL), medPUN ($n=32$; mPUN, 36.4 to 42.1, mean= 39.2 mg/dL), and hiPUN ($n=31$; mPUN, 42.4 to 91.3, mean= 54.3 mg/dL). PUN group influenced ($P < 0.05$) feed/d, ADCBF, FnBF, and Tlncut. hiPun barrows had higher feed/d, ADCBF, and FnBF and reduced Tlncut. Effect of PUN group on feed/d, was nonlinear. Results concur with the reported low phenotypic and genetic correlations among PUN and growth measures [Klindt, et al., J. Anim. Sci. 81(Suppl. 2):36, 2003]. These results suggest that selection against PUN may be accomplished without significant sacrifices in growth performance.

Key Words: Plasma urea concentrations, Growth, Genetic influences

M13 Relationship between performance test traits and subsequent reproductive performance of Yorkshire females. Z. B. Johnson*¹ and R. A. Nugent, III², ¹University of Arkansas, Fayetteville, ²The Pork Group, Tyson Foods, Inc., Springdale, AR.

The objective of this study was to examine relationships between performance test traits and subsequent reproductive performance of Yorkshire females. Performance test records were collected in a commercial swine operation from 1992 to 1999. All females in the breed were grown to 100 d of age (AGE100; $n = 38,979$). At this time pigs were weighed (WT100) and selected for performance testing based on a combination of maternal and performance indexes with more emphasis given to the maternal index. Pigs were weighed at the end of the 77-d performance test (WT177; $n = 32,623$) and ADG calculated. Backfat (BF), loin eye area (LEA), and body length (LEN) were measured. Reproductive traits were number born live (NBA; $n = 3,140$ litters) and weaning weight (WWL; $n = 2,892$ litters) of the first litter. Genetic parameters were estimated using an animal model with litter effects and multiple-trait DFREML procedures. A series of two-trait models was conducted to estimate genetic correlations. Fixed effects for performance traits included contemporary group and either age at 100 d or age at 177 d as a covariate. Contemporary group was the only fixed effect for NBA; while age at weaning was included as a covariate for WWL. Estimates of heritability for NBA, WWL, WT100, WT177, ADG, BF, LEA, and LEN were $0.09 \pm .03$, $0.10 \pm .03$, $0.22 \pm .01$, $0.32 \pm .02$, $0.28 \pm .02$, $0.47 \pm .02$, $0.31 \pm .02$, and $0.23 \pm .02$, respectively. Genetic correlations for NBA with WT100, WT177, ADG, BF, LEA, and LEN were -0.43, -0.20, 0.06, 0.01, -0.17, and -0.11, respectively. Genetic correlations for WWL with WT100, WT177, ADG, BF, LEA, and LEN were 0.55, 0.14, -0.04, -0.05, -0.05, and 0.13, respectively. These correlations indicated that 100-d weight of the mother was more related to NBA and WWL than any performance trait measured. Females that weighed more at 100 d of age had smaller litter sizes, but greater weaning weight of the litter.

Key Words: Swine, Performance Traits, Reproductive Traits

M14 Evaluation of the effects of heterosis on reproductive efficiency and milk yield in South Florida. S. I. Madrid*, T. A. Olson, A. de Vries, C. A. Risco, and P. J. Hansen, University of Florida, Gainesville.

Holstein (H), Brown Swiss (B) and Guernsey (G) cows and their crosses were evaluated in South Florida. Levels of heterosis were determined for 305d ME milk production and days open. The herd was located in Okechobee County, Florida. The cows in this herd were grazed for the majority of the day along with supplemental feeding of concentrates. Records provided by Dairy Record Management Systems (DRMS) were utilized in the analyses. This herd had been utilizing crossbreeding for a period of at least 18 years. During the initial years the herd was composed primarily of Holstein and Guernsey cows. Brown Swiss sires and dams were later added to the herd. Breed composition for the animals in the project were determined by using pedigree records kept in DRMS files. Milk yield was analyzed using a model which included the main effects of year, month of calving, lactation number and breed composition. Heterosis levels for milk yield were 11, -1.4, 2.8, 5, -.05, -.004% for H X G, G X H, B X H, H X B, B X G and G X B respectively. Breed of sire is represented first in the cross. Only the heterosis level observed for the Holstein-sired cows from Guernsey dams was significant ($P < 0.05$). The lowest levels of heterosis for milk yield were found for crosses between the Guernsey and Brown Swiss breeds. Days open were calculated using only the last two calving dates of each cow (DYSOPCD). The data were edited to remove records for days open of less than 70 d, the voluntary waiting period practiced in this herd. The model used in the analyses of days open included effects of year, breed composition and lactation number. The days open for purebred H, B and G cows which were 165, 146, and 164 respectively. Days open for H X G, G X H, B X H, H X B, B X G and G X B were 154, 173, 143, 139, 131, and 179d, respectively. The average days open for all crossbred cows was 20 days shorter than that of the average of the purebred cows. The mean heterosis for days open was 10.5% ($P < 0.05$). Thus, these data indicate that while the effect of heterosis on milk yield was small the advantage for reproductive traits might be substantial.

Key Words: Crossbreeding, Dairy Cattle, Florida

M15 Analysis of sow longevity in commercial herds using competing risks. B. R. Southey*¹, S. L. Rodriguez-Zas¹, R. V. Knox¹, J. F. Connor², J. F. Lowe², and B. J. Roskamp², ¹University of Illinois, Urbana, ²Carthage Veterinary Services Ltd., Carthage, IL.

The length of time a sow remains in a herd or sow longevity is an important component of pork production. Removal of a sow from a herd can be due to many reasons including fertility failure, poor reproduction and litter performance, disease, injury, or death. Competing risks analysis of sow longevity provides a suitable approach to account for the different reasons of removal while accounting for the positive, non-normal and censored sow longevity data. Sow longevity records for 158,940 sows from 32 US commercial herds across five years were analyzed under independent competing risks. The reasons for removal were grouped into common categories including fertility, reproduction, litter performance, disease, injury, old age and death. The Cox proportional hazard model was used to analyze sow longevity including effects of genetic line, herd and year of entry. Genetic line included eight major genetic lines that were present in multiple herds. The relative hazard of removal between the major genetic lines varied depending on removal reason. No difference in hazard of removal was observed for fertility category. For the other removal categories the relative hazard of removal varied among the major genetic lines. For example, the hazard ratio for sow longevity between the Camborough 22 and Camborough 15 lines ranged from 0.43 for old age category to 1.3 for longevity related to poor reproduction. This indicated that Camborough 22 sows had a 60% lower hazard of removal due to old age and a 30% higher hazard of removal due to reproductive reasons than Camborough 15 sows. In contrast, under a single removal cause, the hazard ratio of Camborough 22 relative to Camborough 15 line for sow longevity was 0.87 indicating that Camborough 22 sows had a 13% lower hazard of removal than the Camborough 15 sows. These results illustrate the importance of accounting for removal reason in the analysis of sow longevity. The use of competing risks permits the elucidation of the decision process involved in sow removal and identification of opportunities for management intervention to maximize sow longevity.

Key Words: Longevity, Survival Analysis, Swine

M16 Estimation of correlation between maternal permanent environmental effects of related dams in beef cattle. H. Iwasaki¹, S. Tsuruta^{*2}, I. Misztal², and J. K. Bertrand², ¹Niigata University, Niigata, Japan, ²University of Georgia, Athens.

Correlation (λ) between maternal permanent environmental (MPE) effects of dams and their daughters was estimated using a maternal animal model for beef cattle. Two data sets for weaning weight consisted of 82,138 and 88,639 records of Gelbvieh (GV) and Limousin (LM) breeds, respectively. Numbers of dams and animals in the pedigree file were 39,678 and 121,390 for GV and 52,012 and 155,101 for LM, respectively. The model included fixed effects of contemporary group, sex of calf, age of dam at calving and month of calving; fixed regressions on age of calf; random direct genetic, maternal genetic, MPE and residual effects. The REML procedure was employed with a grid search, in which the likelihood was computed for a series of values for λ . Two models Model 1 without λ and Model 2 including λ were compared by a likelihood ratio test. Model 2 fitted the data significantly better than Model 1. The maximum restricted likelihood was obtained for λ of approximately 0.2 for both breeds. Estimates of residual and direct genetic variances were similar for both models. Compared with those of Model 1, estimates of maternal genetic and MPE variances of Model 2 increased and decreased slightly, respectively, for both breeds. Accordingly, the estimates of maternal heritability and the proportion of MPE variance to total variance for Model 2 were higher and lower, respectively, than those for Model 1. For Model 1, estimates of direct-maternal genetic correlation were 0.26 and 0.59 for GV and LM, respectively, while those for Model 2 were slightly lower (0.20 and 0.54). Pearson and rank correlations for direct and maternal effects were very high (>0.99) for both models. These results indicate that the relationship between MPE effects of two subsequent generations for weaning weight in both breeds is negative but low, and that the consideration of maternal environmental relationships between dams and their daughters in the models does not significantly affect the estimates of (co)variance components and may not be important in genetic evaluations.

Key Words: Maternal Permanent Environmental Correlation, AI-REML, Beef cattle

M17 Effects of climate and photoperiod on feed intake of beef bulls during feedlot performance tests. G. T. Tabler, Jr.^{*}, A. H. Brown, Jr., Z. B. Johnson, E. E. Gbur, Jr., I. L. Berry, D. W. Kellogg, and K. C. Thompson, *University of Arkansas, Fayetteville.*

Climate and photoperiod data were analyzed to identify and quantify impacts on feed intake of beef bulls during 52 post-weaning feedlot performance tests. Feed intake data originated from bulls ($n = 1,874$) in University of Arkansas Cooperative Bull Tests at Fayetteville, Hope and Monticello 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. As formulated, the diet contained 1.6 Mcal NE_m, 0.9 Mcal NE_g and 12% CP per kg DM. Initial age and weight were recorded at start of each test with weights taken at 28-d intervals thereafter. Photoperiod and climate data were obtained from the U.S. Naval Observatory (Washington, DC) and National Climatic Data Center (Asheville, NC), respectively. Variables included maximum, minimum, average, and dew point temperatures; 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. Initial age and initial weight were included in principal components regression as independent variables to adjust for initial animal differences. Principal component analysis was utilized to reduce the number of independent variables in the regression and overcome collinearity concerns associated with photoperiod and numerous climatic variables. Three principal components within each period accounted for 59% to 66% of the variability in explanatory variables. Nine to 14 components accounted for 97% to 100% of variability. Results provide additional information on effects climate and photoperiod have on cattle feeding and indicate photoperiod and climate conditions have differing effects on feed intake of feedlot cattle as feeding periods progress.

Key Words: Beef Cattle, Climate, Feed Intake

M18 Feed efficiency in the West Virginia Bull Test Evaluation Program. E. E. D. Felton^{*}, J. E. Warren, Jr., W. R. Wagner, and J. W. Yates, *West Virginia University, Morgantown.*

The "GrowSafe 4000E" system was installed and used to measure individual feed intake during the 2003-2004 West Virginia Bull Test Evaluation Program. This system of hardware and software consists of feed troughs mounted on load cells. An antenna grid is incorporated in the trough, and animals are fitted with electronic ear tags that are read by the antenna grid. An animal feeding at a trough is identified at five second intervals and feed available in each trough is weighed every second with an accuracy within 50g. The animal identification and feed consumed data are sent wireless via a communication panel to a computer with software to compile individual feed intake and individual feeding events. Bulls arrived at the test station in mid-October, 2003. Following a 3-week acclimation period, bulls were weighed on d 1 and 2: (averaged for on test BW; **IBW**), 42, 77, and 104 and 105 (averaged for off test BW; **FBW**). During the acclimation period and the 105-day test, bulls were fed *ad-libitum* a total-mixed-ration containing 13.6% crude protein and 73.6 and 45.0 Mcals of NEm and NEg per cwt, respectively. A subset of 98 Angus bulls (372 ± 22 days of age, $IBW = 375 \pm 45$ kg, $FBW = 582 \pm 48$ kg) was subjected to correlation analysis of feed:gain data from the beginning of the test to d 42 to various production and descriptive variables. Additional data will be included upon completion of test summary. Weak r-values existed ($P = 0.02$) with frame score (-0.23) and age of the bull (0.24) while much stronger r values existed ($P < 0.001$) with ADG over the entire test period (-0.62) and DMI expressed as a percentage of BW (0.43). There were no detected relationships with birth weight, age of dam, muscle score or longissimus muscle area, back fat and marbling scores measured by ultrasound at the end of the 105 d test period. Many of these variables are important to beef production and are currently used in the selection of sires and dams. These data indicate that it may be possible to also use feed efficiency as an additional selection tool without influencing other important selection variables.

Key Words: Feed Efficiency, Bulls, Beef

M19 Maternal and reproductive performance of crossbred cows mated to moderate or high weaning weight EPD sires. S. M. DeRouen^{*1} and F. A. Thrift², ¹Louisiana State University Agricultural Center, Homer, ²University of Kentucky, Lexington.

Maternal and reproductive performances were evaluated over 5 yr for Angus-, Brahman-, Brangus-, Gelbvieh-, and Gelbray-sired cows when mated to Simmental sires varying in weaning weight (WWT) EPD. Four moderate (MOD) (mean = 9.91 kg WWT EPD) and three high (HIGH) (mean = 17.98 kg WWT EPD) sires were mated to 307 cows by artificial insemination (AI). Accuracies of WWT EPD were > 0.80 . Cows were exposed to clean-up bulls for 60 d following AI. Statistical analyses were conducted using a generalized linear mixed model. Sire type x calf sex interaction was not significant for any response traits studied. A total of 120 AI-sired calves were evaluated. Least squares means for Julian birth date and birth weight for calves sired by MOD and HIGH growth sires were 47.7 d and 41.7 kg and 49.7 d and 44.4 kg, respectively, and did not differ ($P > 0.07$). Weaning weight and 205 d weight for calves sired by MOD and HIGH growth sires differed ($P < 0.04$) and were 271 kg and 248 kg and 284 kg and 261 kg, respectively. A total of 109 cows were evaluated for pregnancy rate while nursing MOD and HIGH growth calves, BW and BCS at weaning, BW and BCS at subsequent breeding, and subsequent pregnancy rate. Pregnancy rates were similar ($P > 0.90$) among cows nursing MOD and HIGH growth calves and were 96.0% and 96.5%, respectively. Body weight and BCS at weaning were 596 kg and 5.47 and 580 kg and 5.39 for cows nursing MOD and HIGH growth calves, respectively, and did not differ ($P > 0.33$). Subsequent BW and BCS at breeding were 600 kg and 5.52 and 579 kg and 5.35 for cows nursing MOD and HIGH growth calves, respectively, and did not differ ($P > 0.19$). Subsequent pregnancy rates were similar ($P > 0.70$) among cows nursing MOD and HIGH growth calves the previous year and were 91.7% and 93.6%, respectively. In conclusion, calf weaning weight differences were similar to sire weaning weight EPD differences and subsequent reproduction was not adversely affected for cows nursing high growth calves.

Key Words: EPD, Reproduction, Weaning Weight

M20 Selection for meat tenderness in Angus. L Praharani*, T. A. Olson, D. D. Johnson, R. L. West, and J. R. Alday, *University of Florida, Gainesville.*

The objective of this study was to evaluate the response to selection of Angus bulls for tenderness based on Warner-Bratzler Shear (WBS) values. The study began with Angus calves born in 1994. About 30-35 bulls were evaluated annually from those born from 1994 through 2000. After evaluation, three or four of the bulls with the highest and lowest WBS values were selected for use. Beginning in 1996, calves were sired by selected bulls. After the bull calves were expected to have reached puberty, at 13 and 14 months of age, semen was collected and frozen. The bulls were then slaughtered and their tenderness was determined using WBS evaluation. The semen from selected bulls was used to inseminate purebred and grade Angus cows at the Santa Fe Beef Unit Angus herd. Warner-Bratzler shear force data from a total of 262 bulls from 45 sires and 195 dams were collected. Analyses were performed to estimate variance and covariance components using AsREML. Genetic trends were plotted as averages of breeding values, estimated by the solution of animal model equations for year of birth, and overall trend was estimated as a regression of all breeding values on year of birth of calves. The average breeding value of progeny of sires selected for tenderness (-0.29 kg) was lower ($P < 0.05$) than that of sires selected for toughness (0.44 kg) over the years of the study. The estimate of direct heritability ($h^2 = 0.41 \pm 0.19$) was quite high. This estimate indicates that selection for meat tenderness in this manner might be effective. The genetic trends for WBS values tended to decrease over the years -0.0038 and -0.0149 kg per year for the progeny of tough and tender selected-sired, respectively. The breeding values of the progeny of both tender and tough selected sires declined. An explanation for declining breeding values of progeny of sires selected as tough is not clear but might be due to the low selection pressure applied in this study, since there were limited numbers of the bulls evaluated and it was not possible to collect freezable semen from all of the bulls prior to slaughter.

Key Words: Selection, Tenderness, Angus

M21 Genetic parameters estimated with multi-trait and linear spline random regression models using Gelbvieh early growth data. H. Iwaisaki¹, S. Tsuruta^{*2}, I. Misztal², and J. K. Bertrand², ¹*Niigata University, Niigata, Japan*, ²*University of Georgia, Athens.*

Estimates of direct and maternal genetic parameters in beef cattle were obtained by a random regression model with a linear spline function (SFM) and compared with those obtained by a multi-trait model (MTM). Most of SFM parameters are on the same scale as in MTM, simplifying validation and implementation. Weight data of 18,900 Gelbvieh calves were used, of which 100, 75 and 17% had birth (BW), weaning (WW) and yearling (YW) weights, respectively. The MTM analysis was conducted with a three-trait maternal animal model. The model included an overall linear partial fixed regression on age at recording for WW and YW, and direct-maternal genetic and maternal permanent environmental effects. The SFM included the same effects as MTM, plus direct permanent environmental effect, and heterogeneous residual variance. Three knots, or breakpoints, were set to 1, 205 and 365 d. (Co)variance components in both models were estimated with a Bayesian implementation via Gibbs sampling using flat priors. For BW with no variability of age at recording, a good agreement was observed between corresponding components of variances estimated from both models. For WW and YW, with the exception of the sum of direct permanent environmental and residual variances, there was a general tendency for SFM estimates of variances to be lower than MTM estimates. Direct and maternal heritabilities estimated with SFM tended to be lower than those estimated with MTM, some of which were particularly high. For example, the direct heritability for YW was 0.59 with MTM and 0.48 with SFM. Estimated negative genetic correlation for direct and maternal effects with SFM were lower than those with MTM. For example, the direct-maternal correlation for WW was -0.43 with MTM and -0.33 with SFM. Estimates by SFM may be superior to MTM due to accounting for constant days and also for random effects. The SFM is simpler to implement than a random regression model with Legendre polynomials.

Key Words: Random Regression, Linear Spline Function, Beef Cattle

M22 Estimated genetic parameters for growth, carcass, and tenderness traits of Brahman steers. D. E. Franke^{*1}, T. Smith¹, J. D. Domingue¹, T. D. Bidner¹, and J. C. Paschal², ¹*LSU Agricultural Center, Baton Rouge, LA*, ²*Texas A&M University, Corpus Christi*, ³*University of Nebraska, Lincoln.*

Purebred Brahman bull calves ($n=430$) were purchased at weaning from private breeders in Louisiana (1996 through 2000) to evaluate genetic (co)variation for growth, carcass, and tenderness traits. Calves were castrated, vaccinated, dehorned, dewormed, and backgrounded and grazed on ryegrass for an average of 120 d over the 5 yr period. Steers were fed in south Texas. Steers were harvested in groups of 20 to 30 head when the group reached 500 to 575 kg BW and 7 to 10 mm fat thickness. Carcasses were electrically stimulated and chilled for 24 hr. A 15-g 24 hr postmortem longissimus muscle sample was taken for calpastatin assay. A primal rib was purchased and 2.54-cm-thick steaks were cut for 14-d aging. Tenderness was determined by averaging the force required to shear six 1.26 cm cores taken parallel to muscle fibers. A full animal model was used to estimate genetic (co)variation in order to compute heritability and genetic correlations. Heritability estimates (\pm SE) were .33 (.14) for feedlot adg, .56 (.15) for hot carcass weight, .51 (.16) for ribeye area, .38 (.17) for fat thickness, .49 (.17) for yield grade, .38 (.16) for marbling score, .21 (.11) for shear force, and .44 (.17) for calpastatin activity. Most genetic correlations were below .25 with similar magnitude of standard errors. Exceptions were -.63 (.25) for yield grade and shear force and -.43 (.17) for marbling score and calpastatin activity. These genetic parameters indicate possible response from selection.

Key Words: Brahman Steers, Carcass Traits, Genetic Parameters

M23 The use of real time ultrasound to estimate variance components for growth and carcass traits in Nelore cattle. C. U. Magnabosco^{*1,2}, F. R. C. Araujo^{1,3}, F. Manicardi⁴, J. R. Hofig Ramos⁵, C. U. Faria², R. B. Lôbo⁶, L. A. F. Bezerra⁶, T. R. Famula¹, and R. D. Sainz¹, ¹*University of California, Davis*, ²*Embrapa Cerrados, Bolsista CNPq*, ³*Aval Serviços Tecnológicos S/S*, ⁴*Grupo OMB*, ⁵*Grupo HoRa*, ⁶*Universidade de São Paulo.*

Real-time ultrasound (RTU) technology was used for collection of data on carcass traits thg Nelore cattle in Brazil, for longissimus muscle area (ULMA), backfat between the 12th and 13th ribs (UFAT), and rump fat at the P8 site (URFAT). The data were collected on ranches in southeastern and midwestern Brazil (Grupo OMB and Grupo HoRa, participants of the Program for Genetic Improvement of the Nelore Breed - PMGRN). The final data set contained 1,721 animals at approximately 15, 18, 21 and 24 months of age, that were produced by 85 different sires. These data were analyzed to estimate genetic parameters and calculate Expected Progeny Differences (EPDs). The pedigree file used for calculation of the inverse numerator relationship matrix contained 25,941 animals, including those augmented so that each animal with data had two ancestral generations. The linear model included fixed effects for contemporary groups (herd-year-season-sex) and age of dam at calving. The model also included random effects for direct genetic effects. Data were analyzed using both a single and bivariate animal model. A Multiple Trait Derivative Free Restricted Maximum Likelihood (MTD-FREML) was used to establish the variance components and genetic parameters. Heritability estimates for ULMA, UFAT and URFAT were 0.29, 0.44, and 0.62, respectively. The EPDs for all traits presented a range that allows the possibility to significantly improve carcass quality in Nelore cattle. Ultrasound scan data produced consistent and heritable results for Nelore cattle and they may be used in genetic evaluation schemes to improve carcass traits.

Key Words: Beef Cattle, Carcass Traits, Genetic Evaluation

M24 Assessment of temperament at weaning in calves produced from diallel matings of Angus, Brahman, and Romosinuano. D. G. Riley^{*1}, C. C. Chase, Jr.¹, S. W. Coleman¹, R. D. Randel², and T. A. Olson³, ¹*USDA, ARS, Brooksville, FL*, ²*TAES, Overton*, ³*University of Florida, Gainesville.*

Objectives were to assess breed differences and estimate genetic effects for measures of temperament in cattle: exit velocity (m/s; higher values may indicate more excitable temperament) of calves when released from a squeeze chute; chute score and pen temperament score, the subjective evaluations of calf behavior when confined in a chute or approached in

an open pen. Scores were rated from 1 to 5; higher scores indicated more nervous or aggressive behavior. Calves ($n = 657$) were from diallel matings of Angus (A), Brahman (B), and Romosinuano (R; tropically adapted Colombian breed). Fixed effects included breed ($n = 9$), calf sex, year ($n = 2$), farm ($n = 3$), day of record ($n = 3$; 0, 24, or 72 h post-weaning). Order through the chute and calf age at weaning were covariates. Random effects were calf and sire. BB (sire and dam breed, respectively) calves had the highest values for exit velocity, chute score, and pen score (2.41 ± 0.1 m/s, 2.42 ± 0.06 , 3.31 ± 0.09); all were higher ($P < 0.05$) than all other breed groups for chute and pen score, and had higher ($P < 0.05$) exit velocity than all but BA and AB. RR calves had the lowest exit velocity (1.66 ± 0.07 m/s), lower ($P < 0.05$) than all but AA, RA, and AR. AA calves had the lowest values for chute and pen score, lower ($P < 0.05$) chute score than all but RR, and lower ($P < 0.05$) pen score than all but RR and RA. Estimates of direct breed effects for exit velocity ($P < 0.001$) were 0.68 ± 0.16 m/s for B and 0.49 ± 0.14 m/s for Romosinuano. Estimates of direct effects for chute and pen score were highly significant for B (0.91 ± 0.1 and 1.13 ± 0.15), A (0.5 ± 0.1 , 0.6 ± 0.14), and R (0.41 ± 0.09 , 0.52 ± 0.13). Estimates of heterosis ($P < 0.05$) were 0.21 ± 0.09 m/s (7.4%) for exit velocity for B with A, 0.12 ± 0.05 (3.1%) for chute score for A with R, and 0.18 ± 0.08 (3.2%) for pen score for R with B. Results suggest that R may be included in similar breeding programs without detrimental temperament changes.

Key Words: Brahman, Romosinuano, Temperament

M25 Estimates of adaptability and stayability for postweaning weight gain in crossbred beef cattle raised in five environments in Brazil. J. C. d. C. Balieiro^{*1,2}, J. B. G. Barros², J. B. S. Ferraz¹, J. P. Eler¹, E. d. S. Balieiro^{*3}, L. G. G. Figueiredo¹, and E. C. Mattos¹, ¹University of São Paulo, Duqu de Caxias Norte, 225. Pirassununga/SP-Brazil, ²University Center of Av. Dr. Octavio da Silva Bastos, S/n. S. João da Boa Vista/SP-Brasil, ³Federal Rural University of Rio de Janeiro, Rodovia BR-465, km 47. Serpédica/RJ-Brasil.

This study was conducted to evaluate adaptability and stability parameters of nine genetic compositions of crossbred European-Zebu cattle raised in five different Brazilian environments. Data ($n=16,546$) from the present study refer to characteristic gain from weaning up to 160 days postweaning. The statistical model included the effects of genetic composition (G), environment (E), GxE interaction and contemporary group within E. Also included was a covariate adjustment for cow's age at calving (linear and quadratic). All sources of variation in the analysis were highly significant ($P < 0.01$). The decomposition of the GxE interaction was accomplished by regression method. Intercepts ($\beta_{0(i)}$) for genotypes 2, 3 and 5 showed the highest weight gains up to 160 days postweaning. On the other hand, the genotypes 7, 9, 8 and 6 showed the smallest postweaning gains. Based on t-tests for the angular coefficients ($\beta_{1(i)}$) adjusted for the environmental index from each environment, it was verified that only genotype 2 had general adaptability. In contrast, genotypes 1, 3, 4 and 5 were classified as having specific adaptability to favorable environments and genotypes 6, 7, 8 and 9 were classified as having specific adaptability for unfavorable environments. The variance components related to the deviations of the regression for the genotypes indicated that all genotypes had low stability. Genotypes 3 and 5 should not be considered completely undesirable since they had high weight gains and coefficients of determination from the regression. The adaptability analysis was efficient in discriminating among genetic types. However, the stability analysis was not effective in discriminating the variance components attributed to deviations from regression. In this case, it was necessary to use another approach (coefficient of determination) to aid in decision making.

Key Words: Adaptability, Crossbred Cattle, Beef Cattle

PSA-Genetics

M26 Interaction genotype and protein level on feed efficiency of Japanese quail in dry tropic weather. J. J. Portillo^{*1}, R. Barajas¹, M. A. Carmona², F. G. Rios¹, and G. Contreras¹, ¹FMVZ - Universidad Autónoma de Sinaloa (Mexico) Carr. Culiacan-Mazatlan km 3.5, ²FES Cuautitlan UNAM (Mexico) Cuautitlan Izcalli, Estado de México.

This study was conducted to evaluate the interaction genotype and protein level and protein level on egg production of Japanese quail, were used 515 females and 200 males of four strains: 1) HH, quails selected for high mature weight; 2) LL, quails selected for low mature weight; 3) HL, reciprocal crosses from males HH with females LL; and 4) LH, reciprocal crosses from males LL with females HH. At 52 days old, the quails was contained in batteries with five levels and four cage by level. In each cage, was allocated six females and two males. With base at arrangement combinatory, five cages of each strain was designated a 16, 19, 21, 24, and 27 % of crude protein (CP) level. During eight weeks, was registered egg production and egg weight from strain and protein level. Each week was measurement the feed intake (FI) only by three days consecutives. To evaluate the interaction genotype-protein level, was utilized a general lineal model of fixed effects by week, strain, protein, and interaction strain-protein level, the tendency on the response was determinate by orthogonal polynomials, a simple lineal regression was used to estimate protein level with better feed efficiency (FE). ANOVA shown effect ($P < 0.01$) in FE by week production, strain, protein level, than as interaction by week x strain, and strain x protein, the tendency by FE was lineal ($P < 0.01$) to strain HH, and quadratic ($P < 0.03$) to strain HL, LH and LL, with CP levels and FE estimated of 26, 20.5, 16, 16 %, and 0.246, 0.248, 0.219, 0.264, to strain HH, HL, LH and LL, respectively. It is concluded, that exist interaction genotype protein in FE to egg production in Japanese quail, and better FE in low mature

weight strain with 16 % CP, than high mature weight strain require 26 % CP.

Key Words: Protein Level, Feed Efficiency, Coturnix coturnix japonica

M27 Interaction genotype - protein level on egg quality of Japanese quail in dry tropic weather. J. J. Portillo^{*1}, R. Barajas¹, M. A. Carmona², F. G. Rios¹, G. Contreras¹, and I. V. Ferrer¹, ¹FMVZ - Universidad Autonoma de Sinaloa (Mexico) Carr. Culiacán-Masatlan km 3.5, ²FES Cuautitlan - UNAM (Mexico) Cuautitlan Izcalli, Estado de Mexico.

To evaluate the interaction genotype and protein level on egg quality of Japanese quail, were used 639 eggs from four strain: 1) HH, quails selected for high mature weight; 2) LL, quails selected for low mature weight; 3) HL, reciprocal crosses from males HH with females LL; and 4) LH, reciprocal crosses from males LL with females HH. At 52 d old, the quails was contained in batteries with five leves and four cage by level. In each cage was allocated six females and two males. With base at arrangement combinatory, five cages of each strain was designated a 16, 19, 21, 24, and 27 % of crude protein (CP) level. From two weeks start hatching and every 14 d, during egg was collected by strain - CP level combination. The next measurement weight, length, width of eggs, dense albumin height, yolk height, and width. From these data, shape index (SI), yolk index (YI), and Haugh Units (HU) were calculated. To evaluate the interaction genotype-protein level, was utilized a general lineal model of fixed effect by week, strain, protein, and interaction strain-protein level, the tendency of the response determinate by polinomial and the means comparison was used contrasts. ANOVA shown effect ($P < 0.03$) in SI, YI, and HU, by week, strain, protein level, and strain x protein level, except to genotype-protein interaction in HU ($P = 0.20$). Was observed lineal response ($P < 0.01$) and difference between 16-19-21 vs. 24-27 % of CP ($P < 0.01$) in SI to strain HH with