

Bioethics

M37 Measuring and managing for sustainability in dairy production: A stewardship scorecard. G. W. C. Clark*, A. A. Whitman, and J. M. Hagan, *Manomet Center for Conservation Science, Brunswick, ME.*

The dairy industry faces huge challenges as consumer values change, investors concerns extend beyond the financial bottom line, and society's expectations of agriculture are being transformed. We are developing a stewardship scorecard that will provide an objective, numerical, science-based assessment of the condition of social, economic and environmental services on farms. Our goal is to develop a tool that allows producers, processors and consumers to assess farm stewardship of dairy products. The key scorecard components and their science-based indicators are

being selected in consultation with dairy farmers and stakeholders (including consumers). Indicator will be screened and selected to meet five criteria: practicality, utility, scientific merit, efficiency, and social relevance. The scorecard will be tested by applying it to 25 dairy farms in the U.S. After the testing phase, the scorecard will be refined based on (1) the field test results, (2) farmer surveys, (3) stakeholder meetings, and (4) scientific peer review. The final version will be distributed with a user's handbook that describes how to apply the scorecard and ways that farmers can change their scores and communicate their performance to stakeholders and processors. The scorecard will be another tool for fostering an awareness of farm stewardship issues.

Key Words: sustainability, scorecard, stewardship

Breeding and Genetics: Beef Breeding, Poultry Breeding, and Genetics of Disease

M38 Milk production and composition during the first 4 months of lactation of Hereford (HH), Angus (AA) and F1 crosses grazing on native pastures Uruguay. A. Espasandin*¹, A. Casal², A. Graña², V. Gutiérrez², and M. Carriquiry¹, ¹*School of Agronomy, UDELAR, Montevideo, Uruguay,* ²*School of Veterinary, UDELAR, Montevideo, Uruguay.*

The objective of this study was measure milk yield and composition in 24 cows (8 HH, 8 AA, and 8 F1) once a month from 30 to 120 days postpartum (DPP), blocked by calving date and body condition at calving. Cows grazed together on native pasture paddock with an average forage mass available of 2400 kg DM/ha. In the morning, cows were drained and separated from their calves and after 6 hours were milked with a portable machine with previous injection of oxytocin (10 IU/cow). Milk was weighted and sampled for chemical composition analysis (protein, fat and lactose). A mixed model was applied to analyze milk yield and composition including cow and calf breed and calf sex as fixed effects, DPP as a covariate and cow within breed as random effect. Means were considered to differ when $P \leq 0.05$. Milk yield (3.8 ± 0.6 , 5.4 ± 0.8 , 4.4 ± 1.1 kg/d for HH, AA, and F1, respectively), and fat (4.2 ± 0.5 , 2.5 ± 0.6 , and $5.0 \pm 0.9\%$ for HH, AA, and F1, respectively) and lactose (4.9 ± 0.1 , 5.2 ± 0.1 , $4.9 \pm 0.1\%$ for HH, AA, and F1, respectively) contents did not differ among cow breeds but protein percentage was greater from HH and F1 than for AA cows (3.2 ± 0.1 , 2.6 ± 0.2 , and $5 \pm 0.2\%$ for F1, HH, and AA respectively). Milk yield was greater during the first 60 DPP and decreased thereafter (5.4 , 5.2 , 3.9 , and 3.5 kg/d ± 0.4 for 30, 60, 90, 120 DPP, respectively). Protein and lactose contents were affected by month of lactation, as protein was less and lactose content was greater during the first 60 DPP (3.0 , 3.0 , 3.3 , $3.2\% \pm 0.07$ and 5.2 , 5.0 , 4.9 , $4.9\% \pm 0.05$ for 30, 60, 90, 120 DPP, for protein and lactose contents, respectively). Fat percentage was not affected by DPP and averaged $3.8 \pm 0.04\%$ during the first 4 months of lactation. Tendencies observed for milk production and composition along lactation were similar to the reported in literature for beef and dairy cattle. Cow breed did not affect milk production and composition except for protein in which F1 and HH showed superiority.

Key Words: milk yield, beef cattle, lactation

M39 Genetic relationships of monounsaturated fatty acid with image analysis traits in Japanese Black cattle. Y. Nakahashi*¹, T. Kato², M. Nakamachi¹, N. Murasawa¹, Y. Hamasaki¹, S. Hidaka¹, and K. Kuchida¹,

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Monounsaturated fatty acids (MUFA) in beef cattle were investigated in large numbers due to the positive correlation with the flavor of marbling. We have studied MUFA and image analysis traits in order to clarify relations between MUFA and marbling shape in the rib eye. However, there are few studies concerning the genetic parameter of MUFA and no investigations on the correlations of MUFA with image analysis traits. The objective in this study was to analyze the relationships of MUFA with image analysis traits genetically. Carcass data were collected from Japanese Black cattle ($n=1,447$) that shipped to a meat processing plant in Hokkaido, Japan. Fat tissues were sampled from the rib eye of every carcass and the fatty acid compositions were analyzed using gas chromatography. Image analysis was performed to calculate the marbling percent (MP), fineness index of marbling (FIM) in rib eye and so on. Using single/multiple trait animal models, genetic analysis was conducted to estimate the heritabilities of all traits and the genetic correlations of MUFA with the image analysis. The heritability of MUFA was estimated as 0.83, indicating the possibility of improvement of the MUFA of Japanese Black. Genetic correlation of MUFA with MP was 0.20, showing a preferable relationship in which increasing MP causes improvement of MUFA. On the other hand, an undesirable correlation between MUFA and FIM was recognized (-0.09), suggesting that the improvement of MUFA is stifled by the number of small marbling flecks preferred in Japanese Black cattle. Therefore, in order to improve MUFA while keeping the fineness of the marbling in rib eye, planned breeding programs considering sire attributes could be effective by using image analysis.

Key Words: genetic parameter, image analysis, MUFA

M40 Genetic analysis of growth traits considering the average numerator relationship matrix and a hierarchical Bayes model for Nellore cattle. L. Shiotsuki*¹, F. F. Cardoso², J. A. II V. Silva³, and L. G. Albuquerque¹, ¹*Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil,* ²*Embrapa Pecuaria Sul, Bage, Rio Grande do Sul, Brazil,* ³*Alta Genetics, Uberaba, Minas Gerais, Brazil.*

The aim of the present work was to evaluate two statistical models to predict the genetic merit of animals with uncertain paternity, a linear mixed model based on average numerator relationship matrix (ANRM)

and a hierarchical animal model (HIER), that considers the uncertainty in paternity attributions of offspring of multiple-sires. Genetic parameter estimates for post-weaning gain (PWG) and yearling weight (YW) obtained with these two models were compared, based on 62,212 records of Nelore animals, offspring of 581 bulls and 27,743 cows. The pedigree data set included information from 75,088 animals. Both models included fixed effects of animal age and age of dam at calving (2-16 years) as linear and quadratic covariables and, as random the animal direct genetic and contemporary groups effects. For YW, maternal genetic and permanent environmental random effects were also included in the models. Deviance information criterion (DIC) and a deviance based on conditional predictive ordinates (DCPO) were used to assess model fit. For PWG, DIC values were 531,166 (ANRM) and 531,033 (HIER) and DCPO values were 522,262 (ANRM) and 522,022 (HIER). For YW, these values were 548,931 and 547,831 (DIC) and 532,536 and 530,366 (DCPO) for ANRM and HIER, respectively. Therefore, for both traits, the HIER was the best fitting model. Postweaning direct heritability estimates obtained with both models were virtually the same (0.20 ± 0.01). For YW, direct heritability estimates were 0.38 ± 0.02 (ANRM) and 0.44 ± 0.02 (HIER) and maternal heritability estimates were 0.12 ± 0.02 (ANRM) and 0.03 ± 0.01 (HIER), showing a different partition of genetic effects in its direct and maternal components between these models. Moreover, the total heritability for YW was 0.37 ± 0.02 (HIER) and 0.31 ± 0.02 (ANRM). These results indicate that selection for growth in this population will achieve faster genetic progress when based on YW and on HIER.

Key Words: growth traits, uncertain paternity, Zebu

M41 Estimates of genetic parameters using random regression on B-spline functions for weights from birth to mature in Nelore cattle. A. A. Boligon^{*1}, L. G. Albuquerque¹, M. E. Z. Mercadante², and R. B. Lobo³, ¹*Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal, São Paulo, Brazil,* ²*Instituto de Zootecnia, Estação Experimental de Zootecnia de Sertãozinho, Sertãozinho, São Paulo, Brazil,* ³*Faculdade de Medicina de Ribeirão Preto, USP, Ribeirão Preto, São Paulo, Brazil.*

The aim of this study was to estimate (co)variance functions using random regression on B-splines for birth to mature weight. A total of 82,064 records from 8,145 females belonging to Nelore Cattle Breeding Program were analyzed. Models included additive direct and maternal effects, and animal and maternal permanent environmental effects as random. Contemporary group was defined including animals born on the same farm, year and season of birth, and belonging to the same group of age at recording (birth and every 45 days of age). Fixed effects were contemporary group and the covariables age of dam at calving (linear and quadratic effect) and orthogonal Legendre polynomials of animal age (cubic regression). Random effects were modeled using B-spline functions, considering different combinations of linear, quadratic and cubic polynomials for each individual segment. Residual effects were modeled using five age classes (0; 1-216; 217-660; 661-960 and 961-2920 days of age). Up to seven knots (six segments) were used for modeling animal additive direct and permanent environmental effects. For maternal genetic and environmental effects only one segment, with two knots in the extremity of the curve, was considered. Fifteen models, with 17 to 81 parameters, were used. A model including quadratic B-spline function with three segments for direct and permanent environmental effects, and one segment for maternal genetic and permanent environmental effects fitted best (47 parameters). Estimates of (co)variances obtained with the B-spline function were similar to that obtained using a multi-

trait (9 traits) and a random regression on Legendre polynomials for all random effects. Direct heritability estimates ranged from 0.27 to 0.43. The largest estimates of maternal heritability were for weights close to 240 days of age. The genetic correlation estimates between weights from birth to 8 years of age were moderate to high (0.32 to 0.95). Selection for weight at any age will promote changes in female mature weight. Random regression on B-splines of age can be used for genetic evaluation of growth in beef cattle.

Key Words: beef cattle, growth traits, random regression

M42 Estimation of genetic parameters for weights, scrotal circumference and testicular volume in Nelore cattle. A. A. Boligon^{*1}, L. G. Albuquerque¹, J. A. V. Silva², R. C. Sesana¹, and J. B. Junqueira¹, ¹*Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal, São Paulo, Brazil,* ²*Alta Genetics Brasil LTDA, Uberaba, Minas Gerais, Brazil.*

Data from 129,575 Nelore cattle born between 1993 and 2006, belonging to the Jacarezinho cattle raising farm, were used to estimate genetic parameters for scrotal circumference measured at 9 (SC9), 12 (SC12) and 18 (SC18) months of age and testicular volume measured at the same ages (TV9, TV12 and TV18) and to determine their correlation with weaning weight (WW) and yearling weight (YW), in order to provide information for the definition of selection criteria in beef cattle. Estimates of (co)variance components were calculated by restricted maximum likelihood method applying an animal model in multiple-trait analysis. The following heritability estimates and their respective standard errors were obtained for WW, YW, SC9, SC12, SC18, TV9, TV12 and TV18: 0.33 ± 0.02 , 0.37 ± 0.03 , 0.29 ± 0.03 , 0.39 ± 0.04 , 0.42 ± 0.03 , 0.19 ± 0.04 , 0.26 ± 0.05 and 0.39 ± 0.04 , respectively. Genetic correlations between the growth traits and scrotal circumference measures were positive and of low to moderate magnitude, ranging from 0.23 ± 0.04 to 0.38 ± 0.04 . On the other hand, high genetic associations were estimated between scrotal circumference and testicular volume at different ages (0.61 ± 0.04 to 0.86 ± 0.04). Correlation estimates between SC and TV measured at the same ages were 0.71 ± 0.03 , 0.75 ± 0.04 , 0.86 ± 0.04 , for 9, 12 and 18 month of age, respectively. Selection to increase scrotal circumference should result in higher WW, YW and testicular volume. In conclusion, in view of the difficulty in measuring testicular volume there is no need to change the selection criterion from scrotal circumference to testicular volume in Zebu breeds' breeding programs.

Key Words: beef cattle, genetic correlation, heritability

M43 Heritabilities, genetic correlations, and genetic trends for age at first calving and calving intervals in a Colombian Blanco Orejinegro-Angus-Zebu cattle population. O. D. Vergara^{1,3}, M. A. Elzo^{*2}, and M. F. Ceron-Muñoz¹, ¹*University of Antioquia, Medellín, Colombia,* ²*University of Florida, Gainesville,* ³*University of Córdoba, Monteña, Colombia.*

Age at first calving and calving interval are traits that have substantial impact on production costs of beef cattle operations in Colombia. However, assessment of genetic variation and evaluation of animals in multibreed populations for these traits is scant. Thus, the objectives of this research were to estimate genetic parameters and trends for age at first calving (AFC), interval between first and second calving (CI1), and interval between second and third calving (CI2) in a Colombian beef cattle population composed of Blanco Orejinegro, Angus, and Zebu

straightbred and crossbred animals. Data were analyzed using multiple trait mixed model procedures. Variance components and genetic parameters were estimated by Restricted Maximum Likelihood. The 3-trait model included the fixed effects of contemporary group (year-season of calving-sex of calf; sex of calf for CII and CI2 only), age of cow at calving (CII and CI2 only), breed direct genetic effects, and individual heterosis. Random effects were cow direct genetic and residual. Relationships among cows were accounted for. Program AIREML was used to perform computations. Heritabilities estimates for additive direct genetic effects were 0.15 ± 0.13 for AFC, 0.11 ± 0.06 for CII, and 0.18 ± 0.11 for CI2. Low heritabilities for AFC, CII, and CI2 suggest that nutrition and reproductive management should be improved to allow fuller expressions of these traits. Correlations between additive direct genetic effects for AFC and CII (0.33 ± 0.41) and for AFC and CI2 (0.40 ± 0.36) were medium and favorable, suggesting that selection of heifers for AFC would improve calving interval. Cow direct genetic AFC, CII, and CI2 yearly means from 1989 to 2004 showed negative trends, suggesting that some selection for these traits existed in this population during these years.

Key Words: cattle, reproduction, trends

M44 Genetic parameters and genetic trends for pre and postweaning growth in a Colombian Blanco Orejinegro-Romosinuano-Angus-Zebu cattle population. O. D. Vergara^{1,3}, M. A. Elzo^{*2}, and M. F. Ceron-Muñoz³, ¹University of Cordoba, Monteria, Colombia, ²University of Florida, Gainesville, ³University of Antioquia, Medellín, Colombia.

Genetic parameters and trends for weaning weight adjusted to 240 d of age (WW240), and weight gain from weaning to 24 mo of age (GW730) were estimated in a Colombian beef cattle population composed of Blanco Orejinegro, Romosinuano, Angus, and Zebu straightbred and crossbred animals. Data were analyzed using multiple trait mixed model procedures. Variance components and genetic parameters were estimated by Restricted Maximum Likelihood. The 2-trait model included the fixed effects of contemporary group (herd-year-season-sex), age of dam (WW240 only), breed direct genetic effects, breed maternal genetic effects (WW240 only), individual heterosis, and maternal heterosis (WW240 only). Random effects for WW240 were calf direct genetic, dam maternal genetic, permanent environmental maternal, and residual. Random effects for GW730 were calf direct genetic and residual. Program AIREML was used to perform computations. Heritabilities estimates for additive direct genetic effects were 0.20 ± 0.003 for WW240 and 0.32 ± 0.004 for GW730. Maternal heritability was 0.14 ± 0.002 for WW240. Low direct and maternal preweaning heritabilities suggest that nutrition should be improved to allow fuller expressions of calf direct growth and cow maternal ability. The genetic correlation between direct and maternal additive effects for WW240 was negative (-0.42 ± 0.009). The near zero (-0.04 ± 0.009) correlation between additive direct genetic effects for WW240 and GW730 suggested that genes affecting preweaning and postweaning growth may differ in this population. Calf, sire, and dam weighted yearly means showed negative trends for direct WW240 and GW730. Maternal WW240 showed near zero trends during these years. Trends for calf direct WW240 and GW730 followed sire trends closely, suggesting that more emphasis was placed on choosing sires than on dam replacements.

Key Words: beef cattle, genetic parameters, genetic trends

M45 Genotype by environment interaction in Nellore cattle for 450 day weight. M. G. Dib^{*1}, I. D. P. S. Diaz², F. R. de Araujo Neto², H. N. de Oliveira^{1,2}, R. B. Lobo³, and L. A. F. Bezerra³, ¹FMVZ-UNESP, Botucatu, SP, Brazil, ²FCAV-UNESP, Jaboticabal, SP, Brazil, ³FMRP-USP, Ribeirão Preto, SP, Brazil.

The object of the current study was to determine if there was a genetic by environmental interaction between the Brazilian states of Sao Paulo and Mato Grosso do Sul for the trait of 450 day weight. The data included weights from 42,160 progeny of 24,476 cows and 1,244 sires recorded from 1991 through 2006. Variance components were estimated using a multiple trait animal model in a Bayesian framework considering weights in the different locations as different traits. The model included fixed effects of contemporary group and effects of animal and residual as random. The genotype by environment interaction was verified through the genetic correlations. Results indicate that the genetic and residual components of variance differ between the two states. Estimates of heritability (SD) for Sao Paulo and Mato Grosso do Sul were 0.4367 (0.025) and 0.3634 (0.019), respectively. The genetic correlation (SD) was 0.9294 (0.031), which does not suggest an important genotype by environment interaction for 450 day weight.

Key Words: 450 day weight, genotype by environment interaction, Nellore cattle

M46 Random regression analyses using B-spline functions to model growth from birth to adult age in Canchim cattle. F. Baldi^{*1}, L. G. Albuquerque¹, and M. M. Alencar², ¹Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal (SP), Brazil, ²Embrapa Pecuária Sudeste, São Carlos (SP), Brazil.

The objective of this work was to use random regression models on B-splines functions, to estimate covariance functions for weights from birth to adult age in Canchim cattle. Data comprised 49,011 weight records on 2,435 females belonging to Southeast - Embrapa Cattle. Fixed effects of contemporary groups (year and month at birth and at weighing), age of dam at calving (quadratic) and a cubic regression on Legendre polynomials of animal age covariable were included in the model. A random regression on b-splines functions of age at recording was applied to model animal and maternal genetic and permanent environmental effects. Residual variances were considered heterogeneous with 4 classes. The same data set was analyzed with a multi-trait model for weights at standard ages (birth, weaning, 12, 18, 24 and 30 months of age, and at 6 years of age). Genetic direct and maternal and maternal permanent environmental effects were considered as random for weights from birth to 24 months of age. For weights after this age only genetic direct effect was considered. A total of twenty analyses, considering linear, quadratic and cubic b-spline functions and up to nine knots, were carried out. Spline functions of the same order were considered for all random effects. A model fitting quadratic b-spline functions, with four knots or three segments for direct genetic and animal permanent environmental effects and two knots for maternal genetic and permanent environmental effects, was the most adequate to describe the covariance structure of the data. Direct and maternal heritability estimates obtained with random regression models were similar to those obtained by multi-trait models, ranging from 0.19 to 0.43 and from 0.01 to 0.05, respectively. Similar direct and maternal genetic correlation estimates between weights from birth to adult age were obtained by random regression and multi-trait models, ranging from 0.42 to 0.97 and from 0.14 to 0.96. Random regression models

using b-spline functions as base functions were adequate to describe the covariance structure of the data.

Key Words: covariance function, genetic parameters, piece-wise polynomials

M47 Genetic parameter estimates for growth traits in Canchim cattle using random regression models. F. Baldi*¹, M. MAlencar², and L. G. Albuquerque¹, ¹Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal, São Paulo, Brazil, ²Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil.

The objective of this work was to estimate covariance functions, using random regression models on Legendre polynomials of age, for weights from birth to adult age in Canchim cattle. Data comprised 49,011 weight records on 2,435 females belonging to Southeast - Embrapa Cattle. The model of analysis included fixed effects of contemporary groups (year and month at birth and at weighing) and age of dam as quadratic covariable. Mean trends were taken into account by a cubic regression on orthogonal polynomials of animal age. Animal and maternal genetic effects and animal and maternal permanent environmental effects were modeled by random regression on Legendre polynomials of age at recording. Residual variances were modeled by a step function with 4 classes. The same data set was analyzed with a multi-trait model for weights at standard ages (birth, weaning, 12, 18, 24 and 30 months of age, and at 6 years of age). Genetic direct and maternal and maternal permanent environmental effects were considered as random for weights from birth to 24 months of age. For weights after this age only genetic direct effect was considered. A total of 12 random regression models with order from two to seven, were used to model the random effects. The model with quadric, cubic, quintic and linear polynomial degrees for direct and maternal genetic and animal and maternal permanent environmental effects fitted the data best. Estimates of direct and maternal heritabilities obtained with random regression models agreed with those obtained by multi-trait model, ranging from 0.19 to 0.38 and from 0.02 to 0.05, respectively. Direct and maternal genetic correlation estimates between weights from birth to adult age obtained by random regression, ranging from 0.39 to 0.92 and from 0.10 to 0.97, respectively, and were similar to those from multi-trait model. Random regression models on Legendre polynomials are well capable to describe the covariance structure of the data.

Key Words: covariance functions, growth curve, orthogonal polynomials

M48 Performance group in G×E study for genetic evaluation of growth in Brazilian Nellore. L. O. C. Silva^{1,2}, S. Tsuruta*¹, J. K. Bertrand¹, A. Gondo², L. A. Josahkian⁴, P. R. C. Nobre⁴, and A. N. Rosa², ¹University of Georgia, Athens, ²EMBRAPA, Campo Grande, MS, Brazil, ³CNPq, Brasilia, DF, Brazil, ⁴ABCZ, Uberaba, MG, Brazil.

The objective of this study was to analyze the importance of G×E interaction when evaluating Nellore in Brazil. Data included 588,461 weaning weights (WW) and yearling weights (YW) from 1,335,354 animals. Data were collected from 1979 to 2007 by Zebu Cattle Brazilian Association (ABCZ). Records from grazing were 97% of the total. A six-trait model was used that considered WW and YW within three performance groups (PG, 1-low; 2-medium; 3-high performance), including 1/3 of the contemporary group (CG) each. PG was created based on the averages of adjusted WW and YW for CG. CG was defined by sex, farm, year,

season, and feeding management. Fixed effects besides CG included age of the animals at weighing within CG (linear covariable) and age of dams at calving (linear and quadratic). Random effects in the model were direct and maternal. Variance components of WW and YW were estimated with Gibbs sampling using five exclusive random samples with 60,000 animals each. The first 50,000 Gibbs samples were discarded as burn-in and the following 250,000 were used to calculate posterior means and SD of (co)variances. Prediction of breeding values and accuracy were also obtained. The ratios PG3/PG2 and PG2/PG1 were 1.15 for WW and 1.2 for YW. Direct and maternal heritabilities for WW (0.18±0.01; 0.24±0.01) and YW (0.29±0.01; 0.14±0.01) within each PG were similar with results from other Zebu breeds. Direct genetic correlations between different PGs for WW and YW were around 0.86±0.03. Maternal correlations were close to the direct ones. These results showed that even in different PGs, similar sets of genes are responsible for expression of WW and YW. Rank correlations between PG1 and PG3 for direct and maternal effect for sires with accuracy ≥ 0.40 were 0.97 and 0.94 for WW and 0.96 and 0.85 for YW. Results indicate no substantial re-ranking of sires in environments with different level of production.

Key Words: Zebu beef cattle, growth weight, G×E interaction

M49 Residual feed intake and reproductive performance of heifers sired by high or low RFI EBV bulls. J. M. Bormann*¹, D. W. Moser¹, T. T. Marston², and K. C. Olson¹, ¹Kansas State University, Manhattan, ²University of Nebraska, Lincoln.

Residual feed intake (RFI) is the difference between an animal's actual feed intake and its predicted intake based on its body weight and growth rate. The objective of this study was to determine differences in performance and fertility between heifers sired by high or low RFI EBV bulls. Bulls with low or high genetic merit for RFI were selected from the Australian Angus Association sire summary and mated to Angus cross commercial cows at the Kansas State University Cow-Calf Unit in 2006. The average RFI EBV for the low RFI (efficient) and high RFI (inefficient) bulls were -0.55 kg (n = 4) and 0.27 kg (n = 5). Heifers (n = 49) were sent to a commercial bull test station for a feed intake and gain test of 57 days. Heifers were allowed *ad libitum* intake of a high roughage, complete diet (approximately 1.05 Mcal/kg ME). Biweekly body weights were collected and used to calculate mid-test body weight and average daily gain. Actual feed intake was regressed on mid-test metabolic body weight and average daily gain to calculate an expected feed intake for each heifer. RFI was calculated by subtracting the expected intake from the actual intake. Heifers were synchronized and bred by AI one time followed by natural service. LSMeans for heifers sired by low and high RFI bulls were 0.11 kg and -0.09 kg (P = 0.62) for RFI, 11.65 kg and 11.46 kg (P = 0.65) for dry matter intake, 18.43 kg/kg and 14.86 kg/kg (P = 0.47) for feed conversion ratio, and 0.72 kg/day and 0.67 kg/day (P = 0.49) for average daily gain. Weaning weight, on-test weight, and off-test weight were also similar between groups (P > 0.05). There was no difference between groups in first service or overall pregnancy rate (P > 0.05). Heifers in this study were being developed at a relatively low rate of gain. Genetic differences in RFI calculated in growing bulls may not have been expressed on the lower plane of nutrition of these developing heifers. There appeared to be no detrimental effect of selection for RFI on reproductive performance of heifers.

Key Words: beef, residual feed intake, breeding value

M50 Association between carcass and meat quality traits, and phenotypic residual feed intake, breed composition, and temperament in Angus-Brahman multibreed cattle. M. A. Elzo*¹, D. D. Johnson¹, D. G. Riley², G. R. Hansen³, G. C. Lamb⁴, R. O. Myer⁴, 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.

Increasing production costs emphasize the need to identify and multiply cattle that are efficient at converting feed into beef of desirable quality. The objective was to study the association between 6 carcass and 6 meat quality traits and breed group (Angus (A), Brahman (B), Brangus, $\frac{3}{4}$ A $\frac{1}{4}$ B, $\frac{1}{2}$ A $\frac{1}{2}$ B, and $\frac{1}{4}$ A $\frac{3}{4}$ B), residual feed intake (RFI) group (high: RFI > 0.85 kg; medium: $-0.85 \text{ kg} \leq \text{RFI} \leq 0.85 \text{ kg}$; low: RFI < -0.85 kg; SD = 1.7 kg), and exit velocity (EV) in 170 steers born in 2006 and 2007. Carcass traits were hot carcass weight (HCW), dressing percent (DP), longissimus muscle area (LMA), fat thickness (FT), kidney, pelvic, and heart fat (KPH), and marbling score (MS). Meat quality traits were Warner-Bratzler shear force (SF), tenderness score (TS), juiciness (JU), flavor (FL), thaw loss (TL), and cooking loss (CL). Data for EV and RFI were from 70-d postweaning feeding trials at a GrowSafe automated feeding facility. Calves were finished at a feedlot in Texas and commercially slaughtered at roughly 14 mm of FT. Carcass data were taken at the slaughter facility, and meat quality data measured at the Florida Meat Processing Lab. Traits were analyzed using single-trait mixed models. Fixed effects were contemporary group (year-pen), RFI group, age of calf, B fraction of calf, calf heterozygosity, and mean EV. Random effects were sire and residual. High RFI steers had smaller LMA ($P < 0.005$) than low RFI steers. High and medium RFI steers had higher ($P < 0.0002$) MS than low RFI steers. Brahman had lighter HCW ($P < 0.0006$), smaller LMA ($P < 0.0001$), thinner FT ($P < 0.02$), lower MS ($P < 0.0001$), higher SF ($P < 0.0003$), and lower TS ($P < 0.0001$) than Angus. Exit velocity was non-significant for either carcass or meat quality traits.

Key Words: carcass, meat quality, feed intake

M51 Temperature and humidity as criteria of between states differences in beef cattle growth rate. M. Lukaszewicz^{1,2}, J. L. Williams*¹, J. K. Bertrand¹, and I. Misztal¹, ¹University of Georgia, Athens, ²Polish Academy of Sciences, Jastrzebiec, Poland.

The division of the US into regions distinguishes between northern ("cold") and southern ("hot") regions, while from East to West three zones are defined (east, mid-west and west). The latter corresponds with humidity distribution across the US. Neither classification perfectly matches the accepted region division leaving, within regions, states that differ climatically from the others. On the other hand GxE studies in cattle address the problem only from the temperature (heat) point of view. The aim of this analysis was to find out whether GxE interaction can only be attributed to temperature differences or if humidity affects beef cattle growth as well. Data were provided by the American Angus Association. Only states which could have been attributed a class of temperature (lower or higher than 55o F annual average) and a class of humidity (lower or higher than 65%) were considered. That excluded states like Kansas, Kentucky, Oregon, Washington, and both Dakotas as either they were spread over two temperature or over two humidity zones. Post weaning gain was highest (169kg, n=680741) in states described as cold/humid, and lowest (146kg, n=420570) in hot/humid ones. Intermediate gains (ca 158kg, n=1077665) were found in hot/dry and cold/dry states. Thus, the difference in gain associated with temperature is only due to high humidity. Records in the 3 groups of states were treated as different traits. Three-trait model included the effects of

contemporary group (sex, age, dam's age) as yearlings and genetic additive effect. Estimates were obtained with Gibbs sampling on 1,477,563 records after removing records with missing information. Heritabilities were 0.20, 0.18, 0.21 (se 0.01 to 0.02) in cold/humid (NE), hot/humid (SE), and "dry" (W) states, respectively. Genetic correlations were all around 0.75 (se=0.02); there may be moderate re-ranking among the regions. Three breeding value estimates could be needed if sires are to be used nationwide.

Key Words: post weaning gain, Angus, climate G×E

M52 Multiple-trait genetic analysis of weight at week 8, age at sexual maturity and initial egg weight in Iranian indigenous chickens. H. Farhangfar*, S. M. Hosseini, and M. E. Navidzadeh, *Birjand University, Birjand, Iran.*

A multivariate animal model was used to estimate variance and covariance components as well as genetic parameters of weight at week 8, age at sexual maturity and initial egg weight for Iranian indigenous chickens. Data set consisted of 3822 records collected from an indigenous chicken flock. The total of progeny was 3822 representative of 179 sires and 1106 dams respectively. In the model, fixed environmental factors of generation (at two levels) and hatch number (at eight levels) along with random direct additive genetic effect were included. The average weight at week 8 (W8), age at sexual maturity (ASM) and initial egg weight (at first week of laying, EW1) were 495 g, 160 d and 39.3 g respectively. The animal model was fit using DMU package for obtaining restricted maximum likelihood estimates of variance and covariance components. For all traits, design matrices were the same. Additive genetic variance components for W8, ASM and EW1 were 1774, 34.46 and 4.71 respectively while environmental variance components were 2234, 81.91 and 18.69 respectively. Heritability estimates of W8, ASM and EW1 were found to be 0.44, 0.3 and 0.2 respectively. Additive genetic correlation between W8 and ASM was -0.03 while it was positively correlated with EW1 (0.23). A positive genetic correlation was found between ASM and EW1 (0.42). At environmental level, W8 were negatively correlated with ASM (-0.14) and EW1 (-0.0008). ASM had a positive environmental correlation with EW1 (0.4). Positive phenotypic correlations were found between W8 and EW1 (0.07) and between ASM and EW1 (0.4) while W8 was negatively correlated with ASM (-0.1).

Key Words: Iranian indigenous chickens, genetic parameters, animal model

M53 Comparative analyses of some growth traits of straight-runs and separate sex reared broilers. O. T. F. Abanikannda¹, A. O. Leigh¹, M. O. Akinsola¹, M. Orunmuyi², O. N. Coker³, and K. A. Binuyo*¹, ¹Lagos State University, Ojo - Lagos, Nigeria, ²Ahmadu Bello University, Zaria, Kaduna State, Nigeria, ³S & D Farms Nigeria Limited, Odeda, Ogun State, Nigeria.

Feeds and feeding are the largest sources of expenditure in commercial broiler production. The need to cut down on the cost of feed / feeding, by reducing wastages and improving feed conversion efficiency of the birds impels an investigation into some genetic and non-genetic factors affecting some growth traits of the birds. This study aims at evaluating growth traits of broiler birds reared as straight-runs (mixed) or reared separately in sex demarcated lots. A total of sixty broiler birds derived from three commercial strains (Anak, Marshall and Ross) were studied, with each strain contributing twenty birds comprising ten each for male and female. However, two of the Anak male birds died two weeks into the experiment. Measurements were taken over a period of eight weeks up to the point when the birds were slaughtered. Three traits of economic

importance studied were initial weight, slaughter weight and average daily gain (ADG). Factors investigated included Rearing Group (G), Breed (B), Initial Weight (I) and interaction between Rearing Group and Breed. The statistical model describing the study was $Y_{ijkl} = \mu + G_i + B_j + I_k + (GB)_{ij} + e_{ijkl}$. Rearing group, breed and interaction of rearing group and breed were all significant ($P < 0.05$) on both the slaughter weight and average daily gain, accounting for about 58% of total variation in both traits. With the exception of Ross strain, separately reared males were heavier and gain faster than females, though not statistically significant ($P > 0.05$), while the separately reared birds were significantly ($P < 0.001$) heavier and gained faster than the mixed birds or straight runs. The study revealed that irrespective of the strain studied, birds reared as separate sex gained better and were heavier at slaughter than those reared as mixed sexes. This method of rearing would be better appreciated in strains that could easily be sexed as male or female, i.e. colour or feather sexed. Further investigation of other productivity indices of broilers reared as separate sex is recommended.

Key Words: mixed sex, separate sex, growth traits

M54 Analysis of androgen receptor gene in dairy bulls. C. Foresta², A. Garolla², D. Zuccarello², and M. Cassandro^{*1}, ¹University of Padova, Agripolis, Legnaro (PD), Italy, ²University of Padova, Padova, Italy.

Aim of this study was to identify the complete sequence of the transcript of the androgen receptor (AR) gene in cattle. At present, no information on the whole sequence of the AR gene is available, both in the NCBI (www.ncbi.nlm.nih.gov) and in the scientific literature: in particular, only some fragments for the exons 1-4-8 are described. Reconstruction of the coding sequence (cDNA) of AR was performed by extraction of RNA from skin biopsy of 6 Holstein Friesian bulls, which was then converted in cDNA by random examers and amplified using primers designed on human AR sequence or partial sequence of bovine AR already existing in literature. All amplified fragments were then sequenced (both forward and reverse) and the chromatograms aligned with the sequence of 8 already known structures of the AR gene (both from human and other species). Through the prediction of the protein sequence and the protein alignment (Clustal W), it was possible to compare the sequences to highlight the differences between the different species under consideration. The results obtained showed that, except for exon 1 (coding for the transactivation domain - NTD) known to be hypervariable, the sequence is highly conserved compared to other animal species. In particular, the serine residues at position 16, 83, 96, 261, 313, 429 and 654, representing the sites of phosphorylation known to activate the receptor, are completely preserved, as well as the region FxxLF, essential for the correct folding of the quaternary structure of the protein. Finally, the analysis of repeated sequences showed that the bull has a shorter poly-GLN primary site (aa 58-91) and a longest poly-GLN secondary site (aa 195-200) compared to man, with a peculiar insertion of 4 additional amino acids in the poly-GLY site (aa 451-476). Moreover, the extension of the sample analyzed and the evaluation of bulls of other breeds will allow us to understand the impact of the sequence variations found in this study, in terms of change in the androgen receptor function of the bull.

Key Words: androgen receptor gene, fertility, Holstein cattle

M55 Evidence for a genetic contribution to bovine viral diarrhoea vaccine response in beef calves. X. Fang^{*1}, T. A. Henrickson¹, C. Maltecca², and M. G. Gonda¹, ¹South Dakota State University, Brookings, ²North Carolina State University, Raleigh.

In this study we hypothesized that Bovine Viral Diarrhoea Virus (BVDV) vaccine response varies among calves and that genetics may contribute to this variation. To test this hypothesis, BVDV humoral vaccine response, as measured by antibody ELISA, was collected from Angus and Angus-Simmental calves (N=85) that were sired by a total of 8 bulls. Calves born between February and April 2008 at the SDSU cow-calf unit entered the study. All individuals were vaccinated with Bovi-Shield GOLD-5, which includes modified-live virus strains type 1 and 2 (Pfizer, Inc., Exton, PA). Two blood samples were collected at time of vaccination (d=0) and post-vaccination (d=41). Day 0 samples were used to measure maternal BVDV antibody and test for persistently infected (PI) BVDV calves, while d 41 samples were used to measure humoral BVDV response to the vaccine. PI calves were detected by real-time RT-PCR for BVDV on RNA isolated from plasma samples (Qiagen, Valencia, CA). Positive controls were included for real-time RT-PCR and viral RNA isolation methods. BVDV antibody ELISA (Idexx, Inc., Westbrook, ME) was used to measure total amount of antibody present at days 0 and 41. Day 0 and 41 antibody concentrations were converted to sample-to-positive (S/P) ratios, and maternal antibody S/P ratios (d=0) were subtracted from S/P ratios at d 41. To investigate a possible effect of genetics on BVDV vaccine response, an ANOVA model including effects of sire, month of birth, sex, and breed composition was fitted. None of the calves tested positive for BVDV by real-time RT-PCR. The mean d 0 and d 41 S/P ratios were 0.744 ($\sigma = 0.400$) and 0.509 ($\sigma = 0.242$), respectively. Sire, month of birth, and gender were significantly associated with BVDV vaccine response ($P < 0.05$). This study is the first to show that sire affects BVDV vaccine response in calves, suggesting that genetics contributes to BVDV vaccine response variation. If genetics contributes to variation of BVDV vaccine response, then selecting high responders to BVDV vaccines may be one strategy for improving calf health.

Key Words: bovine viral diarrhoea virus, vaccine, ELISA

M56 Estimation of genetic parameters and transmitting ability for Minnesota Johne's milk ELISA test. S. A. Attalla^{*1,3}, A. J. Seykora¹, J. B. Cole², and B. J. Heins¹, ¹University of Minnesota, Saint Paul, ²Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, ³Cairo University, Giza, Egypt.

A total number of 45,907 results for Johne's Milk Enzyme-Linked Immuno Sorbent Assay (ELISA) test were received from Minnesota DHIA, of which 40,177 records were from herds with at least one positive Johne's cow. Pedigree information was available for 19,304 Holstein cows from AIPL USDA representing 22,694 total records. Milk ELISA optical density was transformed using a natural logarithm (lnOD). Heritability, repeatability, and breeding values for lnOD were estimated fitting a linear animal model. Variables for statistical analysis were the fixed effects of test date, and age at test day and lab control OD were covariables. Herd, animal, and permanent environmental effects were random effects in the model. All fixed effects were highly significant ($P < 0.001$). Heritability of lnOD was 0.06 ± 0.01 , while repeatability was 0.34 ± 0.02 . The correlations between the breeding values of lnOD for 108 Holstein AI sires that had at least 30 daughters in this study and their corresponding USDA PTAs for milk, fat, protein, productive life (PL), daughter pregnancy rate (DPR) and Net Merit (NM) were calculated. The correlations between lnOD breeding values and corresponding PTAs were: milk (0.01); fat (-0.05); protein (0.0); PL (-0.26); DPR (-0.21); SCS (0.19); and NM (-0.26). These correlations suggest that selection for PL, DPR, SCS and NM could improve the resistance of Holstein cattle against Johne's disease.

Key Words: Johne's disease, genetic parameters, predicted transmitting ability