Breeding and Genetics: Beef and Small Ruminant Breeding

W27   Effects of *Bos indicus* breeding on plasma pregnancy-associated glycoprotein (PAG) concentrations and fetus size in early gestation. P. M. Morelli*[1], D. O. Rae[2], S. E. Johnson[1], and A. D. Ealy[1], [1]*University of Florida, Department of Animal Sciences, Gainesville, [2]University of Florida, Department of Large Animal Clinical Sciences, Gainesville.*

Cross-breeding *Bos indicus* and *Bos taurus* breeds improves various production traits for cattle maintained in hot climates. Limited information exists describing pregnancy specific events that are influenced by these cross-breeding strategies. In this study, transrectal ultrasonography was used to measure fetal size at 52 to 55 d of gestation in cows composed of Angus (>80% Angus; n = 17), Brangus (n = 15) and Brahman (≥25% Brahman; n = 58) genetics. Blood was collected for the measure of plasma pregnancy associated glycoprotein (PAG) content by ELISA. Multiparous cows were used in a timed AI protocol for this study. Multiples sires were used to generate fetuses with varying degrees of Angus/Brahman cross-breeding. Blood was harvested once between d 52 and 55 post-TAI. Day of blood collection and ultrasonography was used as a covariate. PAG concentrations were greater ($P \leq 0.05$) in Brangus and Brahman cows than Angus cows (9.8, 10.4 and 5.9 ng/ml, respectively; SE = 1.93). Fetus size was smaller ($P \leq 0.05$) in Brangus and Brahman cows than Angus cows (27.7, 28.8 and 34.8 mm, respectively; SE = 3.24). No differences in PAG concentrations and fetus size were observed based on the amount of Angus, Brangus and Brahman genetics in the fetus. In summary, both PAG concentrations and fetus size differed based on the degree of Angus/Brahman cross-breeding of the cow but not the fetus. This suggests that the maternal system plays an active role in controlling placental activity and early fetal development, and Brahman-based cows control these events differently than Angus cows during early pregnancy.

Key words: cross-breeding, pregnancy associated glycoprotein (PAG), fetus size

W28   Genetic parameters and genetic trends for growth and reproductive traits in a Colombian multibreed beef cattle population. O. D. Vergara[1] and M. A. Elzo*[2], [1]*University of Cordoba, Monteria, Colombia, [2]University of Florida, Gainesville.*

Genetic parameters and trends for weaning weight adjusted to 240 d of age (WW240; n = 9,668), and weight gain from weaning to 24 mo of age (GW730; n = 1,357), age at first calving (AFC; n = 1,615), and interval between first and second calving (CI1; n = 1,189) were estimated in a Colombian beef cattle population composed of Blanco Orejinegro, Romosinuano, Angus, and Zebu straightbred and crossbred animals. Variance components and genetic parameters were estimated by Restricted Maximum Likelihood. The 4-trait mixed model included the fixed effects of contemporary group (herd-year-season-sex; sex = sex of progeny for CI1), 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; and random effects for AFC and CI1were cow direct genetic and residual. Program AIREML was used to perform computations. Heritabilities estimates for additive direct genetic effects were 0.19 ± 0.003 for WW240, 0.53 ± 0.004 for GW730, 0.11 ± 0.007 for AFC, and 0.05 ± 0.001 for CI1. Maternal heritability was 0.11 ± 0.002 for WW240. The high direct heritabil-

ity for GW730 suggests that selection for this trait is feasible in this population. The genetic correlation between direct and maternal additive effects for WW240 was negative (−0.18 ± 0.009). Correlations between additive direct genetic effects for all traits were close to zero. Calf and cow weighted yearly means showed negative trends for direct growth traits (−0.53 ± 0.19, P < 0. 05 for WW240; −2.64 ± 0.55, P < 0. 001 for GW730), and AFC (−0.04 ± 0.02, P < 0. 05). Cow direct genetic CI1 yearly means showed positive trends (3.01 ± 0.42, P < 0.001). This suggests that some selection for AFC existed in this population during these years and other traits were neglected.

Key words: cattle, growth, reproduction

W29   Combining ability of nine tropically adapted and temperate breeds for growth and ultrasound traits in Colombia. C. A. Martinez[1], C. Manrique[1], M. A. Elzo*[2], and A. Jimenez[1], [1]*Universidad Nacional de Colombia, Bogota, Colombia, [2]University of Florida, Gainesville.*

Colombia is currently using crossbreeding strategies involving tropically adapted and temperate cattle breeds to improve beef cattle productivity for growth and carcass traits under pasture conditions. The objective of this research was to compare the combining ability of sires from 2 tropically adapted *Bos taurus* breeds (Blanco Orejinegro: BON; Romosinuano: RS), 3 tropically adapted *Bos indicus* breeds (Gray Brahman: GB; Guzerat: GZ; Red Brahman: RB), and 4 temperate *Bos taurus* breeds (Braunvieh: BV; Limousin: LIM; Normand: NM; Simmental: SIM) when mated to Gray Brahman cows for birth weight (BW), and adjusted weights (W), ultrasound ribeye area (REA) and backfat (BF) measured at 4 (W4, REA4, BF4), 7 (W7, REA7, BF7), 12 (W12, REA12, BF12), and 15 (W15, REA15, BF15) mo of age. Data were from 352 calves from 2 herds (22 to 100 per breed group) sired by 37 bulls (3 to 12 sires per breed). The model included breed group of calf, contemporary group (herd-year-season-sex) and age of calf (ultrasound traits only) as fixed effects, and sire and residual as random effects. Least squares means (LSM) for BW, W4 and W7 were similar across breed groups, whereas calves from SIM sires were heavier than calves from GB sires at 12 (42.8 ± 9.9 kg; P < 0.0009) and 15 mo of age (35.0 ± 7.9 kg; P < 0.0008). The LSM for REA were similar for crossbred calves from sires of all breeds, except for calves from LIM sires whose REA were larger than those of calves from GZ (11.4 ± 3.0 mm²; P < 0.0078), NM (11.0 ± 2.9 mm²; P < 0.0103), SIM (10.3 ± 2.8 mm²; P < 0.0143) and RB sires (11.3 ± 2.4 mm²; P < 0.0002) at 4 mo of age, and from GB sires at 4 (11.3 ± 2.4 mm²; P < 0.0002), 7 (6.8 ± 1.9 mm²; P < 0.0174), 12 (9.7 ± 1.8 mm²; P < 0.0224), and 15 mo of age (11.3 ± 2.8 mm²; P < 0.0051). The LSM for BF were similar across breed groups and calf ages.

Key words: crossbreeding, growth, ultrasound

W30   Genetic parameters and trends for age at first calving in Brahman cows raised in Brazil. J. C. DeSouza*[1], M. Silveira[2], M. A. Pereira[3], P. B. Ferraz Filho[4], J. A. DeFreitas[5], R. M. DaSilva[2], C. H. M. Malhado[6,10], C. H. M. Cavalari[3], M. F. Mota[7], H. J. Fernandes[8], and W. R. Lamberson[9], [1]*Mato Grosso do Sul Federal University, CPAQ/ Animal Science, MS, Brazil, [2]Student of MSc. of animal science course, UFMS, Campo Grande, Brazil, [3]Brazilian Association of Zebu Breeders, Uberaba, Brazil, [4]Mato Grosso do Sul Federal University, Tres Lagoas, Brazil, [5]Paraná Federal University, Palotina, Brazil, [6]South*

524

J. Anim. Sci. Vol. 89, E-Suppl. 1/J. Dairy Sci. Vol. 94, E-Suppl. 1

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In 1997 the Brahman breed was introduced in Brazil to potentially increase at Brazilian beef cattle production. For this to occur, reproductive traits are very important. The objective of this study was to estimate genetic parameters and genetic trend for age at first calving in Brahman Beef cattle. The data were 5,432 ages at first calving from 1997 at 2008 provided by the Brazilian Zebu Cattle Association and included information on different regions of the country. The genetic parameters were estimated by using the MTDFREML package with an animal model and included the fixed effects of contemporary group (year, season, conception type (1: not in vitro fertilization; VF; 2: in vitro fertilization), nutrition type (1: Pasture, 2: pasture + concentrate, 3: Feed lot) and a random animal effect. The genetic trend was estimated by linear regression of the breeding value of calving interval on cow birth year. The genetic trend was -0.053 d/year ($P = 0.03$) and the $R2$ of model was 0.38. The estimated genetic variance was 8.89 and phenotypic variance was 49.67 yielding a heritability of 0.18 ± 0.05 and the environmental proportion of the total variance was 0.82 ± 0.05. The genetic gain was small, but in the favorable direction. Breeding values averaged -0.107 in 1997 and improved to -0.707 in 2008 for a total reduction in the age at first calving of 0.599 mo. The genetic variance for age at first calving is small and suggests that the trait not a good candidate for direct selection.

Key words: beef cattle, age at first calving, Zebu

W31   Allometric growth study of Guzerá cattle under a performance test on grazing regimen. R. C. Sousa*[1], I. G. Pereira[1], P. V. R. Paulino[2], S. D. J. Villela[1], R. A. M. Oliveira[1], A. P. L. Tonaco[1], F. S. Coelho[1], and F. A. Carvalho Neto[3], [1]Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, MG, Brazil, [2]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [3]Colorado State University, Fort Collins.

A performance test of Guzerá cattle grazing on Brachiaria brizantha pasture was conducted on a private ranch in Brazil during 294 d. The study was assisted by the Brazilian Association of Zebu Breeders. During this performance test the development of the animals were measured by morphometric traits (rump height, body length, and heart girth), scrotal circumference, rib eye area (by ultrasound) and body weight. Forty-five Guzerá bulls were used with an initial body weight of 219.9 ± 38.05 kg and age of 325.8 ± 28.0 d old. The animals grazed on Brachiaria brizantha pastures and were supplemented with loose supplements during the performance test duration to overcome protein deficiencies in the pasture. A 70 d adaptation period was allowed and thereafter the animals were weighed and evaluated every 56 d. An exponential model was used to study the allometric growth of these animals. A log-transformation of the initial model was performed to produce a linear model. Growth was considered isogonic when b = 1 and heterogonic when b ≠ 1 (b > 1, positive and b < 1, negative). The allometric growth of all traits evaluated was heterogonic and negatively correlated to body weight and age of the animals (Table 1). However, coefficients of determination from the allometric equations had moderate values, suggesting that more studies with larger group of animals should be conducted to gather greater amount of information to describe the growth pattern of Guzerá bulls under tropical grazing conditions.

Table 1. Allometric coefficients of morphometric traits, scrotal circumference and rib eye area related to BW of Zebu bulls

Trait	a	b	s(b)	R^2	P-value
RH	54.09	0.16	0.01	0.63	*
BL	32.43	0.24	0.01	0.65	*
HG	31.64	0.28	0.01	0.75	*
SC	0.43	0.71	0.02	0.80	*
REA	1.78	0.51	0.02	0.74	*

*$P < 0.01$. a = intercept of linear regression; b = allometric coefficient; s(b) = standard error of the allometric coefficients; R^2 = coefficient of determination; RH = rump height; BL = body length; HT = heart girth; SC = scrotal circumference, REA = rib eye area.

Key words: beef cattle, morphometric measurements, Zebu

W32   Growth curves of Guzera bulls on grass regimen under performance test. R. C. Sousa[1], I. G. Pereira*[1], P. V. R. Paulino[2], A. V. Pires[1], F. F. Silva[1], R. A. M. Oliveira[1], A. P. L. Tonaco[1], and F. A. Carvalho Neto[3], [1]Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, MG, Brazil, [2]Universidade Federal de Viçosa, Viçosa, MG, Brazil, [3]Colorado State University, Fort Collins.

Data derived from a performance test of Guzera bulls on pasture regimen was used to analyze the growth pattern. Forty-five post-weaning bulls (325.8 ± 28 d old) with initial body weight of 219.9 ± 38.05 kg were used. The animals grazed on Brachiaria brizantha pastures and were also supplemented to attain a body weight gain of up to 1.5 kg/d. All animals were maintained under the same feed regimen for a period of 294 d. Body measurements were taken every 56 d throughout the study. The objective of the study was to develop a nonlinear function that could best describe the growth pattern of these animals. All models tested converged, but it was observed that there was a significant variation on asymptotic weights and mean square error (MSE) between models. The models of Von Bertalanffy and Brody showed more realistic values compared with the other models (Table 1). We observed that the values produced by the Bertalanffy model were slightly lower than the values from the Brody model when comparing the estimates of the asymptotic weights from the 2 models (Table 1). The asymptotic weight estimated by the Gompertz model proved to be a little lower, while the value was much lower than the others in the Logistic model (Table 1). In most studies in the available literature, the Brody model presents the largest estimates of asymptotic weight, and the Logistic model consistently produces lower estimates. It can be observed that the growth curves fitted by Von Bertalanffy and Brody models had lower mean square error (MSE) and higher coefficient of determination when compared with the other models. The Von Bertalanffy model was chosen as it best represented the growth curve of the Guzerá animals as it had the best fit to the data considering the criteria used.

Table 1. Parameter estimates of growth curves of grazing Guzera bulls under performance test

Model	A	B	K	r^2	MSE
Von Bertalanffy	627.97	0.60	0.00	0.97	641.98
Brody	787.71	0.95	0.00	0.97	681.16
Gompertz	568.26	2.53	0.00	0.97	703.73
Logistics	466.39	7.51	0.01	0.96	939.39

MSE = mean square error; A = asymptotic weight when t tends to plus infinity; B = an integration constant, related to the initial BW; K = maturation rate, an indicator of the speed with which the animal approaches its mature; r^2 = coefficient of determination.

Key words: nonlinear models, age, Zebu

W33   Variance components in growth traits of Guzera cattle breed with different models. I. S. Silva*[1], I. U. Packer[2], C. M. R. Melo[3], L. O. C. Silva[4], and R. A. A. Torres Junior[4], *[1]University of Brasília - UnB, Brasília /DF, Brazil, [2]University of São Paulo - USP/ESALQ, Piracicaba/SP, Brazil, [3]University of Santa Catarina - UFSC, Florianópolis/SC, Brazil, [4]Embrapa Gado de Corte, Embrapa Gado de Corte, Campo Grande/MS, Brazil.*

A total of 130,424 body weight records of Guzera cattle collected in 8 periods every 90 d were used to estimate (co)variance components. REML was used with 4 models: model 1 included genetic direct (GA), genetic maternal (GM) environmental permanent maternal (AM) and residual random effects; model 2 excluded GM; model 3 excluded AM and model 4 excluded both GM and AM. Likelihood ratio test did not show significant differences ($P < 0.05$) between models 1 and 2 in almost all ages. Estimates of direct heritabilities h^2 in models 1 and 2 were similar. The values of h^2 decreased from birth to second age then maintained the same value until the weaning and increased after that. Direct heritability estimates for weight in age classes close to 205, 365 and 550 d, by models 1 and 2, were respectively 0.15, 0.12 and 0.14. Estimates of the same parameter obtained by models 3 and 4 were respectively 0.15, 0.14, 0.15 and 0.26, 0.19, 0.17. Heritability estimates from model 3 were larger due to the exclusion of the AM term of the analysis. Estimates of additive variance were greater with model 4. Model 2 adjusted better the data and required lesser processing time. The model comparison indicated that the GM effect did not improve fit.

Key words: beef cattle, maternal effects, estimates of variances

W34   Estimates genetic parameters for growth traits of Guzera cattle breed by single-trait and two-trait analysis. I. S. Silva*[1], I. U. Packer[2], C. M. R. Melo[3], L. O. C. Silva[4], and R. A. A. Torres Junior[4], *[1]University of Brasília - UnB, Brasília /DF, Brazil, [2]University of São Paulo - USP/ESALQ, Piracicaba/SP, Piracicaba/SP, Brazil, [3]Federal University of Santa Catarina - UFSC, Florianópolis/SC, Brazil, [4]Embrapa Gado de Corte, Campo Grande/MS, Brazil.*

The study aimed to estimate components of (co)variance and genetic parameters, comparing different single-trait and 2-trait models, for weight adjusted for the age-standard. A total of 55,063 body weights records adjusted to 120 (W120), 205 (W205), 365 (W365) and 550 (W550) days of age, from 22,949 animals belonging to 46 herds of Guzera breed, referring to the period of 1975 to 2001. In the single and 2-trait analyses 2 models were used to estimate the genetic parameters by the REML: model 1, as a complete model,, included direct and maternal genetic effects, as well as, maternal permanent environmen-

tal and residual effects; the model 2, as a reduced model, included the direct genetic effect and the maternal permanent environmental and residual effects. Likelihood ratio test did not show significant differences ($P < 0.05$) between models 1 and 2 in almost all ages. Estimates and behavior of variances for models 1 and 2 were similar, by the single-trait and 2-trait analyses. In the model 1 the maternal genetic variance estimates were low, mainly before the weaning. Direct heritability estimates by single-and 2-trait analysis for W120, W205, W365 and W550 were 0.15, 0.10, 0.17, 0.14 and 0.13, 0.10, 0.16, 0.15, respectively. Direct heritability estimated by models 1 and 2 were similar in the single-trait and 2-trait analyses. Estimates of maternal heritability were low for all ages. The genetic correlations were similar for models 1 and 2. The direct genetic correlation by models 1 and 2 for W120/W205, W120/W365, W120/W550, W205/P365, W205/W550 and W365/W550 were 0.80, 0.54, 0.54, 0.74, 0.62, 0.95 and 0.80, 0.54, 0.53, 0.74, 0.62, 0.95, respectively. Phenotypic and environmental correlations presented lower values when birth weight was involving. Overall it was observed a good agreement between the results for both models. The comparison between the models indicates that the reduced model was equivalent to the complete model.

Key words: beef cattle, maternal effects, variance components

W35   Real-time ultrasound measurements for the selection of growing animals of Bruna dels Pirineus beef cattle breed. M. Fina, J. Tarres, and J. Piedrafita*, *Grup de Recerca en Remugants, Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain.*

The application of ultrasound technology as a research tool allows the evaluation of carcass attributes in live animals. In addition, these measurements have potential to increase the rate of genetic progress including estimation of heritabilities and genetic correlations in genetic evaluation programs for carcass merits. The objective of this study was to estimate genetic parameters for real-time ultrasound measurements of loin area (LA), loin depth (LD) and subcutaneous fat thickness over the rump (SF) in Bruna dels Pirineus beef cattle, a breed selected for meat from the old Brown Swiss and similar to the American Braunvieh. The measurements were obtained using a Sonovet 2000 ultrasound unit equipped with a 3.5-MHz 17 cm linear transducer. A unique ultrasound technician preformed all measurements. Every animal (n = 352) was scanned 2 to 5 times for each variable to estimate the accuracy of ultrasonic records. The weight at scanning ranged from 158 kg to 608 kg. Intraclass correlations for LA, LD and SF measurements were 0.964, 0.988 and 0.875, respectively. Heritabilities and genetic correlations were estimated using multiple-trait restricted maximal likelihood. The final animal model included only one ultrasonic measurement per animal (the closest to the mean for each animal), fixed effects for year-season (7 breeding year-seasons over a 2.5-yr period) and feedlot, and the interaction of weight by sex as a linear covariate. The pedigree included 936 animals. Heritabilities for LA, LD and SF were 0.37 ± 0.13, 0.36 ± 0.12, and 0.27 ± 0.13, respectively. Genetic correlations between LA and LD, LA and SF, and LD and SF, were 0.63 ± 0.17, 0.36 ± 0.28, and -0.41 ± 0.42, respectively. The estimates of heritabilities and genetic correlations indicate that a relevant additive genetic variance exists for all 3 traits and supports the use of live animal ultrasonic measurements as a selection tool in breeding cattle.

Key words: real-time ultrasound, beef, selection

W36   Linear B-splines to model longitudinal weight records in Tabapuã cattle. G. R. O. Menezes*[1,2], R. A. Torres[2], R. A. A. Torres Júnior[1], L. O. C. Silva[1], A. Gondo[1], and R. F. Euclydes[2], [1]*Embrapa Beef Cattle, Campo Grande, MS, Brazil,* [2]*Federal University of Vicosa, Vicosa, MG, Brazil.*

This work was aimed at evaluating the feasibility of a random regression model with linear B-splines (RRM) to estimate (co)variance components and breeding values for body weight in beef cattle. Data comprised 359,707 body weight records from 1 to 600 d of age on 84,215 animals of the Tabapuã breed. RRM included as fixed effects contemporary group, age of dam and deviation of the animal's birth date to the average day of the calving season. As random effects, direct and maternal additive genetic and direct and maternal permanent environment effects were included. Six residual variance classes were assumed: 1–60, 61–180, 181–300, 301–420, 421–540 and 541–600 d. Six knots located at ages 0, 120, 240, 360, 480 and 600 d were considered. To compare the results obtained with RRM, a multi-trait model (MTM) was applied to standard pre-adjusted weights at 120, 240, 360 and 480 d of age. MTM's fixed and random effects were almost the same of the RRM, except for the direct permanent environment random effect. (Co)variance components were estimated using a Bayesian approach with Gibbs sampling. RRM presented good results, providing reliable (co)variance components and genetic parameters along the range of ages evaluated. Additionally, RRM showed no convergence problem. (Co)variance components and genetic parameters estimates generated by RRM and MTM were similar for all ages evaluated. For instance, direct heritabilities for body weights at 120, 240, 360 and 480 d of age, estimated by RRM and MTM, were 0.20 and 0.18; 0.21 and 0.18; 0.21 and 0.19; 0.24 and 0.19, respectively. These estimates were close to the ones obtained in other studies with Tabapuã cattle. For the ranking based on estimated breeding values, the models were similar, with larger differences among animals with less information, i.e., cows and calves. RRM allowed for better and greater use of available data. Data file used for RRM was 67% larger than the one used for MTM what can improve accuracies of the genetic evaluations. Thus, RRM is a feasible and interesting alternative to be applied in genetic evaluations for longitudinal growth traits in beef cattle.

Key words: random regression, beef cattle, growth

W37   Genetic variability for calf mortality in Nellore cattle. L. C. Magalhães Silva*, F. Baldi, L. G. Albuquerque, and M. J. R. Paranhos da Costa, *São Paulo State University, Unesp, Jaboticabal, São Paulo, Brazil.*

The objective of this work was to estimate genetic parameters for calf mortality in Nellore cattle. Calf mortality (CM) was defined as a binary trait, with 1 = success, indicating a calf born alive after the pregnancy diagnosis and 0 = failure, indicating a calf failing to reach the end of gestation, stillborn, or dead within the first 48 h after calving. Pregnancy diagnoses were performed on cows 90 d after the end of breeding season. After consistency checks 68,307 records for calf mortality from 31,583 cows and 646 sires belonging to Agropecuaria Jacarezinho Ltda, Sao Paulo, Brazil, were available for subsequent analyses. The mortality frequency obtained from the data was of 2.0%. CM was analyzed using a sire model. The age of the cow at the beginning of the breeding season (in classes, ranging from 1 to 13 years) was included as fixed effect in the model, while contemporary group (CG), defined by year, farm and breeding season of the cow and the additive genetic effect of the sire were fitted as random effects. The pedigree file contained 861 sires. Bayesian inference using a threshold model

was applied and a Gibbs Sampler was employed to obtain the marginal posterior mean and standard deviation of all variance components. A single Markov chain of 500,000 cycles was generated with a sampling interval of 100 iterations, using the THRGIBBS1F90 software. The posterior distribution for CM heritability was obtained from effective samples (10,000 samples). The descriptive statistics (mean and standard deviation) and the highest posterior density (HPD at 95%) region were estimated for CM heritability using the BOA package (R program). For CM heritability, the mean $h2 \pm$ standard deviation and HPD [lower bound – upper bound] were 0.21 ± 0.07 and [0.087- 0.37], respectively. The results of the present study pointed out that, applying a sire model to evaluate CM, there is enough genetic variability to select for decreased calf deaths in beef cattle. Financial support: FAPESP.

Key words: calves, heritability, mortality

W38   Selection effect for growth traits on energy requirements in reproduction females of three production cycles. I. D. P. Solar Diaz*[1], F. R. de Araujo Neto[1], G. M. Ferreira de Camargo[1], R. Barbosa Lobo[2], and H. N. de Oliveira[1], [1]*Sao Paulo State University, Jaboticabal, Sao Paulo, Brasil,* [2]*Sao Paulo University, Ribeirao Preto, Sao Paulo, Brasil.*

The objective was to evaluate the effect of selection for growth traits on energy requirements in reproductive females from 3 production cycles (C). Records of weights from Nellore cows were used to calculate the average weights in the reproductive stage (after 730 d). The average number of days that females remain in each category (pregnant lactating, non-pregnant lactating, pregnant nonlactating and empty and dry) for the period of one year considering the average calving interval of 365 (C1), 450 (C2) and 550 (C3) days were calculated as well. The energy requirement was measured by total net energy (T.N.E.) which was obtained by the sum of net energy for maintenance, activity, pregnancy and lactation. The prediction equations of NRC were used. The selection effect was analyzed using the estimates of coefficients of regression which were obtained from a previous analysis (not shown) of genetic parameters from birth to mature ages of cows. A selection intensity of 1.76 u.d.p was used. The following selection criteria were used: weights of 120, 210, 365, 450, 550 and 730 d and the weights gains between these phases. The increase of N.E. was not significant when different selection criteria were used, however the increase was observed between the production cycles. There is a tendency of increase in T.N.E. from C1 (4,864–5,070 Mcal) to C2 (4,935–5,148 Mcal), however the C3 (4,503–4,700 Mcal) was relatively inferior compared with the others. As expected, the nutritional requirements, on an annual basis, decreases with an increasing calving interval, as part of the T.N.E. is assigned to less productive classes (or nonproductive in the case of C3) and therefore less demanding. However, when considering the production of calves, the cost-effectiveness is impaired. In general, considering the genetic parameters used in this study, we conclude that the selection criteria used did not interfere in the females energy requirements regardless of their reproductive efficiency.

Key words: beef cattle, net energy

W39   Effect of model structure on direct and maternal (co)variance and heritability estimates for 210 d weight in Nellore cattle. L. Pascoa*[1,2], A. de los Reyes[2], M. A. Elzo[3], J. L. Ferreira[4], L. A. F. Bezerra[5], and R. B. Lobo[5], [1]*Federal Institute of Brasilia, Planal-*

J. Anim. Sci. Vol. 89, E-Suppl. 1/J. Dairy Sci. Vol. 94, E-Suppl. 1

527

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Actual and adjusted weights to 210 d of age from 72,731 male and female Nellore calves born in 40 PMGRN Nellore Brazil herds from 1985 to 2005 were used to compare the effect of different models on direct and maternal (co)variance and heritability estimates. Four structures of contemporary groups (CG) were defined: CG1: CG_B – semester of birth; CG2: CG_B – trimester of birth; CG3: CG1 – SC; CG4: CG2 – SC, where CG_B: herd – year of birth – management group at each age. Four analytical models were defined: M1: Weight = α + CG1 + SC + DAC + ε; M2: Weight = α + CG2 + SC + DAC + ε; M3: Weight = α + CG3 + DAC + ε; M4: Weight = α + CG4 + DAC + ε; where, α = constant; SC = sex of calf; DAC = class of cow age at calving, ε = random residual effect. (Co)variances were estimated using a derivative-free restricted maximum likelihood procedure, considering CG fixed (F) or random (R). Estimates of additive direct and maternal genetic variance (σ^2_d, σ^2_m) and direct and maternal heritability (h^2_d, h^2_m) were larger in models with semester than with trimester of birth in CG (Table) likely due to greater variation among weights when the season of birth considered in CG was longer. These estimates were similar in models with and without sex of calf in CG. Models with random CG yielded higher estimates of σ^2_d, σ^2_m, h^2_d and h^2_m and lower estimates of residual variance (σ^2_e) than models with fixed CG.

Table 1. Estimates of direct and maternal (co)variances (kg^2) and heritabilities for adjusted / actual weights at 210 days of age in Nellore cattle

M	CG	σ^2_d	σ^2_m	σ^2_e	h^2_d	h^2_m
M1	F	145/153	49/52	234/292	0.31/0.29	0.11/0.10
	R	146/155	49/52	233/291	0.32/0.29	0.11/0.10
M2	F	119/127	42/45	231/290	0.27/0.25	0.10/0.09
	R	121/130	42/45	229/287	0.28/0.27	0.10/0.09
M3	F	142/151	49/51	230/287	0.31/0.29	0.11/0.10
	R	144/153	49/52	229/286	0.32/0.29	0.11/0.10
M4	F	116/123	41/44	226/285	0.27/0.25	0.10/0.09
	R	121/129	42/45	224/281	0.28/0.26	0.10/0.09

Key words: cattle, contemporary group, weaning

W40 Age of dam as phenotypic source of variation for body weight in Nellore beef cattle. D. A. Lino*[1,2], S. Tsuruta[1], I. Misztal[1], E. N. Martins[2], and L. O. C. Silva[3], [1]University of Georgia, Athens, [2]State University of Maringa, Maringa, PR, Brazil, [3]Embrapa Gado de Corte, Campo Grande, MS, Brazil.

Prior to the inclusion of effects in genetic evaluation models, tests should be carried out to quantify their influence. The objectives of this study were to verify the trend caused by age of dam (AOD) on weight and on phenotypic variance of weight in Nellore beef cattle from birth until 385 d. Data from the Brazilian Association of Zebu Breeders were used. A total of 2,915,879 body weight records from 1975 to 2009 were divided into 5 periods of measurement: birth weight (BW), weight taken at age 91 ± 59 d (W1), 188 ± 53 d (W2), 290 ± 86 d (W3), and 383 ± 82 d (W4). The AOD at measurement was divided into 11 categories, ranging from 4 to 14 years. A model separate for each weight considered AOD as a fixed effect. The adjusted phenotypic variance was obtained from the residual variance of the model separately for each AOD class. To compare the effect of AOD in all periods, the estimated values were standardized by phenotypic vari-

ance. The effect of AOD on BW, W1, W2, W3, and W4 explained 1.5, 7.3, 6.3, 4.4, and 3.1% of the differences in weight, respectively. When the standardized values were considered, the changes were basically the same for all periods. The AOD at measurement accounted for 8.9% of the phenotypic variance observed in BW with the highest variance at 4–7 years of age and declining variance outside of this range. For W1, the phenotypic variance was 468 at AOD = 4, increased to 483 at AOD = 7, and declined to 446 at AOD = 14. Therefore, the AOD was responsible for 8.8% of the changes in phenotypic variance for W1. For weight and phenotypic variance of weight, the BW showed a linear trend, whereas W1 showed a quadratic behavior. For W2, W3, and W4, the change in phenotypic variance ranged from 2.9 to 6.0%, without any special trend along AOD. The age of dam influences the phenotypic variance up to 130 d of age but less afterward.

Key words: age of dam, phenotypic variance, beef cattle

W41 Additive genetic variation of residual feed intake and its components in Nellore cattle. M. E. Zerlotti Mercadante*, A. C. Del Claro, S. F. Martins Bonilha, J. N. dos Santos Gonçalves Cyrillo, and R. H. Branco, *Instituto de Zootecnia, Sertãzinho, São Paulo, Brazil.*

The objective was to investigate the importance of additive genetic effects on residual feed intake (RFI) in Nellore cattle. Performance tests for individual feed intake were conducted at Instituto de Zootecnia, Sertãzinho-SP, Brazil. Records of 491 animals (247 males and 244 females), born from 2004 to 2009, progeny of 50 sires and 345 dams, were analyzed. The pedigree file included up to seventh generation of animals with records, and contained 1,652 animals, with 3 sires and 24 dams with own performance and progeny. The averages of test duration, initial age and BW, ADG, DMI and ME were 86 ± 23 d, 290 ± 43 d, 224 ± 53 kg, 0.923 ± 0.220 kg/d, 6.645 ± 1.169 kg/d and 2.151 ± 0.083 Mcal/kg. ADG was estimated as the slope of regression of BW on test d. Phenotypic RFI (RFI_P) was obtained as residuals of linear regression of DMI on MBW ((mid-test BW)$^{0.75}$) and ADG. The model included contemporary group (CG, n = 8), defined by birth yr and sex, as fixed effect and initial age as linear covariate. Variance components were estimated by REML. Genetic RFI (RFI_G) was obtained from linear regression of DMI on EBV of MBW and EBV of ADG, including also the effects of CG and age in the model. EBV were obtained in a 2-trait animal model analysis of MBW and ADG, including CG and age. The heritabilities of DMI, RFI_P and RFI_G were estimated in one-trait animal model analysis, including CG and age (only for DMI). EBV for RFI_P and RFI_G ranged from −0.329 to 0.490 kg/d (SD = 0.136) and from −0.410 to 0.435 kg/d (SD = 0.120), and the average of accuracy values were 0.573 and 0.491 for RFI_P and RFI_G EBV, respectively. The rank correlation between RFI_P and RFI_G EBV was 0.694.

Table 1. Variance components and heritability ± SE for ADG, MBW, DMI, RFI_P and RFI_G

Trait	σ^2 additive genetic	σ^2 phenotypic	h^2±SE
ADG	0.010	0.021	0.464±0.106
MBW	18.853	61.821	0.305±0.094
DMI	0.449	1.000	0.449±0.116
RFI_P	0.037	0.209	0.178±0.098
RFI_G	0.053	0.283	0.186±0.092

Key words: beef cattle, *Bos indicus*, genetic evaluation

528

J. Anim. Sci. Vol. 89, E-Suppl. 1/J. Dairy Sci. Vol. 94, E-Suppl. 1

W42   Relationships among beef cattle temperament and tenderness traits using repeated performance records. T. T. Taxis*[1], W. R. Shafer[2], L. L. Berger[3], D. B. Faulkner[4], J. E. Beever[4], M. M. Rolf[1], D. L. Dow[1], J. F. Taylor[1], C. L. Lorenzen[1], and R. L. Weaber[1], [1]*University of Missouri, Columbia, [2]American Simmental Association, Bozeman, MT, [3]University of Nebraska, Lincoln, [4]University of Illinois, Urbana.*

Beef cattle temperament has been associated with a variety of performance measures, including steak tenderness. The American Simmental Association provided performance data and pedigree records to elucidate the relationship between temperament (exit velocity; EV) and tenderness (Warner-Bratzler shear force; WBSF) in *Bos taurus* breeds. EV were recorded on d 0 (EV1) and d 42 (EV2) of a feeding trial. The edited data set included 2,819 WBSF, 917 EV1 and 976 EV2 phenotypes in 176 contemporary groups (CG) with 13,418 pedigreed animals. Four different statistical models were analyzed. A trivariate and repeated records model were utilized to assess EV, and 2 bivariate models were utilized to assess WBSF. The trivariate animal model with fixed effects (CG, sire and dam breed composition) and a random animal effect was fit revealing a 0.99 genetic correlation between EV observations. A repeated records analysis of EV using the same fixed effects provided a better model fit ($P < 0.0001$; via likelihood ratio). Heritabilities were 0.19 (0.06) and 0.39 (0.08) for WBSF and EV, respectively, with a −0.10 (0.20) genetic correlation. Animals with multiple WBSF measurements, were analyzed using 2 bivariate models (both included WBSF and EV) to elucidate the effects of within animal WBSF variation. WBSF was analyzed using average peak shear force (APSF) and individual core values as repeated records. EV was analyzed using repeated records in both models. Heritability for WBSF using APSF was 0.06 (0.06) and 0.06 (0.05) from the repeated records model. Heritabilities for EV were unchanged in both models. Genetic correlations between WBSF and EV were −0.62 (0.47) and −0.63 (0.47). The analysis using individual core values provided a better model fit (p, 0.00001; via likelihood ratio). A whole genome association study using BovineSNP50 genotypes is planned for WBSF and EV.

W43   Carcass and meat palatability trends in cattle ranging from 100% Angus to 100% Brahman. M. A. Elzo*, D. D. Johnson, J. G. Wasdin, and J. D. Driver, *University of Florida, Gainesville.*

Carcass and meat palatability characteristics constitute key factors for the success of beef cattle operations. Consumers prefer meat that has desirable levels of tenderness, marbling, juiciness, and flavor. Cattle in the Southern region of the US contain some Brahman to enable them to cope with hot and humid climatic conditions, thus decreasing meat tenderness and affecting the desirability of these animals for branded beef products. The objective of this research was to estimate additive genetic differences between Angus (A) and Brahman (B), heterosis, and least squares means (LSM) for 6 carcass and 6 meat palatability traits for groups of cattle ranging from 100% Angus (A) to 100% Brahman. Carcass traits were hot carcass weight (HCW), dressing percent (DP), ribeye area (REA), fat over the ribeye (FOE), kidney, pelvic and heart fat (KPH), and marbling score (MAB). Meat palatability traits were Warner-Bratzler shear force (WBSF), and tenderness (TEND), connective tissue (CTI), juiciness (JUIC), flavor (FLAV), and off-flavor (OFLAV) scores. Data came from 1367 steers from the Angus-Brahman multibreed herd of the University of Florida collected from 1989 to 2009. Estimates of additive genetic breed differences indicated that B carcasses had higher DP ($P < 0.0001$), lower MAR ($P < 0.0001$), smaller REA ($P < 0.0001$), and less FOE ($P < 0.0001$) than A carcasses. Brahman beef was also tougher ($P < 0.0001$), had more

connective tissue ($P < 0.0001$), and it was less juicy ($P < 0.001$) than A beef. Heterosis increased HCW ($P < 0.0001$), DP ($P < 0.017$), REA ($P < 0.0001$), FOE ($P < 0.0001$), and KPH ($P < 0.01$) in crossbred steers. The LSM for HCW, REA, FOE, and KPH increased from A to 1/2 A 1/2 B, and then they decreased toward B. The LSM for MAB, TEND, CTI, and JUIC decreased whereas the LSM for WBSF increased from A to B. Results indicated that crossbred steers with percentage Brahman up to 50% showed limited negative impact on meat quality while maximizing meat yield due to heterosis.

Key words: carcass, meat quality, multibreed

W44   Role of cytoplasmic inheritance on preweaning traits in a closed breeding nucleus Angus herd. J. A. Carrillo* and F. Siewerdt, *University of Maryland, College Park.*

The importance of cytoplasmic inheritance was investigated in an elite Angus herd that has been closed to outside breeding for 70 years. Historical data included full pedigree information on 10,838 animals and phenotypic information (up to 7,986 animals) on body weights collected at birth (WB) and weaning, hock length (HL) at birth and scrotal circumference at weaning (SC). Adjusted body weights to 205 d (W205) were obtained and individual average daily gain from birth to 205 d was also computed. Each animal was traced back to one of 18 founder cows, all from distinct female lineages. Data were analyzed with an animal model that included contemporary group and the random effects of animal, maternal, permanent environment, and cytoplasmic line. The ratios of cytoplasmic variances to phenotypic variances ranged from 0.000 ± 0.002 (WB) to 0.005 ± 0.006 (SC) indicating a very small participation in the determination of genetic and phenotypic variability. In contrast, the much higher genetic maternal variances had ratios to the phenotypic variances ranging from 0.044 ± 0.046 (SC) to 0.156 ± 0.029 (WB) and were typically 50 times higher than the cytoplasmic variances. The observed ranges for cytoplasmic breeding values (BV) for W205, SC, and HL were of 2.62kg, 0.252cm, and 0.053cm, respectively, suggesting that a small but not negligible amount of genetic gain could be amassed by including cytoplasmic BV in the selection index. Selection indexes were computed for all traits individually, with or without inclusion of the cytoplasmic BV. A 20-fold weight on the desired genetic gain was placed on the cytoplasmic BV compared with the direct and maternal BV. Inclusion of the cytoplasmic information in the index reduced the predicted genetic gain in direct and maternal BV by less than 1.5% indicating that this small reduction in genetic gains could be compensated by gains in cytoplasmic BV. Selection for cytoplasmic effects can lead to increased inbreeding by focusing on few maternal lines of animals. Rapid exhaustion of what little cytoplasmic genetic variation is present will happen, unless new variation is created by mutations.

Key words: animal model, quantitative genetics, beef cattle

W45   Heritability and effect of breed and diet on complementary feed utilization traits in Simmental, Angus and crossbred steers. N. V. L. Serão*[1], J. E. Beever[1], D. B. Faulkner[1], M. Pérez-Enciso[2], and S. L. Rodríguez-Zas[1], [1]*University of Illinois at Urbana-Champaign, Urbana, [2]Universitat Autònoma de Barcelona, Barcelona, Catalonia, Spain.*

Phenotypic data from 1,488 steers were used to estimate genetic parameters for average daily gain (ADG), dry matter intake (DMI), gain to feed (GF), residual feed intake (RFI), residual average daily gain (RADG), carcass backfat (BF) and rib-eye area (REA). RADG

J. Anim. Sci. Vol. 89, E-Suppl. 1/J. Dairy Sci. Vol. 94, E-Suppl. 1

529

was adjusted for DMI and mid-test metabolic weight (MMW), whereas RFI was adjusted for ADG and MMW. All analyzes were carried out using Qxpak v 5.03, with an animal model including the pedigree (3,786 animals), the fixed effects of breed (5 levels; Angus (AN), 3/4 AN, 1/2 AN 1/2 Simmental (SM), 3/4 SM and SM), diet (5 levels), breed- diet interaction, days on feed (covariate) and the random effect of harvest group within contemporary group (32 levels). The heritabilities were estimated using maximum likelihood and fixed effects were considered significant at 0.05. ADG presented low heritability estimate ($h^2 < 0.20$), whereas GF, RADG and REA showed moderate estimates ($0.20 < h^2 < 0.40$) and DMI, RFI and BF presented high heritabilities ($h^2 > 0.40$). Breed-diet interaction was significant for BF, REA and RFI. The main effect of diet was significant for RADG and GF, and the main effect of breed was significant for ADG and DMI. The heritability of RADG ($h^2 = 0.30$) was higher than that for ADG ($h^2 = 0.16$). This suggests that genetic selection for RADG would result in higher genetic improvement than for ADG in this population, since the adjustments for DMI and MMW decrease the phenotypic variation of the trait. In contrast, RFI showed a similar heritability to DMI, respectively $h^2 = 0.43$ and $h^2 = 0.42$, suggesting that the adjustment for ADG and MMW did not offer major gains in estimating the heritability in this population. Although the selection for either trait may result in similar genetic gains, RFI represent a more suitable indicator of feed efficiency than DMI. Finally, the estimates for RADG and RFI indicate that, for the population studied, selection based on intake-based indicators is expected to result in superior genetic improvement for feed utilization than selection based on gain-based indicators with lower undesirable increase in body weight.

Key words: genetic parameters, RADG, RFI

W46   Comparison of body weight genetic evaluation accuracy by random regression with splines and multi-trait model in Limousins. M. Lukaszewicz*[1,2], I. Misztal[1], A. H. Nelson[1], J. P. Sánchez[1], and J. K. Bertrand[1], *[1]University of Georgia, Athens, [2]Institute of Genetics and Animal Breeding, Jastrzebiec, Poland.*

This study compared multibreed EPDs obtained by multi-trait (MT) and random regression (RRS) models. RRS allows using weight records outside standard ranges in MT but EPDs by RRS may contain artifacts. The data on birth (BW), weaning (WW), and yearling (YW) weights were provided by the North American Limousin Foundation. After editing, data comprised 1,382,305 BW; 986,777 WW; and 412,977 YW RRS-analysis-ready records. Both models fit direct and maternal additive genetic, contemporary group, animal's age, direct and maternal heterosis effects, and direct and maternal additive genetic means of the breed effects. The RRS fit additionally the direct permanent environment effect. WW and YW record numbers in MT were 94% and 93% of those in RRS. The validity of using RRS was assessed by correlating EPDs from both methods. Correlations between BW direct EPDs, computed on all animals, were 0.99 in both sexes. They dropped to 0.95–0.97 for the later weights. For maternal EPDs the correlations for BW and WW were 0.95 and 0.90 in bulls and 0.96 and 0.92 in cows. In bulls with the RRS EPD accuracy > 0.6 for given trait, the correlations between BW, WW, and YW EPDs for direct effect increased to 1, 0.98, and 0.98 while those between maternal EPDs to 0.99 and 0.96, for BW and WW. For bulls with accuracy < 0.6 under MT and > 0.6 under RRS (for each trait at a time) the correlations between direct EPDs were 0.99, 0.97, and 0.97. For cows with accuracy < 0.45 under MT and > 0.45 under RRS (for each trait at a time) the correlations between direct EPDs were 0.99, 0.93 and 0.91 for BW, WW, and YW while between maternal EPDs 0.71 and 0.86, for BW and WW. When few additional records are available for RRS, RRS and MT provide nearly identical EPD for most animals. Most changes are for animals with additional information beyond that possible with MT.

Key words: body weight EPD accuracy, multi-trait vs. random regression, Limousin

W47   Growth curves for buffaloes (*Bubalus bubalis*) using random regression mixed models with different structures of residual variances. D. M. Bolivar[1,2], M. F. Cerón-Muñoz[2], M. A. Elzo*[3], E. J. Ramirez[2], and D. A. Agudelo[4], *[1]National University of Colombia, Medellin, Colombia, [2]University of Antioquia, Medellin, Colombia, [3]University of Florida, Gainesville, [4]Lasallian University Corporation, Caldas, Colombia.*

The objective of this study was to analyze buffalo growth based on body weight (BW), Longissimus dorsi muscle area (AOL), and fat deposition over the hip (FOH) using random regression mixed models of first (FORRM) and second order (SORRM), each with 9 different variance structures. Ten measurements for each trait were taken on 26 animals during the first performance test (93 d test plus 23 d adaptation period) developed for buffaloes in Colombia. Computations were performed using the lme procedure of the nlme library of program R. Preliminary analyses determined that an SORRM was appropriate for BW and FOH and an FORRM was suitable for AOL. The maximum likelihood ratio (MLR), the Akaike information criterion (AIC) and the Bayesian information criterion (BIC) were used to compare models. The best models were an SORRM with homogeneous residual variances for BW, an FORRM with heterogeneous animal residual variances for AOL, and an SORRM with heterogeneous residual variances among farms times an exponential function of age for FOH. Heterogeneity of residual variances was likely due to environmental differences among farms, and to genetic differences among buffaloes not accounted for by FORRM and SORRM. Fixed intercepts with the best models for each trait were 227 ± 7.90 kg for BW, 34.82 ± 0.99 cm2 for AOL, and 4.19 ± 0.229 mm for FOH. Fixe linear regression coefficients were 1.289 ± 0.073 g/d for BW, 0.0584 ± 0.0042 cm2/d for AOL, and 0.0035 ± 0.0032 mm/d for FOH. The fixed quadratic regression coefficient indicated that BW rate decreased after one year of age whereas FOH rate continued to increase until the end of the test. Random regression coefficients suggested that there was considerable variability among trait curves for individual buffaloes, particularly for FOH.

Key words: buffalo, growth curve, performance test

W48   Estimates of genetic and phenotypic trends for body weight traits of Zandi sheep obtained by a univariate and multivariate animal model analysis. H. Mohammadi* and M. Moradi Shahrebabak, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The objective of the present study was to estimate genetic changes for body weights at different ages in Zandi sheep. Traits included were birth weight (BW, n = 8366), 3 mo weight (3MW, n = 6360), 6 mo weight (6MW, n = 4350), 9 mo weight (9MW, n = 2890), and yearling weight (YW, n = 2430). The data and pedigree information used in the current research were collected at the Breeding Station of Zandi sheep (Tehran province, Iran) during 1991–2007. Variance components were estimated from a 5-trait analysis, based on the best model of analysis

530

J. Anim. Sci. Vol. 89, E-Suppl. 1/J. Dairy Sci. Vol. 94, E-Suppl. 1

for each trait, using the ASReml program. The final model included the fixed effects of year-season, sex of lamb and parity of dam, birth type, and the linear covariate effect of age of dam and random direct and maternal genetic effects. The most suitable model was determined based on likelihood ratio tests for each trait. Breeding values of individual animals were predicted with Best Linear Unbiased Prediction (BLUP) methodology and genetic trends were obtained by regressing the means of predicted breeding values on year of birth for each trait. Direct genetic trends were positive and significant ($P < 0.05$). The additive genetic trends for BW, WW, 6MW, 9MW, and YW using univariate and multivariate analysis were estimated 2.1 and 3.9, 98.5 and 106.28, 89.63 and 95.47, 26.35 and 32.22, 41.53 and 49.83 g/year, respectively. Also, maternal genetic trend for BW was 5.40 and 4.92 g/year. The phenotypic trends for traits were estimated −8.5 and −8.9, −422.2 and −427.2, −90.60 and 90.53, −357.1 and −359.2, −133.32 and −134.31 g/year, respectively. The environmental trends for traits were −11 and −11.5, −444 and −447, −387 and −395, −212 and −215, −296 and −302 g/year, respectively. The results showed that improvement of body weights of Zandi sheep seems feasible in selection programs.

Key words: Zandi sheep, growth traits, genetic and phenotypic trends

W49   Genetic and phenotypic correlations between reproduction and production traits in Zandi sheep. H. Mohammadi* and M. Moradi Shahrebabak, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The objective of this study was to estimate heritabilities and genetic and phenotypic correlations among production and reproduction traits over 4 parities in the Zandi sheep to formulate a breeding plan for this breed. Genetic and phenotypic correlations were estimated between production and reproduction traits in a flock of Zandi sheep reared at the Khojir Research Station by ASREML procedures using bivariate mixed models, included fixed effects (year of mating and age of ewe; for BW traits, additionally sex of lamb; for weaning weight (WW), additionally number of d to weaning as a covariate) and random effects of animal direct genetic, permanent environment (repeated records of ewes) and residual. Production traits investigated were birth weight (BW) and WW, and reproduction traits, including 2 basic and 2 composite traits. The basic traits were conception rate (CR) and total number of lamb born (NLB).The composite traits were total litter weight at birth per ewe lambing (TLWB/EL) and total litter weight at weaning per ewe lambing (TLWW/EL). Direct additive estimates of heritability (h2 ± S.E.) were: 0.24 ± 0.03; 0.26 ± 0.02; 0.05 ± 0.02; 0.14 ± 0.02; 0.11 ± 0.02; 0.10 ± 0.02; for BW, WW, CR, NLB, TLWB/EL and TLWW/EL, respectively. Estimates of the direct genetic and phenotypic correlations between the reproductive and growth traits are shown in Table 1. Genetic correlation estimates between the investigated traits ranged from −0.05 for BW–CR to 0.45 for WW–TLWW/EL. Phenotypic correlations ranged from 0.03 for BW–CR to 0.19 for WW–TLWW/EL. This study provides estimates of genetic correlations that will improve the accuracy of genetic evaluation and prediction of the outcomes from breeding programs for meat objective that include reproduction.

Table 1. Estimates of genetic and phenotypic correlations (±SE) between reproductive and growth traits in Zandi ewe

Genetic correlations	CR	NLB	TLWB/EL	TLWW/EL
BW	−0.05 ± 0.07	0.24 ± 0.10	0.35 ± 0.06	0.13 ± 0.06
WW	0.10 ± 0.04	0.16 ± 0.08	0.23 ± 0.05	0.45 ± 0.07
Phenotypic correlations				
BW	0.03 ± 0.02	0.07 ± 0.01	0.09 ± 0.05	0.05 ± 0.06
WW	0.07 ± 0.02	0.03 ± 0.02	0.09 ± 0.06	0.19 ± 0.06

Key words: covariance components, composite reproductive traits, growth traits

W50   Estimation of genetic trend for some reproductive traits in Zandi sheep breed. H. Mohammadi* and M. Moradi Shahrebabak, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

Knowledge of genetic parameters and trends is necessary to optimize animal breeding schemes. An estimate of the genetic progress achieved by selection programs is necessary to describe the genetic changes progress, to assess the benefits of the selection program and to introduce necessary adjustments. The aim of this study was to estimate genetic parameters and genetic trends of reproductive traits. Genetic parameters from both single-trait and bivariate analyses for reproductive traits were estimated using REML with animal models for Zandi sheep from data collected from 1991 to 2007 at the Breeding Station of Zandi sheep in Tehran province, Iran. Traits included were litter size (LS, n = 5025), litter mean weight per lamb born (LMWLB, n = 4338), litter mean weight per lamb weaned (LMWLW, n = 4172), total litter weight at birth (TLWB, n = 4338) and total litter weight at weaning (TLWW, n = 4172). Estimates of heritability with ASREML software analyses were 0.05 for LS, 0.13 for LMWLB, 0.08 for LMWLB, 0.11 for TLWB, and 0.10 for TLWW. The genetic trends were calculated by regression of the average predicted genetic values per year for each trait versus the dam year of birth. Estimated genetic trends of LS, LMWLB, LMWLW, TLWB and TLWW were −0.001, 0.02, 0.013, 0.023 and 0.26, respectively. From 1991 to 2007, average estimates of breeding values from the multiple-trait analysis increased at a greater rate than average estimates from the single-trait analysis. The rate of yearly genetic improvement was very small for LS, LMWLB, LMWLW, and TLWB traits. However, the reproductive traits of Zandi breed may still be improved by selection. Positive genetic correlations between reproductive traits and growth traits showed that simultaneous genetic improvement of the traits may be possible.

Key words: genetic trends, reproductive traits, Zandi sheep

W51   Estimates of genetic and phenotypic trends for body weight traits of Zel sheep obtained by univariate and multivariate animal model analysis. H. Mohammadi* and M. Sadeghi, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The objective of the present study was to estimate genetic trends for body weight traits at different ages in Zel sheep. Traits included were birth weight (n = 10723), 3 mo weight (n = 8108) and 6 mo weight (n = 5236). The data and pedigree information used in the current research were collected by Jahad-e-Keshavarzi organization (Mazandaran province, Iran) during 1994–2009. Variance components were

estimated from a 3-trait analysis, based on the best model of analysis for each trait, using the ASREML software. The final model included the fixed class effects of year-season, sex of lamb and parity of dam, birth type, the linear covariate effect of age of dam and random direct and maternal genetic effects. The most suitable model was determined based on likelihood ratio tests for each trait. Breeding values of individual animals were predicted with Best Linear Unbiased Prediction (BLUP) methodology and genetic trends were obtained by regressing the means of predicted breeding values on year of birth for each trait. Direct genetic trends were positive and significant for BW, WW and 6MW ($P < 0.05$). The direct genetic trends for BW, WW, and 6MW using univariate and multivariate analysis were estimated 1.90 ± 0.07 and 2.53 ± 1.1, 98.5 ± 10.4 and 105.38 ± 25.2, 73.23 ± 21.2 and 78.46 ± 33.40 g per year, respectively. The maternal genetic trend for BW was 2.94 ± 1.21 and 3.07 ± 2.49 g per year. The phenotypic trends for traits were estimated -6.5 ± 22.60 and $-6.9 \pm 22.50, -152.2 \pm 251$ and -147.2 ± 239, -100.60 ± 48 and 100.53 ± 45 g per year, respectively. The environmental trends, measured as the difference between phenotypic and genetic trends, were -21.1 ± 0.02 and -21.5 ± 0.05, -244 ± 16 and -247 ± 19, -287 ± 30 and -295 ± 26 g per year, respectively. Negative phenotypic and environmental trends could be due to bad environmental conditions, especially to nutrition of the sheep in an unsuitable climate during the study years.

Key words: Zel sheep, growth traits, genetic and phenotypic trends

532

J. Anim. Sci. Vol. 89, E-Suppl. 1/J. Dairy Sci. Vol. 94, E-Suppl. 1