breed on development of novel beef cattle production systems especially on roughage based diets seems to be justified.

Key Words: Feeding intensity, Breed difference, Carcass quality

W80 Evaluation of marbling by US scoring system and video image analysis.

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The visible proportion and distribution of intramuscular fat in M. longissimus dorsi, called marbling, is the most important factor influencing quality grade in the United States and Canada (Boggs et al, 1995). In Europe carcass value is determined by conformation and fatness traits, in spite of it, marbling is often demanded as a primary quality trait of beef by consumers or in labeled products (Chambaz et al, 2002). There have been several methods developed to evaluate intramuscular fat content (Baker, 1986; Rekaya et al, 1999; Hassen et al, 1999; Chambaz et al, 2002). The aim of this research was to determine the correlation between results received by subjective scoring (USA, 1-6) and by video image analysis (VIA). Native Hungarian Grey (HG), and Holstein-Friesian growing-finishing bulls were housed in confinement on deep litter and fed on corn silage, hay and concentrate (6 kg/day) based diets for 210 days in two groups with 10 head of each. Average age and weight at slaughter for HG and HF were 552 and 474 days, and 545 and 578 kg, respectively. Pictures of longissimus muscle cross section were taken by video camera and analyzed by software Terlet V 7.0 developed by Mosoni (2000). Marbling is evaluated using brightness of picture taken. Surfaces with more than 200 brightness units were measured in two replications. Data processing was made with SPSS10 statistical program package. Marbling score for HG bulls was 1.5 when evaluated by subjective scoring and 1.29% determined by VIA. For HF bulls, the values were 1.1 scores and 0.43%, respectively. In terms of marbling significant differences ($P<0.01$) were established between breeds using VIA, while no significant differences were recorded by subjective scoring ($P<0.1$). Correlations between the two marbling evaluation procedures for both breeds (HG: $VIA=0.1133+0.7878*USA$, $r=0.71$; HF: $VIA=-0.7556+1.0778*USA$, $r=0.86$) suggested the appropriateness of both methods in the evaluation of marbling in beef.

Key Words: Marbling, VIA, Cattle breeds

W81 Evaluation of ultrasonic estimates of fat thickness and *longissimus* muscle area in de-haired hanging beef carcasses at chain speed.

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The objective of this study was to evaluate the accuracy of real-time ultrasound measurements of *longissimus* muscle area (REAU) and 12th-rib fat thickness (FTU) in hanging de-haired beef carcasses at regular plant chain speed. A certified ultrasound technician took measurements on 387 head of slaughter cattle using an ALOKA 500V ultrasound unit and Beef Image Analysis (BIA) image interpretation computer software. Carcasses were ultrasounded immediately after de-hairing at a pace of one carcass every 12-15 seconds in a hanging position on the rail. Carcass ribeye area (REAC), carcass fat thickness (FTC) and calculated yield grade (CYG) were collected 24 hours after harvest and scanning. Means for hot carcass weight (HCW), REAU, FTU, REAC, FTC, and CYG were 368.5 32.9 kg, 83.44 9.96 cm^2, 1.10 0.36 cm, 83.79 10.5 cm^2, 1.08 0.46 cm and , respectively. Pearson correlations for REAU and REAC, FTU and FTC, REAC and CYG, REAU and CYG, FTC and CYG, and FTU and CYG were 0.53, 0.72, -0.77, -0.39, 0.86 and 0.65, respectively. These data suggest that ultrasound can accurately assess carcass compositional differences in hanging beef at chain speed. However, the removal of hair prior to scanning is a must to keep up with the speed of the carcass movement every twelve to fifteen seconds.

Key Words: Ultrasound, De-haired, Beef

W82 Effect of breed, sex, and slaughter weight on meat quality of lambs.

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A total of 480 lambs was used to study the influence of breed, sex, and slaughter weight (SW) on meat quality. There were eight treatments arranged factorially with two breeds (Castellana *vs* Merino), two sexes (female *vs* male), and two SW (26 *vs* 31 kg). Each treatment was replicated six times and ten lambs penned together formed the experimental unit. All the lambs received a common pelleted diet based on barley, wheat, and soybean meal. Wheat straw was offered *ad libitum.* Following slaughter, carcasses were stored for 24 h at 2 ± 1 C. Then, samples from the *longissimus* muscle from the left side of two lambs per replicate were obtained and divided into two portions. Water holding capacity, chemical composition, and color were measured in the first portion (L1, 6th to 10th dorsal rib) and shear force was measured in the second portion (L2, 11th to 13th dorsal rib). Samples from L1 were stored at -20 C, whereas samples from L2 were previously stored for three d at 4 C and then frozen. Loins from Castellano lambs had more fat content than loins from Merino lambs (4.6 *vs* 4.2 %; $P < 0.05$), and loins from females had more fat content than loins from males (4.8 *vs* 4.0 %;$P < 0.05$). Loins from females had lower a* and higher L* values ($P < 0.05$), and had less cooking losses (21.3 *vs* 19 %; $P < 0.05$) than loins from males. An increase in slaughter weight increased fat content of the loin (5.30 *vs* 3.49 %; $P < 0.05$). Loins from lambs slaughtered at 31 kg had greater cooking losses (21.4 *vs* 18.9 %; $P < 0.05$), and higher a* but lower L* values ($P < 0.05$) than loins from lambs slaughtered at 26 kg. Also, SW tended to increase shear force (Warner-Bratzler values of 7.67 and 6.74 kp; $P < 0.10$). It is concluded that meat quality of lambs can be adapted to different markets by manipulating breed, sex, and weight at slaughter.

Key Words: Lambs, Slaughter weight, Meat quality

W83 Cholesterol level and sensory evaluation of lambs of various hair x wool sheep crosses.

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The cholesterol level and sensory evaluation were compared in six lambs from each of the following genotypes: 1) St. Croix hair sheep, 2) St. Croix x wool sheep, 3) Callipyge wool x St. Croix, 4) Dorper hair sheep x St. Croix, 5) Dorper x wool, Callipyge wool x wool, and 6) wool x wool. Meat cholesterol was extracted by chloroform-methanol mixture and the cholesterol levels were determined by spectrophotometric measurement of the color generated by the reaction of cholesterol with glacial acetic acid-$FeSO_4$-H_2SO_4. A 9-point hedonic ballot ranging from 9 (like extremely) to 1 (dislike extremely) was used for the sensory evaluation based on the following index: flavor, tenderness, juiciness and overall quality. The general linear model (GLM) ANOVA procedures and Fisher's LSD multiple-comparison test were used to determine the difference among genotypes. Cholesterol levels (mg/100g fresh meat) were 249.6, 170.1, 73.2, 130.7, 149.2, 50.4 and 116.5, respectively. The cholesterol level in the hair sheep (St. Croix) is significantly higher ($P < 0.05$) than all the other genotypes and the lowest is in the Callipyge crosses. Significant differences ($P < 0.05$) existed between genotypes for every sensory characteristic measured. St. Croix had the highest overall sensory acceptance rating (6.8) and the lowest in the Callipyge wool x wool. As cholesterol correlates to fat composition of the tissue these differences may account for the differences found between crosses in the sensory evaluation data.

Key Words: Cholesterol, Sensory evaluation, Sheep

Breeding & Genetics

W84 Estimation of correlations of reproductive traits with blood serum IGF-I concentration in Angus beef cattle.

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The objectives of this study were to obtain estimates of heritabilities and genetic (rA1A2), environmental (rE1E2), and phenotypic (rP1P2) correlations of insulin-like growth factor I (IGF-I) concentration with scrotal circumference (SCR), percentage of motile (MOT) and morpho-

logically normal (NORMAL) sperm cells, calving rate (CR), and age of heifers at first calving (AFC). Data were obtained from an ongoing experiment that involves Angus beef cattle divergently selected on the basis of blood serum IGF-I concentration at the Eastern Ohio Resource Development Center. Selection was based on the mean IGF-I concentration of three blood samples taken at d 28, 42, and 56 of the 140-d postweaning test. Data were analyzed using SAS and MTDFREML. Fixed effects, which included birth year, IGF-I line effect, season of birth, age of dam, sex, mating number and on-test age, were tested for significance and only significant effects were included in the subsequent analyses. (Co)variance estimates were obtained using an animal model that did not include maternal genetic or permanent environmental effects. Calving rate was coded as either 1 (conceived) or 100 (did not conceive) and was treated as a repeated measure. Environmental correlations of calving rate with mean IGF-I concentration for matings other than the first were ignored, because including IGF-I measurements for each mating resulted in non-permissible heritability estimates for IGF-I measurements. Correlations with mean IGF-I concentration were small, except that genetic correlations of mean IGF-I with SCR, MOT, and CR were moderate to high. These results suggest that selection for blood serum IGF-I concentration should result in a decrease in age at first calving and increases in all remaining variables.

			Mean IGF-I		
Variable	N	h2	rA1A2	rE1E2	rP1P2
Mean IGF-I	1,848	0.32			
SCR	825	0.51	0.35	0.01	0.14
MOT	596	0.09	0.43	0.02	0.07
NORMAL	765	0.43	0.00	0.09	0.07
CR	2,092	0.13	-0.41	0.02	-0.06
AFC	294	0.26	0.14	-0.09	-0.10

Key Words: Insulin-Like Growth Factor I, (Co)variance Component Estimation, Reproduction

W85 Molecular characterisation of myostatin gene in mexican Beefmaster cattle.

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The production of animals with superior muscle structure is of great importance to food animal agriculture. Dysfunction of myostatin gene has been reported in mammals. In bovine the loss of this gene activity have been associated to double-muscled phenotype present in some european cattle breeds. Beefmaster is one of the main breeds in Tamaulipas, Mexico. Due to the role of myostatin gene in muscle development, the objective of this study was to analyze a coding region containing mutations which potentially altering the myostatin gene expression. Eighty-seven individuals of Beefmaster cattle were blood- sampled and the DNA extracted was used to amplify a 548-bp from exon II. Mutation analysis of this region was achieved using both Base Excision Sequencing Scanning and nucleotide sequencing. We detected some sequence variations in our tested population: nt 374-51 (T-C Transition); nt 374-50 (Transition G-A); nt 414 (Transition C-T); nt 374-16 (Deletion 1). The nucleotide changes founded were grouped in three haplotypes A,B and C. The first one does not contain mutations, whereas B and C present the 3 transitions and the deletion changes, respectively. The data from this study indicate that mutations founded in Beefmaster were identical to those previously reported in other non double-muscled breeds. Therefore exon II from myostatin gene does not make a useful molecular marker to selection of those individuals with superior muscle mass in Beefmaster cattle.

Key Words: Myostatin, Beefmaster cattle, Mutation

W86 Association between promoter region insulin-like growth factor-I polymorphism and genetic merit for production traits in Holstein sires.

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DNA was extracted from blood samples from dairy sires at the time of enrollment into a progeny test program. Of these animals, genetic merit information based on at least 40 daughters eventually became available on 309 sires, from which population means and standard deviations (SD) were calculated. 204 bulls were found to be either one SD greater than or one SD less than the mean for either one or more of the following traits: milk yield (MY), fat yield (FY), fat percent (F%), protein yield (PY) and protein percent (P%) and were included in subsequent analysis. A 264bp fragment spanning a polymorphic site 512 bp upstream from initiation site of insulin-like growth factor-I (IGF-I) was amplified using 5'-ATTACAAAGCTGCCTGCCCC-3' as forward and 5'-CACATCTGCTAATACACCTTACCCG-3' as reverse primers. Bulls were genotyped using single strand conformation polymorphism techniques. Two distinct alleles were found in this population and designated in accordance with previous reports. Genotypic frequencies were compared between +1 and -1SD groups for each trait using the Frequency procedure of SAS. Further, trait means for AA, AB and BB genotypes were compared using GLM procedure. Genotypic distribution was different between -1SD and +1SD groups F% and P% ($p<.05$ and $p<.02$, respectively), as more BB genotypes were present in -1SD than in +1SD groups for both traits. Comparing trait means among -1SD$_{P\%}$ and +1SD$_{P\%}$ indicated that BB genotypes had less P% than AA or AB genotypes (-0.013% vs 0.041% or 0.044%, $P<.01$). Further in that same subpopulation of bulls, BB genotypes had greater milk yield than AA or AB genotypes (883 vs 520 or 401 lbs, $P<.01$). A similar pattern of differences among genotypes occurred when comparing means among -1SD$_{F\%}$ and +1SD$_{F\%}$ bulls, as components were less in BB animals while milk yield was greater ($P<.03$). Results were slightly different among -1SD$_{M}$ and +1SD$_{M}$ bulls, as milk yield only approached significance ($P=.07$), while components again were less among BB than AA or AB animals ($P>.03$). Data indicate that BB genotype may be associated with increased milk yield and decreased fat and protein percentage in dairy animals.

Key Words: IGF-I, Polymorphism, Yield Traits

W87 Genetic polymorphism at the kappa casein locus in Holstein and Iranian native cattle Sarabi by use of PCR-SSCP.

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Methods have been devised for detecting polymorphism in the bovine k-casein genes using the polymerase chain reaction (PCR) followed rather by restriction enzyme digestion (to reveal a RFLP) or by single strand conformation polymorphism and to demonstrate CSN3 polymorphism in blood sample of Iranian native cattle (Sarabi n=66) and Holstein-Frisian (n =102). The PCR products (453 bp) were heat-denatured, loaded onto non-denaturing polyacrylamide gels, and Ethidium Bromide stained. Each variant yielded patterns clearly distinguishable from the others. Reference DNA sample from cows and bulls, which were previously genotyped at DNA level with PCR-RFLP, were used to develop the optimal conditions of PCR-SSCP. The optimal condition for SSCP were 8 % polyacrylamide gels (49:1 acrylamid: bis-acrylamid ratio), with 5 % glycerol and constant running temperature of 4oC. Estimated gene frequencies of Holstein and Sarabi were 0.8284 ±0.0265, 0.1716 ±0.0265 and 0.7652 ±0.0361, 0.2348 ±0.0361 for A and B alleles respectively. The observed heterozygosity for Sarabi and Holstein were 0.3484 0.452 and 0.2843 0.452 respectively .The estimated gene diversity from sum of squares of allele frequency represented by Bruce, for Sarabi and Holstein were 0.3593 ±0.053 and 0.2843 ±0.053 respectively. Based on information at this locus and based on chi-square test statistic, no evidence was found of disequilibrium in two populations. Comparison of allele frequencies in this study with other cattle breeds indicates that there was no significant difference between observed and expected frequencies in both Sarabi and Holstein populations. The only significant differences observed are those between the two breeds of this study with Jersey and Brown Swiss from other study.

Key Words: Single strand conformation polymorphism, PCR-RFLP, Sarabi cattle

W88 Type trait evaluations and heritabilities of Holstein dairy cattle in northeastern Iran.

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This study was conducted to evaluate measures of type traits and their relationships and heritabilities for Holstein dairy cows by using data from 520 dairy cows of Kenebist Farm (Astan Ghods Razavy, Mashad, Northeastern Iran). Type traits were divided into two categories. First, the traits that classifiers measure were stature, size, pin set, rump length, pin width, rear udder height,rear udder width and teat length; their means (and standard deviations) were 140.93(3.98),198.60(9.44),2.31(2.20),52.35(2.54),20.17(1.79),26.08(4.37) ,16.43(2.57), 5.19(0.99) cm, respectively. Second, the traits that classifiers estimate in a scale from 1 to 9 were chest width, loin, body depth, rear leg side view, foot angle, fore udder attachment, suspensory ligament, udder depth, front teat placement, rear teat placement,and angularity; their means (and standard deviations) were 5.33 (1.40), 4.94 (1.00), 6.93 (0.98), 5.44 (0.85), 5.77 (1.26), 5.98 (1.66), 6.38 (1.76), 5.04 (1.21), 4.16 (1.37), 5.99 (1.43), and 6.92(0.85) respectively. Heritabilities of traits were based on a derivative-free restricted maximum likelihood (DFREML) method with an animal model. The estimated heritabilities for pin set, pin width, rear udder height, rear udder width, and rump length were 0.23, 0.37, 0.27, 0.25, and 0.24, respectively.

Key Words: Type trait, Heritability, Dairy cattle

W89 Performance of Holsteins that originated from embryo transfer or twin births.

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Concern has continued on possible bias in genetic evaluations of animals from embryo transfer (ET) due to preferential management. Performance of ET Holsteins was documented and compared with that of Holsteins from single and twin births. Of particular interest was the milk, fat, and protein yields, somatic cell score (SCS), and productive life (PL). The first ET animal recorded in the Holstein Association USA herdbook was in 1962. During the 1960s, 1970s, 1980s, and 1990s, number of ET Holsteins was 18, 1947, 103,436, and 269,064, respectively; numbers peaked in 1993 and have declined since. Of those ET animals registered, 88, 82, 85, and 66%, respectively, were female. Pedigree merit of ET cows registered was superior to population mean for milk, fat, and protein yields by 133, 7, and 5 kg, respectively, and pedigree merit of ET bulls was superior by 339, 13, and 12 kg. Females were $>98\%$ of registered twins. Pedigree merit of registered offspring from parents having twins was nearly identical to population mean for cows (difference of 3, 0, and 1 kg for milk, fat, and protein), but pedigree superiority for twin bulls was 113, 5, and 4 kg, probably indicating selective registration. Means for ET cows ($n = 10,277$; mean of 1.02 full sisters per ET cow) and their full sisters were virtually identical for standardized yield, yield deviation, and genetic merit for milk, fat, and protein. If ET cows were treated preferentially, their full sisters received equal preference. Mean SCS of ET cows (3.1) did not differ from their full sisters or the population mean, but PL of ET cows was high, and even 0.6 mo longer than their full sisters. Mean yield deviations for twins ($n = 6514$; mean of 1.02 full sisters resulting from single births per twin) were 93, 5, and 3 kg less for milk, fat, and protein, respectively, than those of their full sisters from single births; this could be due to smaller size at birth and calving. Mean twin SCS (3.1) did not differ from their full sisters, but mean twin PL was 0.4 mo shorter. Genetic merit of ET bulls ($n = 3512$; mean of 1.3 full brothers per ET bull) differed little from their brothers for all yield and component percentages, SCS, and PL. ET animals have contributed positively to genetic improvement, but the number of these animals is declining.

Key Words: Embryo transfer, Genetic evaluation bias, Twin

W90 Measures of lactation persistency for Iranian Holstein dairy cattle.

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The four persistency measures used in this study were 1) partial yield from day 100 to 305 divided by accumulated production for the total 305 d, 2) $PD = 110[(m60 - m280) - (y60 - y280)]$, 3) ratio of yield at day 60 to yield at day 280 of lactation, and 4) MAME (maxiumum/mean). A univariate model was applied for the first three lactations; for first lactation, a multivariate model also was used. Heritabilities based on the univariate model for milk, fat and protein were 0.286, 0.165, and 0.301; 0.208, 0.194, 0.163; and 0.168, 0.109, 0.142 for first, second and third lactations, respectively. Heritabilities of persistency measures from the univariate model were estimated to be 0.068 to 0.107, 0.071 to 0.136, and 0.064 to 0.083 for milk; 0.032 to 0.047, 0.031 to 0.058, and 0.028 to 0.046 for fat; and 0.038 to 0.086, 0.081 to 0.086, and 0.070 to 0.096 for protein for first, second, and third lactations, respectively. Heritabilities of 305-d yield based on the multivariate model for first lactation were the same as from the univariate model. Heritabilities increased for some measures when using the multivariate model and ranged from 0.067 to 0.132, 0.076 to 0.098, and 0.048 to 0.095 for milk, fat, and protein, respectively. Genetic correlations between measures of persistency and 305-d yield were 0.038 to 0.764., 0.100 to 0.450, and 0.127 to 0.461 for milk, fat, and protein, respectively. Phenotypic correlations had similar trend to genetic correlations.

Key Words: Lactation persistency, Iran, Dairy cattle

W91 Genetic correlations between boar semen traits.

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Currently boars selected for commercial use as AI sires are evaluated on grow-finish performance and carcass characteristics. If AI sires were also evaluated and selected on semen production, it may be possible to reduce the number of boars required to service sows thereby improving the productivity and profitability of the boar stud. The objective of this study was to estimate genetic correlations between boar semen traits; total sperm cells (TSC), volume collected (SV), number of extended doses (ND), and acceptance rate of ejaculates (AR). Semen collection records for 842 selected boars and two generations of pedigree data were provided by NPD USA. Genetic parameters were estimated using animal models and MTDFREML software. Breed, farm and contemporary group were included as fixed effects, and were significant ($P < .0001$) in all four traits. Heritability estimates were .44 for TSC, .44 for SV, .46 for ND and .16 for AR. The genetic correlations between TSC and SV, TSC and ND, and TSC and AR were .75, .98 and -.06, respectively. Genetic correlations between SV and ND, SV and AR, and ND and AR were .70, -.04 and -.02, respectively. Boar producing ejaculates with greater volume had more total sperm cells and produced more extend doses. The acceptance rate of ejaculates was not genetically correlated with the other recorded semen traits.

Key Words: Heritability, Semen, Pig

W92 Effect of selection for testosterone production on testicular morphology and daily sperm production in pigs.

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The objective of this study was to measure indirect responses in morphological testicular characteristics and daily sperm production to divergent selection for testosterone. Duroc boars from lines divergently selected 10 generations for testosterone production in response to GnRH challenge followed by random selection were used. In generation 21 endogenous testosterone in the high (H, $n=54$) and low (L, $n=44$) testosterone lines averaged 490 ng/ml and 278 ng/ml ($P<0.01$), respectively. Plasma FSH concentrations did not differ significantly between the lines. Boars from generation 20 were castrated at 211 d of age and 97 kg. After adjustment for body weight, average paired testicular weights for H ($n=46$) and L ($n=13$) were 417 g and 457 g ($P<0.01$), respectively. Testicular tissue samples were used to determine volume density of Sertoli cells, sperm per gram of testis, total daily sperm production, and total testicular sperm. No significant differences were detected between lines for volume density of Sertoli cells, sperm per gram of testis, total daily sperm production, or total testicular sperm adjusted for age. Selection for testosterone concentration in response to a GnRH challenge is an effective method of changing testosterone concentration. However, indicators of male fertility did not differ significantly between lines. Thus, selection for testosterone is not recommended as a method of improving sperm production in pigs.

Key Words: Selection, Reproduction, Pigs

W93 Effect of selection for high or low mature weigth and its reciprocal crossing on reproductive response in Japanese quail.

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To determine the effect of selection for high or low mature weight and its reciprocal crossing on reproductive response in Japanese quail. Two hundred eighty Japanese quail breeders (240 females and 40 males) were grouped in four genotypes that consist 1) Quails selected for high mature (HH); 2) Quails selected for low mature (LL); 3) Reciprocal crosses from males HL with females LL (HL); and 4) Reciprocal crosses of males LL and females HH (LH). The quails were allocated in groups of batteries with five levels and four cages by level and were fed with a diet containing 21% CP and 2,900 kcal of ME/kg. During 10 weeks, egg production, egg weight, feed intake, and feed efficiency were measured daily. During weeks 3, 6, and 9, the hatchability and fertility were measured. Preplanned contrasts of HH vs. LL, pure vs. crosses, and HL vs. LH were performed. During weeks 1 to 2, the crosses had higher ($P<0.03$) hatchability than pure breeds improved ($P<0.05$) feed efficiency. During weeks 3 to 7, eggs production of crosses was lower ($P<0.01$) than pure breeds. Crosses increased ($P<0.01$) egg weight, and decreased weight, and feed intake, and improved ($P<0.04$) feed efficiency. Hatchability of HH pure breed quails was lower ($P<0.01$) than other treatments. In week 8 to 10, the crosses increased ($P<0.01$) egg weight over pure breed quails. Fertility of the cross LH was higher ($P<0.01$) than other treatments. It is concluded that the crosses between Japanese quails selected for high and low mature weight have shown a little advantage for reproductive purposes.

Key Words: Crosses, Japanese quail, Hatchability

W94 Effect of selection of high or low mature weight and its reciprocal crossing on egg quality characteristics in Japanese quail.

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To determine the effect of selection for high or low mature weight and its reciprocal crossing on egg quality characteristics in Japanese quail breeders (240 females and 40 males), four genotypes were grouped in 1) Selected for high mature weight (HH); 2) Selected for low mature weight (LL); 3) Reciprocal crosses from males HH with females LL (HL); and 4) Reciprocal crosses of males LL with females HH (LH). The quails were allocated in seven groups (one male and six females), placed in metal wire cages as part of two cages batteries with five levels and four cages by level, and fed with a diet containing 21% CP and 2,900 Kcal of ME/kg. During 10 weeks, 20 eggs from each treatment were weekly collected. The following traits were measured: weight, egg length and width, dense albumin height, yolk height and width, and shell weight. From this data, shape index, yolk index, and Haugh units were calculated. Preplanned contrasts of HH vs. LL, pure vs. crosses, and HL vs. LH were performed. During the ascending part of hatching curve, the crosses had higher ($P<0.02$) egg weight. The cross HL had higher ($P<0.02$) yolk height and yolk width. During the plateau phase, the crosses increased ($P<0.05$) egg weight, shell weight, and albumin height. The cross HL improved ($P<0.05$) shell weight and yolk width over the cross LH. In the end of hatching curve, the crosses increased ($P<0.05$) egg weight, and egg wide over pure breeds. The cross HL increased ($P<0.02$) egg width, yolk width and yolk height over the cross LH. It is concluded that the crosses between quails selected for high and low mature weight improves some egg quality characteristics, and in those crosses, the main benefit is obtained using males selected for high mature weight.

Key Words: Selection by weight, Japanese quail, Egg quality

W95 Heritability estimates for semen charcteristics of inbred and non-inbred Hereford bull.

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Our objectives were to determine the influence of inbreeding on post-thaw semen characteristics measured by computer assisted sperm analyzer (CASA) and determine if post-thaw semen characteristics are heritable. Frozen semen samples were obtained from two inbred (Line1, n= 11 and Prospector, n= 7) and a non-inbred line (n= 9) of Hereford bulls. Average inbreeding level of each group was 0.27, 0.45, and 0.0 respectively. Semen samples were collected from 1978 to 2000. For CASA analysis four straws (0.5 ml) from each bull were evaluated. Cells were analyzed by mixed model analysis using a model that contained line and age at collection as fixed effects and individual bull as a random effect. No significant differences between groups of bulls were found for motility or progressive motility (Table 1). For average path velocity (VAP), cell elongation (ELON), and cell area (AREA) significant differences were between bull groups. Mean separation (Table 1) indicated that Line1 had larger cell area and were not as elongated as the Prospector and non-inbred group cells. The higher VAP for Line1 bulls is an indicator that Line1 cells are faster moving and perhaps more robust. Method R for a single trait was used to estimate heritability for semen characteristics. The heritability estimates would indicate relatively large amount of additive genetic variation present across bull groups, which could be utilized in a selection program. The lack of significant differences for motility and progressive motility across bull groups was surprising and indicates no inbreeding depression was exhibited for post-thaw semen characteristics. One explanation for this could be that indirect selection pressure was placed on these characteristics as inbreeding was increased.

Table 1. LS means and heritabilities of semen characteristics

	Line 1	Non-inbred	Prospector	Heritability
Motile (%)	0.90±0.03	0.91±0.02	0.90±0.02	.82±.01
Progressive (%)	0.31±0.04	0.29±0.03	0.25±0.03	.79±.01
VAP (mm/sec)	91.23±12.57^a	69.17±9.64^b	57.37±8.46^b	.36 *pm*0.04
ELON (%)	43.02±1.31^a	45.15±1.00^b	45.95±0.87^b	.34±0.0 5
AREA (mm)	7.08±0.33^a	6.44±0.25^b	6.3±0.22^b	.33±0.04

^{ab} Within a row, different superscripts differs at the $p< 0.1$ level.

Key Words: Semen characteristics, Heritability, Inbreeding

W96 Estimates of genetic parameters os carcass traits in limousin cattle.

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The current genetic evaluation of carcass traits for the North American Limousin Foundation (NALF) utilizes bivariate analyses. This study used NALF field records to estimate variance components to develop a multivariate evaluation. Weaning weight (WW), carcass weight (CW), ribeye area (REA), back fat (BF) and marbling score (MS) were analyzed with MTDF-REML (derivative free restricted maximum likelihood) using bivariate and trivariate linear models. Contemporary group and AOD (age of dam) were fit as fixed effects and age at slaughter and at weaning as covariates. Six analyses were performed (CW-WW; REA-MS; MS-BF; CW-REA and WW-CW-REA, WW-BF-MS). Random maternal and permanent environment effects were included for WW. A total of 31,063 pedigree records and 18,368 performance records were used. Heritability estimate for CW in the bivariate analysis of CW and WW were 0.41. The genetic correlations between CW and WW were 0.77. Heritabilities estimates for BF and MS were 0.37 and 0.31, with genetic correlation of -0.07. For CW and REA, the heritabilities were 0.30 and 0.34, with genetic correlation of 0.45. The REA and MS heritabilities were 0.35 and 0.33 and genetic correlation of -0.37. For trivariate WW-CW-REA analyses heritabilities were 0.43 for CW and 0.34 for REA, with genetic correlation between CW and REA of 0.50. For WW-BF-MS analysis heritability for BF was 0.38 and 0.30 for MS, with genetic correlation of 0.13 between BF and MS. The heritability for CW increased when estimated in a model that included WW. The genetic correlation between BF and MS was small, therefore selection for marbling can be implemented without increasing fatness. The genetic correlation between REA and MS was moderately negative. Further work is required to determine the impact on variance component estimates of including ultrasound data along with carcass and growth data.

Key Words: Carcass traits, Maternal effects, Heritabilities estimates

W97 Colorado State University Center for Genetic Evaluation of Livestock: Current approaches to performing large scale beef cattle genetic evaluations.

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The purpose of this paper is to review methodology for conducting beef cattle genetic evaluations performed by the Colorado State University Center for Genetic Evaluation of Livestock (CSU-CGEL). This methodology includes the specification of the type of model used, components that make up the model and solutions reported for each analysis. The CSU-CGEL performs contract genetic evaluations world wide for 15 different clients including breed associations, private ranches, and composite and pure-bred mating system cooperatives. These evaluations consist of the traits birth weight, weaning weight, yearling weight, docility, stayability, heifer pregnancy rate, calving ease, mature cow maintenance energy requirements, pulmonary arterial pressure, fat thickness, marbling score, rib eye area, carcass weight and quality grade that can be placed in the categories of growth, reproduction, carcass, longevity and behavior. The approach used to determine criteria for inclusion in the statistical model is the same for all analyses, even though the actual model for a given analysis differs for each category. For example, the growth traits birth weight and weaning weight are analyzed in a bivariate model as well as weaning weight and yearling weight, but weaning weight EPD reported are from the birth weight/weaning weight analysis. These traits are run together because they are genetically correlated and the increased amount of information adds accuracy to the prediction. Weaning weight is included in the carcass analysis, but for a different reason than it was included in with the growth traits. Weaning weight is analyzed with carcass traits to account for selection bias seen when calves are either selected as replacements or as slaughter animals. The production of EPD is its own unique puzzle, but if done properly provides producers with the most advanced tools currently available to help them increase the profitability of their operation.

Key Words: Beef cattle, Genetic evaluation, Expected progeny differences

W98 Identification and characterization of an AFLP marker for protein yield in Canadian Holsteins.

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A total of 200 cows, including 100 high and 100 low EBV for protein yield were used for genome-wide screening of QTL (quantitative trait loci) linked markers for protein yield in Canadian Holsteins using selective DNA pooling and amplified fragment length polymorphism (AFLP) approaches. These cows were selected from an experimental population of 5445 animals and used to form 5 high and 5 low performance pools with 20 animals per pool. AFLP analysis was performed on these pools using 80 selective primer combinations. The PCR products of selective amplifications were electrophoresed and electropherogram readings were standardized by dividing the sum of peak heights of standard length fragments. Standardized peak heights of AFLP fragments were log transformed and compared between high and low pools. A 288 bp fragment, generated using the E-ACG/T-CAT primer combination, was found to differ most significantly (P¡0.001). The difference was also confirmed by AFLP genotyping of individual cows. The AFLP fragment was then extracted from the gel and sequencing analysis revealed a C/T substitution responsible for this AFLP polymorphism. This marker was genotyped on all high and low performance animals using a Bi-PASA (bi-directional PCR amplification of specific allele) technique along with approximately equal addition of new animals into each pool from both tail of EBV distribution. Allele “C” was twice as frequent in low than in high performance animals (0.28 vs. 0.14, P¡0.01). A BLAST search against GenBank databases showed evidence that this AFLP marker is orthologous to an intron region of the human *TCF7L2* gene. Based on comparative maps between human and bovine genomes, we genotyped two additional markers in this AFLP marker region on a bovine/hamster RH panel. RHMAP analysis assigned this AFLP marker and the bovine *TCF7L2* gene on bovine chromosome 26 (BTA 26).

Key Words: AFLP, Selective DNA pooling, Dairy cattle

Nonruminant Nutrition

W99 Enzyme addition as a tool to improve early postweaning piglet performance.

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A total of 192 crossbreed piglets (Pietrain*Large white x Large white*Landrace), 50 % male and 50 % female, weaned at 21 days and weighting 6.5 kg were used to determine the effect of addition of an enzymatic complex (CE n 34) containing 275 U/kg of endo-1,3(4)-β-glucanase (E.C. 3.2.1.6), 400 U/kg of endo-1-4-β-xylanase (E.C. 3.2.1.8) and 3,100 U/kg of α-amylase (E.C. 3.2.1.1) to diets on performance. There were two experimental treatments based on enzyme supplementation (500 mg/kg) to a basal diet. The experimental design was applied in both the prestarter (21 to 40 d of age) and the starter diet (40 to 60 d of age). Nutritive value of the diets was 10.08 MJ NE/kg and 14.7 g/kg lysine for Prestarter and 10.03 MJ NE/kg and 13 g/kg lysine for Starter, and were based on barley, wheat and maize. Each treatment was replicated 8 times and 12 piglets caged together formed the experimental unit. Data were analyzed by using the GLM procedure of SAS. At 40 d of age, piglets fed the enzyme supplemented diet showed higher body weight (9.34 vs 8.35 kg, $P<.01$); daily gain (124 vs 72 g/d, $P<.05$); feed intake (247 vs 193 g/d, $P<.05$); and better feed conversion (2.05 vs 2.83 kg/kg, $P<.05$) than animals fed the unsupplemented diet. However, from 40 to 60 d control animals showed better feed conversion (1.44 vs 1.56 g/g, $P=.03$) and similar growth rate than enzyme supplemented piglets (528 vs 428 g/d, $P>.05$), so that, global differences (21 to 60 d of age) on performance were not significant. In addition, piglets fed the enzyme supplemented diet tended to be cleaner (5= very good, 0=very poor) than control animals at 40 d of age (3.31 vs 2.81, $P=.07$), but differences disappear thereafter. In conclusion, enzyme addition improved piglet performance in the prestarter period, but for the global period these differences disappeared, probably due to compensatory growth.

Key Words: Enzyme supplementation, Piglets

W100 Xylanase, glucanase and amylase supplementation to piglet diets.

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A study was designed to assess the efficacy of an enzyme complex (CE n 34) containing 275 U/kg of endo-1,3(4)-β-glucanase (E.C. 3.2.1.6), 400 U/kg of endo-1-4-β-xylanase (E.C. 3.2.1.8) and 3,100 U/kg of α-amylase (E.C. 3.2.1.1), supplemented at 3 doses (T2: 400, T3: 500 and T4: 600 mg/kg) to a pelleted diet based on cereals (wheat, maize, barley) on the performance of newly-weaned piglets, in comparison with a negative control group (T1, 0 mg/kg). The experimental diets were fed in two phases: as prestarter pellets from weaning (21 d) to 42 d and as starter pellets from 42 to 63 d of age, to 16 replicates of 10 piglets per treatment. The prestarter and starter diets, respectively, were formulated to contain 12.5 MJ ME/kg and 15 g/kg lysine and 12.6 MJ ME/kg and 13.5 g/kg lysine. Data were analyzed as a completely randomized block design using the GLM procedure of SAS. For the overall period of growth, piglets fed on T3 (500 mg/kg of enzyme complex) gained more weight than piglets fed on either T1 or T4, with the piglets fed on T2 having an intermediate value (17.51, 18.09, 18.49, 17.55 kg for T1 to T4, respectively, $P<.05$). Feed intake was not affected by dietary treatment, but piglets fed on T3 had better feed conversion ratios than those fed on T4, with pigs fed on both T1 or T2 having intermediate values (1.601, 1.584, 1.536, 1.614 g feed/g gain for T1 to T4, respectively, $P<.05$). Neither mortality nor piglet uniformity was affected by dietary treatment. It was concluded that i) the addition of the enzyme complex to a diet for piglets improved their growth, and ii) the dietary concentration of the enzyme complex resulting in the optimal performance was 500 mg/kg.

Key Words: Enzymes, Piglets

W101 Enzyme supplementation to piglet diets.

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A study was designed to assess the efficacy of an enzyme complex (CE n 34) containing 275 U/kg of endo-1,3(4)-β-glucanase (E.C. 3.2.1.6), 400 U/kg of endo-1-4-β-xylanase (E.C. 3.2.1.8) and 3,100 U/kg of α-amylase (E.C. 3.2.1.1), when added at 2 concentrations (T2, 500 and T3, 600 mg/kg) to a pelleted diet based on cereals (wheat, maize, barley) on the performance of newly-weaned piglets, in comparison with a negative Control group (T1, 0 mg/kg). Diets were fed in 2 phases: Prestarter from weaning (21 d) to 35 d and Starter from 35 to 57 d of age, to 15 replicates of 10 piglets per treatment, in 3 blocks (weanings). Nutritive value of the diets was 10.55 MJ NE/kg and 16.1 g/kg lys for Prestarter and 10.37 MJ NE/kg and 12.5 g/kg lys for Starter. Data were analyzed as a completely randomized block design by using the GLM procedure of SAS. Piglets fed enzyme supplemented diets were heavier than Controls at 35 (9.2, 9.7 and 9.7 kg, $P<.01$) and at 57 d of age (18.2, 19.2 and 19.2 kg for T1, T2 and T3 respectively, $P<.01$). Enzyme addition improved piglet growth by 16% from 21 to 35 d (195, 227 and 226 g/d, $P<.01$), by 5% from 35 to 57 d (404, 426 and 424 g/d, $P<.01$), and by 8% from 21 to 57 d of age (322, 349 and 347 g/d for T1, T2 and T3 respectively, $P<.01$). Enzyme supplementation also induced improvements in feed intake from 21 to 35 d, from 35 to 57 d and for the overall period (445,