BREEDING AND GENETICS

31   Selection for loin eye area using real-time ultrasound technology in Landrace swine. D. L. Kuhlers*, S. B. Jungst, and B. L. Anderson, *Auburn University, AL.*

With the availability of ultrasound technology to the swine industry, it was of interest to discover if selection for loin eye area (LEA) based on this technology would be effective. Furthermore, it was of interest to know what correlated responses could be expected from LEA selection. In a three-generation single-trait selection study with an unselected control line, 985 pigs, sired by 63 sires and out of 149 dams, were evaluated for real-time ultrasound of 10th-rib LEA and backfat thickness (BF) scanned with an Aloka 500V ultrasound machine. Pig weights at 168-d weight (W) were also recorded. Using a single-trait mixed animal model with full-relationship matrix. EBVs for LEA were calculated and used in selection of replacement breeding stock each generation. The control line pigs were selected within litter with EBVs as close to 0 as possible. Generation interval was one year with no overlapping generations. To evaluate the results of the selection, a multiple-trait DFREML analysis was conducted using the fixed effects of generation, sex and linear and quadratic covariates on W (for BF and LEA) and random animal and common litter effects. Estimates of heritabilities were .48, .54, and .37, for LEA, BF, and W, respectively. Genetic correlations estimates between LEA and BF, LEA and W, and BF and W were –.22, –.08, and .60, respectively. Common litter effects as a proportion of the phenotypic variance were .05, .02, and .06, for LEA, BF, and W, respectively. Differences in line-generation means of the EBVs (S–C) for LEA were 2.4, 5.2, and 6.9 cm^2 in generations 1, 2, and 3, respectively. Carcass LEA line differences were similar. For the correlated trait BF, the (S–C) line EBV differences were –.22, –.22, and –.11 cm, and for W, (S–C) line EBV differences were –3.9, –4.4, and –1.6 kg, for generations 1, 2, and 3, respectively. The results to date indicate selection for ultrasound loin eye area is an effective method for changing LEA. However, changes in W have been consistently in the undesirable direction.

Key Words: Pigs, Loin eye area, Selection

32   Optimization of Genetic Nucleus testing facilities using genetic correlations between pre-test weight and off-test performance. D. A. Henderson, T. H. Short, E. R. Wilson, and C. R. Looper*, *PIC USA, Franklin, KY.*

Sow herd sizes at the genetic nucleus level are maintained to fill available testing spaces. If sow herd sizes are increased to increase selection intensities, either additional testing facilities must be constructed or a preselection criterion must be established. Genetic correlations between weight at on-test (STWT) and performance traits at off-test were calculated using 11,726 dam line records (3 lines) and 7,592 sire line records (4 lines) from pigs born at a genetic nucleus farm. Reproductive traits in dam lines were not evaluated. An animal model was used in a series of two trait evaluations to estimate genetic correlations using the statistical package MTDFREML. Genetic correlations with teat number, leg score, and P_2 backfat were low ($| r_g |$ = .10 to .20) while genetic correlations with average daily feed intake (ADF) and days to 100kg (DAYS) were moderate ($| r_g |$ = .45 and .52, respectively). Preselection of pigs at on-test based on a selection index comprised of STWT, predicted ADF, and predicted DAYS would allow larger sow herds and optimize selection intensities and rate of genetic improvement for a fixed test facility.

Key Words: Pigs, Selection, Correlations

33   Relationships between growth and maternal traits in a pig dam line. D. A. Henderson*, T. H. Short, E. R. Wilson, *PIC USA, Franklin, KY.*

Genetic relationships between litter size, growth and carcass traits, and maternal ability were estimated in a commercial dam line. There were a total of 29,868 litter and performance test records and 2,187 litter weaning weight (LWWT) records from pigs born after January, 1990 at two PIC genetic nucleus farms. Up to three parities of litter records were included. An animal model with pedigrees traced back to base animals was used to estimate (co)variances in a series of two trait evaluations. Genetic correlations between total number born (TNB) and most growth traits and TNB and LWWT were low ($|r_g| < .18$). Three genetic correlations were greater than .25: TNB and days to 100kg (DAYS), $r_g = .35$; LWWT and DAYS, $r_g = -.35$; and LWWT and leg score, $r_g = .26$. This indicates that slower growing gilts have the genetic potential to produce larger litters. Also, faster growth and lower leg scores were genetically associated with increased milking ability (as measured by LWWT). The genetic correlation between TNB and LWWT was –.02, which is expected as litters are standardized within 24 hours after farrowing.

Key Words: Swine, Reproduction, Growth

34   Estimation of dominance variance in swine. M. S. Culbertson[1]*, J. W. Mabry[1], I. Misztal[1], and N. E. Gengler[2], [1]*University of Georgia, Athens and* [2]*FNRS Universitaire des Sciences Agronomiques, Gembloux.*

179,485 Yorkshire reproductive and 239,354 Yorkshire growth records were used to estimate additive and dominance variance by Method R. Estimates were obtained for number born alive (NBA), 21 day litter weight (LWT), days to 230 lbs. (DAYS), and backfat at 230 lbs. (BF). The single-trait models for NBA and LWT included the fixed effects of contemporary group and regression on inbreeding percentage and the random effects mate within contemporary group, permanent environment, additive, and dominance. The single-trait models for DAYS and BF included the fixed effects of contemporary group, sex, and regression on inbreeding percentage and the random effects permanent environment, additive, and dominance. Final estimates were obtained from 6 samples for each trait. Regression coefficients for 10% inbreeding were found to be –.23 for NBA, –.52 kgs for LWT, .02 for DAYS, and equivalently 0.0 for BF. Estimates of additive and dominance variances expressed in percent of phenotypic variances were 8.75 ± .49 and 2.15 ± .73 for NBA, 8.06 ± 1.05 and 6.28 ± .94 for LWT, 33.19 ± .41 and 10.28 ± 1.48 for DAYS, and 43.63 ± .94 and 4.77 ± .68 for BF. The ratio of dominance to additive variances ranged from .78 to .11. Results did not indicate a relationship between relative magnitude of additive and dominance estimates or between regression on inbreeding percentage and dominance estimates. The relative importance of dominance effects appears to be greater for reproductive traits and measures of growth than for measures of carcass composition.

Key Words: Swine, Dominance, Variance

35   Daily activity and core body temperature of mice selected for high and low heat loss. M. R. Mousel and M. K. Nielsen, *University of Nebraska, Lincoln.*

Daily activity (A) and core body temperature (T) were investigated in lines of mice selected for high (MH) or low (ML) heat loss and unselected controls (MC). Lines were created by selecting for 16 generations. All lines were replicated three times. At Generation 15, divergence between MH and ML relative to the MC mean was 53% for heat loss and 21% for feed intake. Collection of A and T data was done at Generation 20 using mice between 13 and 20 wk of age. An average of 9 animals per replicate-sex-selection-line class were recorded with a total number of 164. Data were accumulated using implanted transmitters (Mini-Mitter Co, Sunriver, OR) and continuous automated collection. Six mice, one of each sex of the 3 lines, were measured contemporaneously. Because transmitters were surgically placed in the peritoneum while the mice were under anesthesia, mice were allotted 1 d to recover from surgery before measurement. Measurement was for the subsequent 3 d. Mice were kept with their usual cohort during data recording. Activity was recorded for each half hour and then summed for the day; T was averaged daily. The 24-hr A means were transformed to log base 2 to lessen heterogeneity of variance within lines. Selection lines were significantly (P<.004) different for both A and T. Differences were due to selection (MH – ML, P<.001), and there was no evidence of asymmetry of response (P>.31). Retransformed from log base 2 to the scale of measurement, mean A counts were 301, 196, and 148 for MH, MC, and ML, respectively. Mean core temperatures were 37.2, 36.9, and 36.7 C for MH, MC, and ML, respectively. Females had greater A (P<.0001) and T (P<.006) than males. There was no evidence of a line × sex interaction for either A or T (P>.50). Overall phenotypic correlation between T and log base 2 of A was .36 (P<.001), however the pooled within line-sex correlation was not different from zero. Phenotypic and genetic relationships between A and T are different.

Key Words: Mice, Energy utilization, Activity

36   Variance component estimates for weekly body weights in New Zealand White commercial rabbits. J. I. McNitt[1] and S. D. Lukefahr[2]*, [1]*Southern University and A&M College, Baton Rouge and* [2]*Texas A&M University, Kingsville.*

The objective was to compare variance components due to direct genetic and common litter effects for weekly body weights in New Zealand White rabbits. Records for 5,874 rabbits born in 1,123 litters from 1985 to 1996 at Southern University, involving weaning weight (W0) and as many as five subsequent weekly body weight measurements (W1, W2, W3, W4, W5), were analyzed. Experimental rabbits were reared under commercial herd environmental conditions involving standard feeding, housing and management practices. Rabbits were marketed at a minimum body weight of 1,600 g, regardless of age. Single trait animal models included fixed effects of year-season-parity and a covariate for age (except for weaning weight), and random additive genetic, common litter and residual effects. There were 714 inbred rabbits with an average inbreeding coefficient of .116. Direct heritabilities were .107±.04, .105±.04, .156±.04, .188±.05, .260±.05 and .301±.06 for W0, W1, W2, W3, W4 and W5, respectively. Common litter effects consistently decreased: .713±.02, .651±.02, .584±.02, .518±.02, .417±.02 and .304±.02 for W0, W1, W2, W3, W4 and W5, respectively. These results suggest that to improve accuracy of selection, potential replacement candidates should not be marketed before 56 d (W4).

Key Words: Rabbits, Heritability, Growth

37   Linkage mapping of the leptin receptor gene to pig chromosome 6. A. L. Vincent*, L. Wang, and M. F. Rothschild, *Iowa State University, Ames.*

The leptin receptor (LEPR) is the high affinity receptor for leptin, a hormone secreted by adipose tissue to regulate fat deposition and satiety. Mutations in LEPR have been associated with obesity in both the mouse (db/db) and the rat (fa/fa). LEPR is a single transmembrane protein closely associated with the gp130 signal transduction of class I cytokine receptors. To genetically linkage map LEPR in the pig, published human cDNA sequence (Genbank HSU43168) was used to design PCR primers. Several sets of PCR primers spanning approximately 600 bp in the cDNA were used to amplify pig genomic DNA. A *HinfI* polymorphism was identified in an approximate 3.8 kb fragment. The ends of this fragment were sequenced to confirm that the pig LEPR gene had been amplified. The exonic sequence from the 5' and 3' ends of the fragment had 95% and 93% positives at the amino acid level, respectively, with the corresponding human sequence. The *HinfI* pattern produced fragments of approximately 2.1kb, 700bp, 395bp, 340bp, 230bp, 130bp, 50bp, and 40bp in the A allele, and 2.1kb, 700bp, 395bp, 240bp, 130bp, 110bp, 50bp, and 40bp in the B allele. Individuals from the PiGMaP reference families were genotyped and these data were analyzed for two-point linkage using CriMap. LEPR was significantly linked to seven published markers on pig chromosome 6. A multiple-point analysis was done to produce a best chromosome 6 map including all linked loci. This analysis corresponds with the recent physical mapping of LEPR in our lab to 6q3.3-q3.5 (Ernst et al., 1997). Financial assistance from Dalgety and PIC USA is greatly appreciated.

Key Words: Porcine, Leptin receptor, Mapping

38   Pinpointing QTLs on Chromosome 7 for Performance Traits in the Pig. L. Wang*, T.-P. Yu, H. W. Chung, C. K. Tuggle, and M. F. Rothschild, *Iowa State University, Ames.*

Improvements in the porcine genetic map and availability of resource families to study performance traits in the pig have made it possible to reexamine previous findings linking certain traits to genes or chromosomal regions. Previous studies have suggested that the porcine major histocompatibility complex on chromosome 7 may be linked to some performance traits including birth weight, growth and backfat. In a previous study, Rothschild et al. (1996) examined the association of chromosome 7 to several performance traits using five single molecular markers. In this study we have a total of 10 markers (S0064, TNFalpha, S0102, S0078, S0158, S0066, SW304, SW1083, S0101 and S0212, in part kindly provided by the U.S. Pig Genome Coordination Program) on chromosome 7 and have used an interval mapping approach to determine if Quantitative Trait Loci (QTL) exist for the traits. The total pigs used ranged from 241 to 330 and were from four Chinese × American resource families. The traits were birth weight, body weight at 21 and 42 days, average daily gain, several fat measurements and meat color, marbling and firmness scores. The data were analyzed for each breed cross separately and also pooled. In three of the four families, the region from TNFalpha to S0078 tended to be associated with first rib, last rib, tenth rib, lumbar fatness and average backfat thickness. An association was found between markers S0064 and TNFalpha for loin eye area in the Minzhu × Hampshire family. For other families some associations were seen for the other traits. For the pooled data, the region near S0212 was associated with 21 day body weight and that near S0078 with 42 day body weight. The results, though not statistically significant, were in reasonable agreement with previous findings indicating that chromosome 7 may certain QTL for growth and carcass traits in pigs. Increased accuracy of the analysis and significance of the results could be obtained with more F2 animals per family and some additional markers.

Key Words: Pig, QTL, Mapping

39   Progress toward an interval map for birth weight and early growth quantitative trait loci on pig chromosome 13. T.-P. Yu*, L. Wang, M. F. Rothschild, and C. K. Tuggle, *Iowa State University, Ames.*

A genome scan by Andersson et al., 1994 (Science 263: 1771-1774) identified a birth weight and early growth quantitative trait loci (QTL) on pig chromosome 13. PIT-1, which is a transcriptional regulatory factor of the growth hormone, prolactin and thyrotropin b subunit genes, was mapped on pig chromosome 13. We have reported that the pig PIT-1/MspI polymorphism is associated with pig birth weight in the ISU resource families as well as the Edinburgh resource families. The Uppsala resource families were also PIT-1/MspI genotyped. PIT-1 was linkage mapped to the region which is very close to their identified early growth and birth weight QTL on pig chromosome 13. We are attempting to confirm the birth weight QTL region on pig chromosome 13 in the ISU resource families and clarify the role of PIT-1 gene in the putative QTL region. Four microsatellite markers: Swr1008, S0068, Sw398 and Sw1056 were selected to genotype the ISU resource families which include four families with a total of 327 animals. The microsatellite genotyping was performed by using fluorescent-labelled primers kindly provided by the U.S. Pig Genome Coordination Program and the ABI automated genotyping system (Perkin-Elmer). The S0068 and Sw398 markers were multiplexed in a PCR reaction as were the Sw1056 and Swr1008 markers. Then all these four markers were multiloaded, electrophoresed and analyzed with Genescan software. The alleles were identified by using Genotyper software. By using a total of 1528 genotypes, the pig PIT-1 gene and these four microsatellite markers were linkage mapped in the ISU resource families by using the CRIMAP program. The results showed that these loci are in the same order as on the USDA-MARC map (Rohrer et al., 1996, Genome Research 6:371-391). The linkage distance (cM) between the markers are: Swr1008-9.3-S0068-13.3-PIT1-11.6-Sw398-16.6-Sw1056. This linkage map information will be used to interval map birth weight and early growth QTL on pig chromosome 13.

Key Words: Pig PIT-1, Microsatellites, QTL, Linkage map

40   Microsatellite variation in Yorkshire, Large White, and Hampshire swine. S. L. Kacirek*, P. I. Dimsoski, and K. M. Irvin, *The Ohio State University, Columbus.*

The objective was to study the microsatellite loci variation in Yorkshire, Large White, and Hampshire pigs. With the development of the Yorkshire breed in the U.S., we expect the two breeds may now represent two gene pools. The microsatellite variation in the Hampshire breed was used as a reference family to help us define the relationship between the Yorkshire and Large White breeds. Thirty individuals of each breed were chosen according to least relatedness criteria. Eighteen dinucleotide microsatellites were randomly chosen for analysis. DNA was extracted from blood or semen samples and amplified by the Polymerase Chain Reaction. The PCR products were loaded into 6% polyacrylamide sequencing gels and allele frequencies were estimated. Calculated parameters include: heterozygosity levels, the exact test of Hardy-Weinberg equilibrium, F_{st} values, test for distribution of allelic frequencies, and genetic distances. The mean number of alleles per locus was 4.2. The allele frequencies ranged from 0.02 to 0.90. Average heterozygosity levels for Yorkshires and Large Whites, respectively were 0.53 and 0.60. Alleles at six loci in both the Yorkshire and Large White populations were according to Hardy-Weinberg equilibrium. The three most discriminating loci between the two lines were: SW703, SW995, and SW1067 with F_{st} values of 0.24, 0.22, and 0.19, respectively. Results indicate that the two breeds, due to many generations of selection, diverged enough so that their differences were significant enough to be measured by microsatellite variation. Due to the variation in the populations, we conclude that the Yorkshire and Large White breeds represent two distinct populations.

Key Words: Pigs, Microsatellites

41   Pit-1 gene *Hin*fI RFLP and growth traits in double-muscled Belgian Blue cattle. R. Renaville*, N. Gengler, I. Parmentier, F. Mortiaux, S. Massart, C. Bertozzi, A. Burny, and D. Portetelle, *Faculty of Agronomy, Gembloux, Belgium.*

Pit-1 is a pituitary-specific transcription factor that regulates growth hormone, activates prolactin and has a role in pituitary cell differentation and proliferation. Our preliminary study in dairy cattle showed a *Hin*fI RFLP at the Pit-1 gene and postulated that allele A was probably associated to milk performances. The aim of this study was to search for eventual association between Pit-1 polymorphism using the *Hin*fI enzyme and growth and feed consumption traits of 350 double-muscled Belgian Blue bulls. A PCR strategy was used to amplify a 451-bp fragment from blood white cells DNA. Growth performances were weighed between 7 and 13 months of age and included body weight (BW), average daily gain (ADG), shoulder height (SH), and feed efficiency (FE). Digestion of PCR products with *Hin*fI revealed two alleles : A allele was not digested (451bp fragment) and B allele was cut at one restriction site, generating two fragments of 244 and 207 bp. The allelic frequency was 53 % and 47 % for A and B, respectively. Three patterns were observed, with the frequencies of 20, 44.5 and 35.5 % for AA, AB and BB, respectively. A mixed linear model was used with pattern as fixed effect and additive polygenic as random effect. Linear contrasts were fitted. The BB pattern was found significantly superior to AB and AA patterns for BW at 7 months of age (P<0.01 and P<0.05). The AA and BB patterns were significantly superior to AB for shoulder height at 13 months of age (P < 0.001). No relationships were observed between ADG or FE and the Pit-1 genotypes. In conclusion, this study made evidence of interesting relationships between Pit-1 RFLP and growth traits in beef cattle. The B allele could be associated to early body weight. (Ministery of Agriculture, Research grant 5744A).

Key Words: Pit-1, RFLP, Growth

42   Integration of four published bovine linkage maps. S. M. Kappes, J. W. Keele, R. T. Stone, and C. W. Beattie, *USDA-ARS Meat Animal Research Center, Clay Center, NE.*

Livestock genetic linkage maps have been developed to identify loci that influence economically important traits. Identification of quantitative trait loci (QTL) can improve selection accuracy and intensity of economically important traits. The first bovine linkage maps contained 313 (Bishop et al., 1994), 171 (Barendse et al., 1994) and 159 (Georges et al., 1995) linked markers with an average marker interval exceeding 10 centimorgans (cM). Although loci have been detected with these maps, marker density and informativeness limits resolution of the locus location and efficiency of subsequent marker assisted selection (MAS). Additional markers have been developed and linked but they are found on several different maps (Ma et al., 1996; Barendse et al., 1997; Kappes et al., 1997). A comparison of these maps will augment QTL detection and resolution and MAS by identifying all available markers in specific regions of the genome. We have genotyped markers (Kappes et al. 1997) that are in common with other bovine maps (322/689, Barendse et al., 1997; 181/239, Ma et al., 1996 ; and 74/149, Georges et al., 1995) to allow comparison of the linkage groups. The four maps contain 1774 unique markers with a range of 132 (chromosome 1) to 31 (chromosome 27) unique markers per chromosome. Common linkage group distances were calculated relative to the Kappes et al. (1997) map by determining the distance between the two most external common markers for each linkage group and combining the 29 autosomal and × chromosomal distances. The relative common linkage group distances were 94% (949/1005 cM; Georges et al., 1995), 107% (1763/1655 cM; Ma et al., 1996), and 134% (3330/2491 cM; Barendse et al., 1997) of the Kappes et al. (1997) map. Differences in linkage group length can be caused by genotypic errors and specific parental recombination rates. Marker order of common markers is similar between the four maps. The information provided by these four maps will augment QTL detection and resolution and subsequent MAS in cattle.

Key Words: Bovine, Linkage map

43   Identification of RAPD markers linked to quantitative trait loci controlling milk protein yield in Holstein dairy cattle. R. L. Park*, S. Xiong, J. K. Day, R. N. Thwaits, and W. R. Andersen, *Brigham Young University, Provo, UT.*

In dairy cattle, milk yield and composition are controlled by a large number of polygenes. In an intensely selected population, those polygenes with large effects are near fixation. In this approach we utilized the RAPD technique and bulked DNA samples from highly selected bulls to facilitate the identification of polymorphic markers linked to quantitative trait loci (QTL) responsible for protein yield in Holstein dairy cattle. DNA was isolated from semen samples of 33 bulls provided by Atlantic Breeders Association. Two DNA bulks were prepared according to PTA (Predicted Transmitting Ability) protein records. The high performance bulk (n = 18) had a mean PTA protein yield of 49.39 and the low bulk (n = 15) had a mean PTA protein yield of –11.07. Genome scans were then conducted by screening for polymorphic markers between the two bulks with approximately 1500 random 10-mer primers. A set of polymorphic markers were identified. Candidate markers were then confirmed with individual DNA screening. Four markers associated with the high performance group were then tested on DNA samples isolated from blood drawn from 16 selected cows from Brigham Young University (high group: n = 10, mean PTA protein = 64.60; low group: n = 6, mean PTA protein = –1.0.). The results indicated that those markers significantly associated with the high protein yield (χ^2 test: $p \leq 0.026$). SCAR markers are being developed for further tests on samples from other intensely selected populations. Our results demonstrated that RAPD can be used to generate predictable DNA markers that could be used in a marker assisted selection breeding program.

Key Words: RAPD, DNA polymorphism, Milk protein yield, Dairy cattle

44   Identification of Sequence Tagged Sites in the Asian Elephant (*Elephas maximus*). N. E. Elavsky, C. W. Ernst, L. A. Messer*, and M. F. Rothschild, *Iowa State University, Ames.*

Limited research has been done in the area of elephant genetics. To date, gene identification has essentially related to evolutionary studies. Further identification of genes in elephants could provide additional information for evolutionary studies and also provide information for evaluating genetic diversity in existing elephant populations. Our objective was to identify sequence tagged sites (STS) in the Asian elephant for the following genes: melatonin receptor 1a (MTNR1A), retinoic acid receptor beta (RARB), and leptin receptor (LEPR). These genes are highly conserved among mammals and all may play a role in reproduction. Heterologous primers for PCR were designed from sequences available in other species. An approximately 500 base pair (bp) fragment for MTNR1A, a 180 bp fragment for RARB, and a 350 bp fragment for LEPR were obtained by amplifying genomic Asian elephant DNA. The LEPR fragment included an intron of 164 bp. All PCR products were sequenced and comparison computations were made at the nucleotide and amino acid (aa) level to sequences available in GenBank. Sequence identities for MTNR1A between elephant and pig, human, sheep, mouse, rat and chicken ranged from 71% (chicken) to 84% (pig) for nucleotide sequence and from 76% (chicken) to 87% (mouse) for aa sequence. Sequence identities for RARB between elephant and pig, human and chicken ranged from 82% (chicken) to 97.8% (pig) for nucleotide sequence and 97% (chicken) to 100% (pig and human) for aa sequence. Identities for LEPR between elephant and pig, human, mouse and rat ranged from 90.1% (rat and mouse) to 96.9% (pig) for nucleotide sequence and from 89.3% (rat and mouse) to 96.4% (pig) for aa sequence. This work represents some of the first sequencing work in the Asian elephant.

Key Words: Elephant, Sequence tagged sites, Receptor genes

45   A decision support system to deal with genotype by environment interactions. T. S. Stewart, S. Newman, M. Goddard, and M. Gregory, *Purdue University, W. Lafayette, IN, CSIRO, Rockhampton, QLD, Univ. of New England, Armidale, NSW, and Central Queensland Univ., Rockhampton, QLD.*

A major limitation to crossbred mating programs in tropical areas has been the lack of information on the impact of genotype-environment interactions. A decision support tool was developed to predict performance of alternative genotypes for 17 performance traits under tropical environmental conditions. Descriptors of environmental stress are ambient temperature, ticks, worms and nutrition availability. The approach used to predict animal performance is to first predict performance in a benign (zero stress) environment. Impact of environmental stresses is characterized by determining the reduction in growth performance due to each environmental stress. Environmental regression equations are non-linear multiple regressions accounting for environmental stressor and the percent of the animal's genotype that is a tropically adapted breed. For maternal traits, percent adapted genotype of the dam is also included in the regression. Performance of other traits is predicted by regressing the trait on the stressed weight of the specific genotype. A database of 18 breeds was developed to characterize breed performance in a benign environment. Environmental regression equations were developed by pooling information in reports relating performance to temperature, internal and/or external parasite levels. Users provide descriptions for temperature, parasites and nutrition for breeding, growing and finishing phases of production. They construct a mating plan using a graphical interface. Predicted performance is displayed as a bar graph including all genotypes in the mating plan or a table listing performance of all traits for a genotype in both the benign and described environment. Work is continuing to include economic inputs to combine the values of all traits and to allow inclusion of genetic evaluation information for individual sires or dams.

Key Words: Decision support, Genotype environment interaction, Beef Cattle, Genetics, Crossbreeding

46   Heat tolerance in Tuli × Angus, Senepol × Angus, Brahman × Angus, Senepol, Brahman, and Angus heifers. A. C. Hammond[1]*, C. C. Chase, Jr.[1], T. A. Olson[2], and R. D. Randel[3], *[1]USDA, ARS, Brooksville, Florida, [2]University of Florida, Gainesville, and [3]Texas A & M University, Overton.*

Heat tolerance was investigated in 29 Tuli × Angus (T×A), 17 Senepol × Angus (S×A), 23 Brahman × Angus (B×A), 30 Senepol (PS), 35 Brahman (PB), and 13 Angus (PA) heifers (365 ± 3.4 kg) by measurement of rectal temperature (RT, °C) and respiration rate (RR, breaths per min) under ambient conditions in central Florida. Differences among breeds in temperament score (TS, 1 to 5) and plasma cortisol (CORT, ng/mL) were also investigated. Measurements were obtained on three summer and three winter dates in 1995. Data are presented for Aug. 16 (the hottest summer date) and Dec. 13 (the coolest winter date) with avg. ambient temperatures and relative humidities of 33.0 and 24.0 °C and 63.5 and 59.5%, respectively. Data for RT were transformed (log [RT − 37]) prior to analysis. In Aug., RT and RR were higher (P < .001) in PA (40.9, 74 ± 2.7) than in PB (40.0, 39 ± 1.6), PS (39.6, 50 ± 1.8), and crossbred heifers (40.0, 60 ± 1.8; 39.7, 55 ± 2.3; and 40.2, 48 ± 2.0 for T×A, S×A and B×A, respectively), and RR was higher (P < .001) in B×A (48 ± 2.0) than in PB (39 ± 1.6). There was no difference in RT for PS vs S×A or PB vs B×A in Aug. In Dec., RT did not differ for any of the five contrasts, but RR was slightly lower in PB (32 ± .5) than in PA (34 ± .7, P < .01) and B×A (36 ± .6, P < .001). On both dates, TS and CORT were higher (P < .01) in PB than PA (TS: 3.6 ± .14 vs 2.4 ± .24 and 2.8 ± .12 vs 2.3 ± .20; CORT: 53 ± 4.4 vs 30 ± 7.1 and 40 ± 2.1 vs 23 ± 3.5; for PB vs PA in Aug. and Dec., respectively). In Dec., CORT was also higher (P < .001) in PB (40 ± 2.1) than in B×A (27 ± 2.6). These data indicate that heat tolerance in crosses of tropically adapted breeds (Tuli, Senepol, Brahman) with a temperate breed (Angus) are similar to heat tolerance displayed by purebred tropical breeds (Senepol, Brahman).

Key Words: Beef Breeds, Heat Tolerance, Subtropics

47   Evidence for the existence of a major gene influencing hair length and heat tolerance in Senepol cattle. T. A. Olson[1], A. C. Hammond[2], and C. C. Chase, Jr.[2], *[1]University of Florida, Gainesville and [2]USDA, ARS, Brooksville, Florida.*

The heat tolerance of 28 calves from Angus(A) sires and Senepol(S) × Hereford F_1 dams was evaluated to investigate the existence of a major gene influencing heat tolerance. Calves were evaluated for hair length, rectal temperature (RT), respiration rate, and BW. Purebred A calves (n = 10) were included as controls. Measurements were taken on three consecutive weeks during summer and also during late fall. The ambient temperature surpassed 32.5° C on two of the summer dates and averaged 23.3° C during the fall. A subjective system (1 to 4) was used to evaluate hair length. The three lowest scores (1⁻, 1 and 1⁺) describe the extremely short-haired "slick" condition of purebred S cattle and their F_1 crosses with temperate *Bos taurus* breeds. One of the A calves was coded as a 1⁺, the others, 2 and higher. Twelve of the 28 crossbred (25% S) calves were coded as slick-haired (1⁻, 1 or 1 1⁺) and 16 as normal-haired (2⁻ and higher); the 12:16 ratio does not differ significantly from 1:1. Data for RT were transformed (log [RT - 37]) prior to analysis. The RT of the slick calves was lower (P < .02) than that of the A on two of the summer and two of the fall dates. The RT of the slick calves were lower (P < .04) than that of normal-coated counterparts (also 25% S) on two of the three summer dates. The RT of A-sired 25% S calves with normal haircoats was not different (P > .07) from that of A calves on any date. Respiration rate was not influenced by hair coat type or breeding in any consistent manner. The slick calves were heavier (P < .05) than the normal-haired and A calves on the last weigh date. A group of 15 Charolais-sired calves from S × A F_1 dams was also scored for hair length in late September. Seven of these calves were coded as 1's and eight as 3's or 4's, for a 7:8 ratio of slick:normal. These data suggest that a major gene for hair length and heat tolerance may exist in the Senepol breed.

Key Words: Heat Tolerance, Genetic Control, Senepol

48   Genetic relationships among direct and maternal components of milk yield and weaning gain in a multi-breed beef herd. S. P. Miller* and J. W. Wilton, *University of Guelph, Ontario, Canada.*

Objectives were to determine the genetic relationship between milk yield of the beef cow and maternal weaning gain and estimate genetic parameters for Milk Yield (MY) and Weaning Gain (WG). Data spanning 1980 to 1993 from a multi-breed beef herd involving primarily 8 different breeds (Angus, Charolais, Gelbvieh, Hereford, Maine Anjou, Pinzgauer, Simmental, and Tarentaise) were used to obtain 2207 records on WG (200-d, kg) and 1826 records on MY (200-d, kg), which were obtained by machine milking after oxytocin injection. Bivariate (WG and MY) REML estimates of (co)variances were obtained modeling breed and heterosis of calf and cow using a partial regression approach. Animal effects included the calf and the cow contributing to each record designated as ($Calf_{WG}$, Cow_{WG}) and ($Calf_{MY}$, Cow_{MY}) for (Calf, Cow) contributions to WG and MY, respectively. Permanent environment effect of the cow was modeled for MY, with 693 levels. Genetic effects of 2926 animals were included. Estimates of breed differences were generally similar for Cow_{WG} and Cow_{MY}. Heterosis was estimated at 8.2, 2.5, 6.8 and 5.4 percent of mean for $Calf_{WG}$, Cow_{WG}, $Calf_{MY}$, and Cow_{MY}, respectively. Permanent environment effect of the cow for MY represented 9 percent of phenotypic variance. Heritability estimates were 0.22 and 0.23 for $Calf_{WG}$ and Cow_{WG} and 0.23 and 0.35 for $Calf_{MY}$ and Cow_{MY}. A genetic correlation between Cow_{WG} and Cow_{MY} of 0.76 indicates that maternal weaning gain evaluations are a good indication of milk yield.

Key Words: Beef cattle, Milk yield, Maternal effects

49   Heritabilities of and genetic correlations among sex-specific traits in beef cattle. R. K. Splan[1]*, L. V. Cundiff[2], and L. D. Van Vleck[2,3], [1]University of Nebraska, Lincoln, [2]USMARC, Clay Center, and [3]Lincoln, NE.

Data from 3459 beef heifers and 4080 of their steer paternal half-sibs were used to estimate genetic parameters of and among female growth and reproductive traits and male carcass traits. Estimates of heritability for adjusted 205-d weight, adjusted 365-d weight, age at puberty, calving rate and calving difficulty measured on females were .13, .37, .46, .07 and .12, respectively, with estimates for calving rate and calving difficulty expressed on a binomial scale. Estimates of heritability for hot carcass weight, retail product percentage, fat percentage, bone percentage, rib eye area, estimated kidney, pelvic and heart fat percentage, adjusted fat thickness, marbling score, Warner-Bratzler shear force, taste panel tenderness, taste panel juiciness and taste panel flavor measured on steers were .37, .64, .53, .47, .57, .43, .43, .71, .24, .29, .00 and .04, respectively. Estimates of genetic correlations were positive for heifer weights with hot carcass weight, estimated kidney, pelvic and heart fat percentage, rib eye area, adjusted fat thickness and taste panel flavor of steers, and negative with retail product percentage. Warner-Bratzler shear force and taste panel tenderness were unfavorably correlated with heifer weaning weight, but showed no relationship with yearling weight. Age at puberty was correlated with taste panel tenderness and flavor but with no other carcass trait. Calving rate was positively correlated with traits involving carcass fatness. Calving difficulty was unfavorably correlated with measures of carcass tenderness. Results imply selection for some traits expressed in one sex of beef cattle may yield undesirable responses in traits expressed in the opposite sex.

Key Words: Genetic Parameters, Carcass Traits, Reproductive Traits

50   Evaluation of maternal EPD selection line, weaning weights and measured milk production in first lactation Angus cows. J. F. Baker, *University of Georgia, Tifton.*

First lactation records (n=73) for Angus cows from high (HEPD) or low (LEPD) weaning weight maternal sires were used to estimate effects of line on weaning weights. Bulls were selected based on maternal weaning weight EPD's (MILK) provided by the American Angus Association. The difference between the average HEPD and LEPD was 18.14 kg. while average yearling weight EPD's were similar; 21.77 kg for HEPD and 22.68 kg for LEPD. Bulls selected had to have MILK accuracy values in excess of .5 and were near the average for birth and yearling weight EPD's. Daughters were reared at two locations (Ti and Re) in South Georgia and mated A.I. to a single sire then a short natural service season for first calf at two y. Calves were not creep fed. Males at Re were castrated and implanted; but left intact at Ti and no implant. The average calving date was January 31 with weaning in late August. Cows were milked four times, with the first measurement at about 45 d average post-partum, the fourth occurred just prior to weaning and the other measurements were approximately equally spaced between the first and last. Milk production was significantly correlated with age adjusted weaning weight for three of the four milk estimates (.37, .16, .44, and .37 respectively). Line and location were significant sources of variation for milk production estimates and weaning weights but the interaction was non-significant. The difference between the average weaning weights of HEPD and LEPD lines was 10.19 kg and less than predicted by grandsire EPD's.

Key Words: Beef cattle, Milk production, Breeding value

51   Variance component estimates for scrotal circumference, age at puberty in heifers and hip height in Brahman cattle. C. A. Vargas[1]*, T. A. Olson[1], M. A. Elzo[1], C. C. Chase, Jr.[2], and P. J. Chenoweth[1], [1]University of Florida, Florida and [2]ARS-USDA, STARS, Brooksville, Florida.

Variance and covariance components were estimated for scrotal circumference (SC, n=287), age at puberty in heifers (AAP, n=292), and hip height in both sexes (HH, n=684) between 1984-1996 in the Brahman herd at the Subtropical Agricultural Research Station, Brooksville, Florida. Measurements on SC and HH were taken at 18 mo of age. A multitrait animal model was used to estimate (co)variances. The fixed effects were year (YR), and age of dam (AOD), and age at measurement (AAM) for SC, YR and AOD for AAP, and YR, SEX, AOD and AAM for HH. The MTDFREML package was used for the computations. Starting values were obtained by fitting a single trait animal model for each trait. Estimates of heritability of SC, AAP and HH were .28, .42 and .65, respectively. Estimates of genetic correlations between SC and AAP, AAP and HH, and SC and HH were −.32, .25 and .19, respectively. Estimates of environmental correlations were −.13 between AAP and HH, and .19 between SC and HH. Estimates of genetic parameters indicate that selection of sires for increased scrotal circumference should be a viable means to reduce age at puberty in heifers.

Key Words: Beef cattle, Reproduction, Variance components

52   Estimates of genetic parameters for preweaning growth traits in the Turipana Romosinuano herd in Colombia. M. A. Elzo[1]*, C. Manrique[2], G. Ossa[3], and O. Acosta[4], [1]University of Florida, Gainesville, [2]Universidad Nacional, Colombia, [3]CORPOICA, Colombia, [4]ICA, Colombia.

The Romosinuano (R) herd at Turipana, Colombia, is the main source of germplasm of this breed in the world. Most of the R cattle in Costa Rica, Venezuela, Brazil, and the U.S.A., can trace their pedigrees back to the Turipana herd. It is important to document the genetic variability of this herd for traits of economic interest. Thus, estimates of direct (D) and maternal (M) additive genetic covariances were computed for birth weight (BW) and weaning weight (WW) using 2058 records from a R-Zebu crossbreeding program conducted at Turipana between 1980 and 1992. Covariance estimates were obtained by restricted maximum likelihood, using an expectation-maximization algorithm for multibreed populations. The model used had contemporary group and age of dam as fixed effects, additive genetic effects (calf, dam), and nonadditive genetic effects (sire × breed group of dam) as random effects. Covariances among random effects were accounted for. Heritability estimates were: .14 (BWD), .12 (WWD), .41 (BWM), and .33 (WWM). Additive genetic correlation estimates were: .27 (BWD, WWD), .71 (BWD, BWM), .25 (BWD, WWM), .28 (WWD, BWM), .75 (WWD, WWM), and .36 (BWM, WWM). Given the small size of the data set available, these estimates need to be viewed with caution. However, the total number of R cattle in Colombia is less than 4000. This number is even smaller in other countries. Thus, to obtain more reliable estimates of genetic parameters for this breed, data from all countries that have R cattle will be needed. Good international cooperation is essential to achieve this goal.

Key Words: Genetic parameters, Growth, Cattle

53   Relationships between estimates of heterosis and dominance variance for post-weaning gain in US Limousin cattle. N. Gengler[1]*, I. Misztal[2], and J. K. Bertrand[2], *[1]FNRS Faculté Universitaire des Sciences Agronomiques, Gembloux and [2]University of Georgia, Athens.*

The objective of this study was to estimate the dominance variance for post-weaning gain in Limousin cattle and to relate it to heterosis. The data included 215,326 post-weaning gains from 205 to 365 days, provided by the North-American Limousin Foundation for the August 1996 genetic evaluation. Extended pedigree files contained 476,175 animals. Parental dominance sub-classes were formed and related using the method of Hoeschele and VanRaden. A total of 538,635 classes were created. Variance components were estimated using Method R. Fixed effects in the model included contemporary group and covariates for inbreeding, breed composition (Limousin or British) and heterosis estimated using the breed composition of the parents. Six samples representing 50% of the animals were drawn and analyzed. Two models were used. Model 1 contained the fixed effects described above and a random animal genetic effect. Model 2 included a dominance effect in addition to the effects contained in model 1. Dominance effects were represented as related parental sub-class effects, with the dominance variance being four times the estimated parental sub-class variance. Estimates for inbreeding depression, breed composition and heterosis were all small and not affected by inclusion of dominance effects. Estimates of additive variance (expressed as a percent of the phenotypic variance) were also only slightly affected with 21% ± 1.1%. Estimates of dominance variance (expressed as a percent of the phenotypic variance) were 10% ± 1.5%. Such a high value, representing 48% of the additive estimate, may indicate that dominance is important for post-weaning gain. Also high dominance variance was observed despite low heterosis estimates; these estimates were not affected by the inclusion of dominance in the model.

Key Words: Beef cattle, Heterosis, Dominance variance

54   Genetic parameter estimates of carcass traits in Charolais cattle. N. Caron[1,2]*, R. A. Kemp[1], and G. M. Weiss[2], *[1]Agriculture and Agri-Food Canada, Lethbridge and [2]Canadian Charolais Association, Calgary.*

A total of 3994 carcass trait records from the Conception to Consumer program (an organized progeny test) were used to estimate genetic parameters. Calves were born and raised to weaning ($\bar{x}$=215.6d) in several commercial herds in Western Canada from 1975 to 1996. At weaning, all calves were placed in one commercial feedlot until reaching the desired slaughter endpoint. All calves were progeny of 170 Charolais sires mated to cows of various breed types. Measurements on carcass weight (CW), ribeye area (REA) and average fat thickness (AFAT) were used to estimate lean yield (LY) using the following equation: LY (%) = 59.76 −.027 CW (kg) + .212 REA (cm²)− .703 AFAT (mm). Variance components were estimated using MTDFREML in a 4-trait sire model with priors estimated from preliminary single trait and pairwise analyses. Sire relationships were included through a sire-maternal grandsire relationship matrix. The model included 196 contemporary groups (herd × sex × date on-test) and 48 dam breed types as fixed effects and the linear covariate age at slaughter within year. Coefficients of variation for LY, CW, REA and AFAT were 5.20, 11.78, 11.97 and 30.55 %, respectively. Heritability estimates for CW, REA, AFAT and LY were .15, .36, .30 and .38, respectively. Genetic correlation estimates for CW with REA and AFAT were .36 and .07, respectively, and −.39 between REA and AFAT. Genetic correlation estimates were .01, .78 and −.87 for LY with CW, REA and AFAT, respectively. Genetic improvement programs for composite traits need to consider the genetic relationships among the composite and component traits to ensure desired progress towards breeding goals.

Key Words: Beef Cattle, Genetic Parameters, Carcass

55   Genetic parameter estimates for carcass and yearling ultrasound measurements in Brangus cattle. D. W. Moser[1]*, J. K. Bertrand[1], I. Misztal[1], L. A. Kriese[2], and L. L. Benyshek[1], *[1]University of Georgia, Athens and [2]Auburn University, AL.*

Carcass measurements of 12th rib fat (CARCFAT), ribeye area (CARCREA), and weight (CARCWT) on 3,484 Brangus and Brangus-sired fed steers and heifers and yearling weights (YWT) and ultrasound measurements of 12th rib fat (USFAT) and ribeye area (USREA) on 7,369 Brangus breeding bulls and heifers were analyzed to estimate genetic parameters. Data were analyzed using a multiple-trait animal model and an average information REML algorithm. The model included fixed effects for contemporary group, breed of dam, covariates for age at slaughter or measurement, and random effects for animal and residual error. Heritabilities (diagonal), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) are listed in the table below. Standard errors ranged from .023 to .048 for heritabilities and from .053 to .113 for genetic correlations. Genetic correlations between corresponding carcass and ultrasound traits were positive and moderate in magnitude. Yearling ultrasound measurements of breeding cattle may be of use in predicting breeding values for carcass traits.

	CARC-FAT	CAR-CREA	CARCWT	USFAT	USREA	YWT
CARCFAT	.60	−.14	.25	.57	.11	−.05
CARCREA	−.05	.39	.24	−.02	.59	.35
CARCWT	.33	.41	.68	.01	.31	.78
USFAT	.27	−.01	.01	.38	.06	.05
USREA	.04	.19	.14	.13	.28	.40
YWT	−.02	.14	.40	.19	.39	.40

Key Words: Beef cattle, Genetic parameters, Ultrasound

56   Association of the double-muscling locus on bovine chromosome two (BTA2) with carcass traits. E. Casas*, J. W. Keele, S. D. Shackelford, T. S. Sonstegard, T. P. Smith, M. Koohmaraie, S. M. Kappes, and R. T. Stone, *USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

The locus causing double-muscling (mh) in cattle is located on the proximal region of BTA2. The objective was to assess the effects of a single copy of this locus on carcass traits. Two half-sib families were developed using either a Belgian Blue × MARC III (n=219) or a Piedmontese × Angus (n=187) sire. Four microsatellite markers within the first nine centimorgans (cM) of BTA2 linkage group were used to determine the presence or absence (grand-parental origin) of the mh locus. Two additional markers, at 28 and 47 cM, were used to confirm that the locus affecting the traits was in the proximal region of BTA2. Carcass traits evaluated were rib eye area (REA; cm²), retail product yield (RP; %) USDA yield grade (YG), marbling (MA), fat thickness (FAT; cm), estimated kidney, pelvic and heart fat (KPH; %), and longissimus tenderness measured as shear force at 3 (S3) and 14 (S14) days postmortem. Data were analyzed with a model that included the fixed effects of sire and sex, and hot carcass weight as a covariate. F-statistics were obtained at 1 cM intervals to identify the position and effect of the locus. Allelic difference at the mh locus increased (P<.01) for REA and RP, and decreased MA, YG, FAT, and KPH. The effect of the mh allele (mh/+ − +/+) was 1.38, 1.47, −.9, −1.41, −.7, and −.8 residual standard deviations, respectively. Allelic differences due to the mh locus were similar for both sources (Piedmontese or Belgian Blue), supporting historical evidence that the mh locus is the same in both breeds. Individuals inheriting the mh allele had an advantage for carcass composition, but had decreased marbling scores compared to those inheriting the alternative allele. Thus, mating schemes that maximize production of mh/+ genotypes provide a viable approach for improving carcass composition.

Key Words: mh, Double Muscling, QTL

57 Identification of quantitative trait loci for traits influencing energy utilization in mice. D. E. Moody*, D. Pomp, and M. K. Nielsen, *University of Nebraska, Lincoln.*

Lines of mice differing in energy expenditure have been developed through long-term divergent selection for heat loss (HL) as a model to study the genetic regulation of energy utilization in livestock. The objective of this study is to screen the mouse genome to identify chromosomal regions harboring quantitative trait loci (QTL) influencing HL and correlated traits. An F2 population (n=560) was created from a high HL selection line (MH) and the inbred line C57BL/6J, whose mean HL is 4 SD lower than MH. Phenotypes were recorded for HL measured in direct calorimeters, body weights at 3 (BW3), 6 (BW6), and 10 (BW10) wk, individual feed intake (INT), and percent subcutaneous (SUB), gonadal (GON), and brown adipose (BAT) tissues. Selective genotyping of 94 F2 mice with high or low HL compared to siblings was carried out using 40 fully informative microsatellite markers (65% genome coverage). Chi-square analysis was used to identify differences in allele frequencies between high and low HL groups. Different (P<.05) allele frequencies were found for markers on chromosomes 1 (M1), 2 (M2) and 3 (M3). The complete F2 population was genotyped for these markers and analysis of variance was used to determine the effect of marker genotype on phenotype. Evidence of QTL influencing HL was found at M1 (P=.0001), M2 (P=.0009) and M3 (P=.0002) with each locus having an effect of .5 SD. M1 and M3 had significant effects on BAT (P=.0008, .5 SD; and P=.005, .4 SD, respectively), and M1 had effects of .77 (P=.0001) and .39 (P=.006) SD on BW3 and BW6, respectively. Genotype by sex interactions for M2 were significant for BAT (P=.003), SUB (P=.02) and BW6 (P=.02). No significant effects of M1, M2 or M3 genotypes were detected for INT, GON or BW10. These results indicate that QTL influencing HL are linked to M1, M2 and M3, and these or other linked QTL also effect BAT. Further investigations of these chromosomal regions may facilitate a greater understanding of the genetic regulation of HL and its relationship to energy utilization.

Key Words: Quantitative trait loci, Mice, Energy utilization

58 Comparative gene mapping of human chromosome 13 in pigs. H. S. Sun[1]*, L. Wang[1], M. F. Rothschild[1], A. Robic[2], and C. K. Tuggle[1], [1]*Iowa State University, USA and* [2]*INRA, Laboratoire de Genetique Cellulaire, France.*

Previous comparative mapping between the human and pig genomes suggested complete conservation of human chromosome 13 (HSA13) to pig chromosome 11 (SSC11). The objectives of this study are comparative gene mapping of pig homologs of HSA13 genes and to examine gene order within this conserved synteny group by physical and/or genetic assignment of each locus. A detailed HSA13 to SSC11 comparison was chosen since the comparative gene map is not well developed for these chromosomes and a rearranged gene order within conserved synteny groups was observed from the comparison between human chromosome 13 and bovine chromosome 12 (Sun et al., Genomics, in press). Genes selected for this study are fms-related tyrosine kinase (FLT), retinoblastoma susceptibility gene (RB1), serotonin receptor subtype 2 (HTR2), esterase D (ESD), endothelin receptor B (EDNRB) and coagulation factor 10 (F10). Heterologous primers for PCR were designed from regions that were highly conserved between the human and a second species. Fragments amplified from the pig genome were sequenced to confirm the homology and pig sequence tagged sites (STSs) were submitted to the GenBank database. Four pig STSs have been developed and three loci were physically mapped using a somatic cell hybrid panel to SSC11 with 85-93% concordance. Subchromosomal assignment of these loci on SSC11 localizes ESD and RB1 to SSC11p11-15 and EDNRB to SSC11q11-17. Genetic linkage data also confirmed the assignment of EDNRB to SSC11 with a close linkage to markers S0230 and S0009 with the recombination frequencies of 0.05 (LOD = 23.91) and 0.07 (LOD = 16.63), respectively. Results from this study will improve the comparative map between human chromosome 13 and pig chromosome 11 and provide more information to examine gene order within this conserved synteny group.

Key Words: Pig, Human, Comparative gene map

59 Effects of heart fatty acid-binding protein (h-FABP) on intramuscular fat and production traits in pigs. F. Gerbens[1], J.W.M. Merks[2]*, J. H. Veerkamp[3], and M.F.W. te Pas[1], [1]*DLO-Institute for Animal Science and Health (ID-DLO), Lelystad,* [2]*IPG, Institute for Pig Genetics B.V., Beuningen, and* [3]*University of Nijmegen, Nijmegen, The Netherlands.*

The h-FABP is a protein involved in intracellular fatty acid transport expressed predominantly in muscle cells. Therefore the h-FABP gene is a candidate gene to account for the variation in intramuscular fat (IMF) content. To investigate this relation the porcine h-FABP gene was sequenced and 3 RFLPs were identified with HaeIII, HinfI and MspI. The RFLP alleles showed different distributions in several pig breeds. The h-FABP gene was assigned to pig chromosome 6 [Gerbens et al., Mamm. Genome in press]. The role of the genetic variation in the h-FABP gene for intramuscular fat % (IMF %) and the production traits 180 days age-adjusted body weight (BW) and 110 kg weight-adjusted backfat thickness (BFT) was examined in purebred, halothane-negative Stamboek and Dumeco Breeding Duroc pigs. In total 98 pigs were genotyped for each RFLP and BW and BFT data were recorded. In addition IMF% was determined in a sample of the loin of 41 pigs. Data were analysed statistically with a multi-variate animal model using heritabilities for BW, BFT and IMF of 0.35, 0.45 and 0.5 respectively. Haplotype, sex and farm were included in the model as fixed effects. Although all haplotypes were present, one of the homozygous haplotypes for each RFLP was quite rare i.e. <8%. With respect to IMF%, differences up to 10% were detected between the haplotypes. These contrasts failed to attain statistical significance due to the small number of animals analysed for IMF and the unbalanced ratio of haplotypes. For BFT, no significant differences were detected. BW differed significantly between both homozygous HaeIII RFLP haplotypes (8.3 kg, P<0.05). In conclusion, results from this limited study indicate that h-FABP clearly influences growth rate and may affect IMF deposition, whereas it does not affect carcass fatness. The use of the h-FABP RFLP tests and their application in breeding programs is patent pending.

Key Words: Pigs, Genetics RFLP, Candidate gene

60 Estimation of chromosomal position and effects of the callipyge allele (CLPG) using quantitative measurements of carcass traits. B. A. Freking*, J. W. Keele, S. M. Kappes, R. T. Stone, C. W. Beattie, and K. A. Leymaster, *USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Nine Dorset rams of CLPG phenotype and 114 Romanov ewes were used to develop a resource flock of 355 F2 lambs segregating for the CLPG allele to provide genotypic and phenotypic data to estimate chromosomal position, test gene action, and quantify allelic effects of genotypes on carcass traits. The parent generation consisted of matings of eight F1 sires and 138 F1 dams. Lambs were serial slaughtered in six groups at 3-wk intervals starting at 23-wk of age to estimate accretion rates of carcass components. A linkage group of 22 loci (mean of 720 informative meioses/marker) spanned 86.3 centimorgans (cM) of ovine chromosome 18. Probabilities for each genotype at the CLPG locus were calculated at 1 cM intervals (0-106). Contrasts of genotypic probabilities produced coefficients to evaluate alternative models for gene action. Statistical models developed fit effects of sex, year, sires, and contrast specific linear and quadratic regressions on age at slaughter. Contrasts tested included additive, maternal dominance, and paternally derived polar overdominance (PO) effects. Lack of fit F-tests (3 df) indicated PO [Aa-(AA+aA+aa)/3], where 'A' = CLPG allele, was the only significant contrast. A 3 df F-test of PO from an analysis of total carcass fat-free soft tissue regressed on carcass fat was maximum at position 91 cM (F = 43.3; P < .0001). Residual standard deviation units for PO at position 91 cM and 215 d age were for carcass: weight, .20; dress %, 1.35; length –.82; loin area, 2.07; protein, 1.13; water, 1.03; fat, –1.26; and ash, –.03, respectively. These results, based on analysis of genotypic probabilities and quantitative trait data, confirm assignment of CLPG locus to telomeric region of chromosome 18 and support the polar overdominance model of gene action. Efforts for further marker development need to be directed toward the telomeric region of chromosome 18 to improve resolution of the locus.

Key Words: Sheep, Carcass, Callipyge

61   Posterior probabilities of scoring errors in genetic marker data. R. M. Thallman, G. L. Bennett, J. W. Keele, and S. M. Kappes, *USDA-ARS Meat Animal Research Center, Clay Center, NE.*

The objective was to develop a quantitative method of identifying potential errors in genetic marker data. Scoring errors (SE) cause problems in estimation of map distance, marker order and the effects and positions of quantitative trait loci. Several programs are available for identifying likely SE based on the presumption that marker data represents genotypes. They generally identify inconsistencies but often do not indicate which animal is responsible. An alternative approach is to view the marker data as phenotypes which arise from unobserved genotypes at the marker locus. The model incorporates a prior error probability. Consequently, errors have less effect than when genotypes are assumed to be observed without error. Posterior error probabilities (PEP) are calculated by summing the posterior genotype probabilities (PGP) of all genotypes that are inconsistent with the observed marker phenotype. The PGP for an individual (I) can be partitioned into prior allele probabilities for I's sire (S) and dam (D) conditional on marker data related to I through S or D, respectively, and a likelihood of marker data on I or related to I through I's progeny. The priors and likelihoods can be calculated recursively in terms of one another. PGP are computed by iteratively calculating priors from the top of the pedigree to the bottom and likelihoods from the bottom of the pedigree to the top. Ninety-one sires used in a twinning rate selection experiment were scored for 16 microsatellite markers on bovine chromosome 1. Markers were independently scored twice and discrepancies were resolved prior to the analysis. PGP were calculated for the 91 sires and for 132 common ancestors that were not scored. PEP were calculated for the sires that were scored. Three marker phenotypes had error probabilities greater than 0.10. Each of these corresponded to combinations of phenotypes that were mutually exclusive under the assumptions of no errors and Mendelian inheritance. PEP can be used to efficiently prioritize animals to be checked for SE.

Key Words: Genetic markers

62   Heterosis levels for performance and carcass traits in Yorkshire, Large White and Hampshire swine and their crosses. M. J. Barhorst, K. M. Irvin, and S. Moeller, *The Ohio State University, Columbus.*

The objective of this study was to measure heterosis in various breed combinations of Yorkshire (Y), Large White (LW), and Hampshire (H) swine. Females from Y × Y, Y × LW, LW × Y, and LW × LW combinations were then mated to Hampshire boars. The resulting offspring were evaluated for mid test average daily gain (MIDADG), total average daily gain (TOTADG), backfat (BF), adjusted backfat to 105 kg (ADJBF), loin muscle area (LMA), adjusted loin muscle area to 105 kg (ALMA), lean gain per day on test (LGDOT), and percent lean (% lean). The test was conducted at The Ohio State University Swine Evaluation Station, Columbus. There were 99 pigs represented (half barrows and half gilts), on test from 15.51 kg to 106.13 kg. Feed consumed per amount of gain (F/G) was calculated from the start of the test to 105 kg. F/G values for the four breed combinations are means on a per pen basis: Y × LW, mid test = 2.21, total test = 2.89, LW × Y, mid test = 2.14, total test = 2.84, Y × Y, mid test = 2.26, total test = 2.81, LW × LW, mid test = 2.26, total test = 2.85. BF was measured at the 10th rib at the end of the test using real-time ultrasound. Heterosis values expressed were: % lean = −1.602% (P=.0555), MIDADG = 3.724% (P=.0517). Heterosis values for the remaining traits were: TOTADG = 2.717%, BF = 4.306%, ADJBF = 4.126%, LMA = −3.084%, ALMA = −3.107%, and LGDOT = −0.323% (all P>.10). Yorkshire and Large White pigs had similar origins, were developed separately, and are registered the same. Heterosis values for early growth detected increased gain for the crosses of Yorkshire and Large White compared to the pure lines. Heterosis levels detected could be utilized in the development of breeding plans for the pork industry.

Key Words: Heterosis, Pigs, Performance

63   Central test performance of Rambouillet rams as a predictor of progeny performance for growth and wool traits in feedlot and range environments. M. W. Salisbury*, G. R. Engdahl, C. J. Lupton, D. F. Waldron, C. B. Scott, and B. J. May, *Angelo State University, San Angelo, TX and Texas Agric. Exp. Station, San Angelo.*

A study was conducted to examine the effects of sire's performance on performance of 34 Rambouillet rams (9 centrally tested sires, 4 offspring/sire) on a 140 d pen trial followed by a 140 d pasture trial. Regressions of progeny performance (weight gain, fleece weight, wool average fiber diameter, and average staple length) on sire's central test performance were used to estimate the relationship between central test performance and progeny performance in feedlot and range environments. The nine sires represented a wide range of performance on central test. The model used for each trait included a fixed effect for type of birth of the lamb (single or multiple), a linear regression for age of the lamb in days at the start of the feeding period, a covariate for sire's performance, a covariate for dam's performance and random effects for sire and residual error. The covariate for dam's performance was dam's BW at breeding for gain traits, grease fleece weight of the dam for fleece weight traits and staple length, and average fiber diameter of the dam for fiber diameter traits. The regression coefficients of progeny performance on sire's performance were +.46 (P < .01) and −.02 (P < .1) for gain, +.34 (P < .01) and +.23 (P < .1) for clean fleece weight, +.41 (P < .01) and +.39 (P < .01) for average fiber diameter, and +.33 (P < .05) and +.09 (P < .1) for average staple length in the feedlot and range environments, respectively. There was a strong relationship between sire's performance as measured on 140-d central performance test and progeny performance in a similar environment. When progeny performance is measured on a relatively low nutrition environment, the relationship between central test performance and progeny performance was weakened for growth rate, fleece weight, and average staple length.

Key Words: Sheep, Wool, Central performance test

64   Relative proportions of insulin-like growth factor binding proteins in postweaning purebred Angus cattle divergently selected for blood serum insulin-like growth factor I concentration. M. E. Davis*, D. A. Stick, C. W. Ernst, and R.C.M. Simmen, *The Ohio State University, Columbus.*

Postweaning characteristics of insulin-like growth factor I (IGF-I) and associated serum IGF-binding proteins (IGFBP) were investigated in 68 purebred Angus calves born in fall 1992 as part of a divergent selection experiment for serum IGF-I concentration. Blood samples were collected from individual animals by jugular venipuncture at d 28, 42, and 56 of the postweaning period. Serum IGF-I concentrations were determined by RIA and four serum IGFBP (24, 30, 34, and 38 to 42 kDa species) were identified by Western Ligand blotting. Relative amounts of the individual serum IGFBP were determined by densitometric analysis of resultant autoradiographs. Proportion of serum 38 to 42 kDa IGFBP was not affected by sampling date (P > .10). Sampling date had an effect (P < .001) on the relative amounts of the 34 and 30 kDa IGFBP. However, proportions of these two IGFBP varied in an inconsistent fashion throughout the postweaning period. Proportion of 24 kDa IGFBP decreased (P < .0001) with time. Bulls exhibited greater proportions of the 38 to 42 and 24 kDa IGFBP species (P < .0001) than were observed in heifers, which displayed more 34 kDa IGFBP (P < .0001). Relative amount of the 30 kDa IGFBP was unaffected by sex (P > .10). Proportions of the four IGFBP did not differ between the high and low IGF-I selection lines (P > .10). Residual correlations between serum IGF-I concentration and relative proportions of the 38 to 42 and the 24 kDa IGFBP were .11 (P < .04) and −.11 (P < .05), respectively. The IGFBP percentages were not significantly correlated with body weight or postweaning ADG. Interactions among fixed effects suggest a complex relationship of proportions of serum IGFBP with sex, age, and serum IGF-I concentration.

Key Words: Beef cattle, Insulin-like growth factor, Insulin-like growth factor binding proteins

65 Preweaning performance of Angus-, Brangus-, Gelbvieh-, and Gelbray-sired calves. S. M. DeRouen* and J. M. Turpin, *Louisiana State University Agricultural Center, Homer.*

Angus (A)-, Brangus (Ba)-, Gelbvieh (G)-, and Gelbray (Gb)-sired progeny (n=464) were evaluated for preweaning traits over 3 yr. First-cross Brahman-Hereford dams were randomly mated to A, Ba, G, and Gb bulls to produce spring- and fall-born calves. Percent Brahman breeding was 25% in A- and G-sired calves and 43.75% in Ba- and Gb-sired calves. A total of 27 sires (6 to 9 sires per sire breed) were used. Calf birth weight (BWT), average daily gain (ADG), actual weaning weight (WWT), 205 d adjusted weaning weight (A205), and weaning hip height (HHT) were analyzed by a generalized linear mixed-model procedure (PROC MIXED in SAS). Season of birth was significant for ADG and A205. Spring-born calves had greater ($P < .01$) ADG and A205 than fall-born calves. Sire breed did not affect ($P = .23$ to .80) any of the preweaning traits. Angus- and G-sired calves, however, tended to rank higher for ADG, WWT, and A205 than Ba- and Gb-sired calves. Results from this study indicate that similar preweaning performance was achieved among straightbred-sired and Brahman derivative composite-sired calves. These progeny will be evaluated for potential as replacement heifers, stockers, feeders, and carcasses.

Sire breed	BWT, kg	ADG, g	WWT, kg	A205, kg	HHT, cm
A	34.8	835	218	206	115
Ba	35.5	809	213	201	116
G	37.1	823	219	206	116
Gb	36.6	805	214	202	115

Key Words: Beef cattle, Preweaning traits, Brahman

66 Comparative evaluation of three restrictive selection indices in beef cattle breeding. J. Tõzsér*, A. Kovács, N. Nagy, S. Bedõ, and Z. Szakács, *University of Gödöllõ.*

Three restrictive selection indices have been evaluated in this study. Apart from the American Index (Index-1) further ones (Indices 2,3, respectively) were developed on various theoretical principles taking into account recommendations provided by Fitzhugh and Taylor (1971), Andersen et al. (1981), and Menissier et al. (1986). In order to be able to compare indices figure of 668 male and 754 female calves were recorded at the Limousin seedstock herd Hajdzúzoboszló for the period 1970-1989. Suitability of selection indices having been developed were evaluated by simulated selection. Both birth weight and adjusted live weight for one year of age were included in all indices. Among all selection indices positive relationship were found (r=0.36–0.39). Smaller decrease of birth weight for both sexes was shown when using Selection Index 1(USA) for the best 10% (–0.52kg–1.83kg, respectively), but greater decrease with the using of Indices –2, –3 for the best 10% –7.82–(–8.72), –5.93–(–7.43)kg. Just the same index tended to increase live weight adjusted for one year of age at the highest rate (for the best 10% –71.5–86.76kg, respectively). Findings reveal that all selections indices can effectively be recommended to develop paternal lines and/or families with low weight transmitting ability.

Key Words: Limousin, Simulated selection

67 Comparison of BLAD carrier and non BLAD carrier top bulls. Á. Jánosa* and J. Dohy, *Gödöllõ University of Agricultural Sciences, Institute of Animal Husbandry; Gödöllõ, Hungary.*

Bovine leukocyte adhesion deficiency (BLAD) is a recessive, monofactorial lethal genetic disorder mainly in the Holstein breed and especially in very well known top bulls. The purpose of this study was to investigate if there were differences between carrier (BL) and non carrier (TL) bulls concerning production, reproduction and some important type traits. To achieve the intent we completed the comparative evaluation with the results of 107 Hungarian Holstein and 153 Dutch Holstein bull's progeny testing. We estimated the averages of the TPI(=(6*PTA Fat)+(14* PTA Protein)+(80*PTA Final Score)+(70*PTA Udder Score) /Hungary/ and the INET (=-0.15 PTA Milk+2 PTA Fat+12 PTA Protein) /The Netherlands/. From the data it can be concluded that differences between two groups are significant in favour of the group of BLAD carriers. It is suggested that to prevent such genetic disorders from spreading further among dairy cattles and to control it as well as possible, attempts should be made with cooperation of involved countries. Important is the identification of BLAD carriers and planning of mating programs to avoid mating of carriers.

Progeny testing results of the BL and the TL bulls used in Hungary

Number of bulls	Number of daughters	Average of TPI
BL bulls (n=13)	692	920
TL bulls (n=94)	7548	852

Total performance indexes of the BL and the TL Dutch Holstein bulls
(J. Dohy-A. Jánosa-J. Vági, 1996)

Genotypes of progenies of BL sires	BL		TL		Difference
	n	INET	n	INET	INET
Grandsons of the Carlin-M Ivanhoe Bell	3	574	30	487	87
Sons of the Ripvalley Na Bell Troy	1	593	3	448	145

Key Words: Holstein-Friesian, BLAD, Breeding value

68 Sire effect on the body weight and measurements of Holstein-Friesian young bulls. P. Polgar, and F. Szabo, *Pannon University of Agricultural Sciences, Georgikon Faculty, Keszthely, Deak F. u. 16. 8361 Hungary.*

Body weight and body measurements taken monthly between 60 and 365 days of age from performance test of 832 Holstein Friesian young bulls in Hungary were evaluated. The duration of the examination period was 14 years between 1977-1991. Least Square & Maximum Likelihood computer program (ANOVA) were used for data processing. According to the results statistically proved ($P<0.01$) sire effect was found in the body weight between 60 and 365 days of age at every weighing of the animals. Decreasing tendency of the 365-day weight data was found that means that the progeny generation (428,35kg ± 36,28kg) were 53,75kg ($P<0,01$) lighter than the sire generation (482,1kg ± 33,71kg). The body measurements of progeny and sire generation differed significantly ($P<0.01$), too but no significant differences were found in the height at withers of the evaluated young bulls. Differences: (a) height at withers 2,22cm, (b) body length 5,67cm, (c) chest depth 5,88cm, (d) chest width 3,37cm, (e) chest girth 11,83cm, (f) rump length 5,2cm, (g) 1. rump width 4,24cm, (h) 2. rump width 3,38cm, (i) leg girth 0,65cm. The variables of body measurements in multiple regression analysis for body weight at weighing to 365 days entered different equations: sire generation.: Y = −1229,13+7, 32a+(−4,26b) + (−4,78c) + (−5,55d) + 3,79e+10,2f + (−52,17g) + 62,81h + 20,33i progeny generation.: Y=−466,79 + (−0,32a) + 0,81b + (−0,33c) + (−1,9d) + 2,15e + (−1,34f) + 1,76g + 6,54h + 14,73i

Key Words: Holstein, Bulls, Generation, Body weight, Body measurements

69   Heterosis and maternal effect on weaning weight of Hungarian Simmental, Hereford and Angus F1 calves. F. Szabo[1]*, K. Szentpali[2], J. Tari[2], J. Dohy[3], and E. Szucs[3], [1]*Pannon University, Georgikon Faculty, Keszthely, [2]Mezofalva Ltd, and [3]Gödöllő University, Hungary.*

Weaning weight of straightbred Hungarian Simmental (HS), Hereford (HE) and Angus(A) and that of reciprocal crossbred HS×HE and HE×A F1 calves were evaluated in Hungary based on more than 600 animals. Calves were born in spring season, kept and creep fed on pasture in summer, weaned in fall at the age of 6-7 months. Weaning weight were adjusted to 205-day of age. Least Squares and Maximum Likelihood Computer Program (Harvey 1990) were used for data analyses. The average weaning weight of straightbred male and female calves were as follows: 219.1 kg (HS), 196.3 kg (HE), 215.2kg (A) ($P<0.01$). Significant maternal effect ($P<0.01$) were found in the weaning weight of calves from both reciprocal crossings. 11% positive effect in case of HS×HE reciprocal crossbred calves due to HS dams and 8% positive effect in HE × A reciprocal crossbred calves due to A dams. Heterosis effect were also found in the results of both F1 calf groups. That was 7.8% in HS×HE F1, and that of 5.5% in case of HA × A F1 calves ($P<0.01$). It seemed that the bigger the genetic distance between the breeds, the higher the maternal and heterosis effect in the weaning weight of their crossbred progeny.

Key Words: Straightbred, Crossbred, Beef calves, 205-day weight

70   Effects of a metallothionein/bovine growth hormone transgene on components of growth in mice. M. Kaps*, A. S. Moura, W. R. Lamberson, *University of Missouri - Columbia.*

The objective of the study was to determine the effects of a metallothionein/bovine growth hormone transgene on rate and duration of components of growth in mice. Mice were produced by mating hemizygous transgenic males to nontransgenic females in an outbred background. Weights on 147 mice were taken ten times from birth to 84 d of age. Between 28 and 84 d, mice were 6 times anesthetized and measured for electrical conductivity. Fat free mass (FFM) and body fat (BF) were predicted on the basis of conductivity and body weight. A logistic curve ($y=A/(1+exp(k*(b-t)))$), where y is FFM or BF, t is age in days, k and b are curve parameters) was used to fit the data for each animal for FFM and BF, respectively. The function and its first, second and third derivatives for FFM and BF, were used to explain the following: asymptotic final weight, relative growth rate, maximum daily gain (inflection point), age at inflection, total duration of growth, age and mass at the beginning of accelerated growth, duration of and daily gain in the accelerated growth. A mixed model was fitted with animal and litter as random, and transgenotype and sex as fixed effects. Transgenotype × sex interaction effects were found for: final FFM ($P<.05$), relative growth rate of FFM ($P<.01$), age at inflection for FFM ($P<.05$), FFM at inflection ($P<.05$), FFM at beginning of accelerated growth ($P<.05$), length of accelerated FFM growth ($P<.01$), final BF ($P<.05$), BF at inflection ($P<.01$), age at beginning of BF accelerated growth ($P<.01$). In addition, transgenotype main effects were found for: FFM daily gain at inflection point ($P<.01$), duration of FFM growth ($P<.01$), age at beginning of FFM accelerated growth ($P<.01$), FFM daily gain in accelerated growth ($P<.01$), BF growth rate ($P<.05$), duration of BF growth ($P<.05$), BF at beginning of accelerated growth ($P<.01$). The transgene had a greater effect on males than females. Also, transgenic males began to accumulate fat later, but eventually gained more fat than transgenic females.

71   Gene action of the oMt1a-oGH transgene in two lines of mice with distinct selection backgrounds. F. Siewerdt[1,3]*, E. J. Eisen[1], J. D. Murray[2], and J. S. Conrad-Brink[2], [1]*North Carolina State University, Raleigh, [2]University of California, Davis, and [3]CNPq, Brasília.*

The objective was to determine the kind of gene action associated with the oMT1a-oGH sheep growth hormone transgene. Sires homozygous for the transgene insert were mated to dams of two lines. One line had a background of selection for increased 3 to 6 wk body weight gain (M16) and the other was a randomly selected control (ICR). F2 populations were obtained from both lines (TM and TC, respectively). A quantitative PCR analysis determined the genotype of each mouse with respect to the transgene. Mice received 25 mM $ZnSO_4$ in drinking water from 3 (weaning) to 8 wk to stimulate the activity of the transgene. Weekly body weights (BW) were obtained from 3 to 8 wk in males and to 10 wk in females. Males were dissected at 8 wk and weights obtained on epididymal and subcutaneous fat pads. Females were mated at 10 wk to unrelated males. On day 16 of pregnancy, females were killed. Live and dead fetuses and corpora lutea (CL) numbers were recorded. In TC, sex by genotype interactions were significant ($P<.05$) for BW from 5 to 8 wk and for weight gain (WG) from 3 to 6 wk. Positive estimates ($P<.01$) were found for additive and dominance effects, and the effect of the transgene on BW was larger in females. In TM the interactions were significant ($P<.05$) from 4 to 8 wk and for WG from 3 to 6 wk. Additive and dominance effects on BW in males were negative ($P<.01$) from 3 to 6 wk. In females the transgene had overdominance effect on BW from 6 to 8 wk ($P<.01$). In both lines additive effects for WG from 3 to 6 wk in males and overdominance for females were found. Complete dominance was observed for WG from 6 to 8 wk. Negative additive and dominance effects ($P<.01$) were present for fat pads, except for subcutaneous fat pad in TC. Reproductive traits were not affected, except for the additive effect found for CL in TC. Favorable additive and dominance effects on WG and on fat traits, and no adverse effects on reproduction make the use of the transgene feasible.

Key Words: Transgene, Mouse, Growth Hormone

72   Zinc concentration affects growth, fat content and reproduction in oMt1a-oGH transgenic mice. E. J. Eisen[1]*, C. B. Peterson[1], I. J. Parker[1], and J. D. Murray[2], [1]*North Carolina State University, Raleigh and [2]University of California, Davis.*

Attachment of the sheep metallothionein 1a promoter to the sheep growth hormone gene (oMT1a-oGH) has resulted in a closely regulated transgene in mice that can respond to elevated levels of zinc ions provided in the drinking water. The objective of this study was to explore the effect of zinc ion concentration on postweaning growth, fat content and female reproduction. At weaning (3 weeks), hemizygous oMT1a-oGH mice were assigned randomly to receive 0, 12.5, 25, 37.5 or 50 mM $ZnSO_4$ in distilled water for 5 weeks. Males were killed at 8 weeks and fat pad weights were obtained. Females received tap water from 8 to 10 weeks and then were mated to unrelated non-transgenic fertile males to obtain ovulation rate and embryo survival. Mortality rate was increased ($P<.05$) at 37.5 mM (15.2%) and 50 mM (33.3%) $ZnSO_4$ compared with lower levels. Postweaning growth was highest at 12.5 mM $ZnSO_4$ followed by 25 and 37.5 mM, respectively. At 50 mM $ZnSo_4$, 8 week-old males were 20% smaller than controls while females did not differ ($P>.05$) from controls. Epididymal (EFP) and subcutaneous (SFP) fat pad weights decreased linearly ($P<.01$) with increased dose of $ZnSO_4$, while on a percentage of body weight basis, EFP and SFP decreased quadratically ($P<.01$). Mice receiving 12.5 mM $ZnSO_4$ had their EFP and SFP as a percentage of body weight reduced ($P<.01$) to 54.1% and 65.9% of controls (0 mM), respectively. No differences ($P>.05$) in female fertility were detected. Females receiving $ZnSO_4$ supplement had higher ($P<.05$) ovulation rates than controls, but there were no differences ($P>.05$) in ovulation rates among the zinc levels. A decrease ($P<.05$) in pre- and post-implantation embryo survival was detected at 37.5 mM $ZnSO_4$. These results indicate that zinc dosage affects phenotypic expression of the oMT1a-regulated oGH transgenic mice, and the dose responses are trait-dependent.

Key Words: Growth Hormone, Transgene, Mice

73 Maternal behaviors in mice selected for large litter size. C. F. Chiang*, R. K. Johnson, and M. K. Nielsen, *University of Nebraska, Lincoln, NE.*

Thirty-two lactating mice with their pups from two different litter size selection lines (LS, directly selected for 21 generations to increase litter size, and LC, unselected control) were used in each of three replications to characterize lines for maternal behavior. Half the litters in each replication were standardized to an equal number of pups on day one of lactation; half nursed their natural litters. Litter sizes of LS vs. LC lines in the first, second, and third replication were $12.3\pm.6$ vs. $10.6\pm.6$, $15.9\pm.5$ vs. $13.1\pm.5$, and $17.3\pm.6$ vs. $13.2\pm.6$ pups, respectively. Activity budgets during 30-min observation periods from day 2 to 22 of lactation were recorded. Lactation period was divided into five stages (day 2 to 4, 5 to 8, 9 to 12, 13 to 17, and 18 to 22). Behavioral categories included nursing, licking, and retrieving pups, nest building, resting with pups, resting alone, eating and drinking, grooming, and other activities. Categories 1 through 5 were summed as an index of maternal care. Variances of behavioral traits were similar in standardized and non-standardized groups, so data were analyzed together. Interactions of line $\times$ stage of lactation and line $\times$ litter standardization were not significant for any trait ($P>.05$). LS mothers spent more time nursing pups than LC mothers ($64.6\pm1.4\%$ vs. $54.8\pm1.5\%$, $P<.05$), and litter weight gain tended to be greater for LS litters. The maternal index tended to be greater for LS mice suggesting they spent more time with their pups ($68.2\pm2.7\%$ vs. $61.2\pm2.8\%$, $P<.1$). LS mice tended to spend less time resting with their pups than LC mice, especially in the second and third replication. Selection for larger litters altered maternal behavior. Change in maternal behavior was independent of size of litter being nursed suggesting a correlated response in maternal behavior to LS selection.

Key Words: Mice, Litter size, Maternal behavior