Breeding and Genetics II

T22   Fine mapping of a bovine twinning rate QTL. E. S. Kim*[1], J. Cruickshank[1], M. Dentine[1], P. J. Berger[2], and B. W. Kirkpatrick[1], *[1]University of Wisconsin, Madison,, [2]Iowa State University, Ames.*

A twinning rate quantitative trait locus (QTL) has been previously detected on chromosome 5 in the North American Holstein dairy cattle population. The objective of the current study was to refine the map location of this QTL. In the previous work the strongest evidence for this QTL was obtained from analysis of an extended, four-generation sire family. In that work a total of 122 sires were genotyped with microsatellite markers for which sire families were informative in a linkage analysis. In the current study additional genotyping was performed to provide complete marker genotypes for all 14 markers used previously. The additional genotypes permitted deduction of paternally and maternally inherited marker haplotypes for all sons. The 14 markers used were located between 66 cM and 120 cM on the USDA linkage map for chromosome 5. The patriarch of this extended family was heterozygous Q q for the twinning rate QTL based on results of the previous linkage analysis where Q denotes the allele associated with increased twinning rate. Association between haplotype and twinning rate was evaluated with a model that included effects of sire, paternally inherited haplotype nested within sire and maternally inherited haplotype. Separate analyses considered either all possible haplotypes, or a dichotomous classification of allele Q-associated or non-Q associated haplotype, based on the haplotype associated with allele Q in the patriarch of the extended family. A significant (P<0.005) effect of maternally inherited haplotype was observed for the marker bracket flanking the 74-76 cM region of chromosome 5. This linkage disequilibrium analysis (effect of maternally inherited haplotype) provides additional evidence of the twinning rate QTL and suggests a narrowed region for potential QTL location.

Key Words: Twinning Rate, QTL Mapping, Linkage Disequilibrium

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T23   Massive verification and mapping of SNP in cattle using the Illumina® BeadStation 500G genotyping system. C. Li*[1], B. Murdoch[1], Z. Wang[1], S. Mckay[1], J. Williams[2], R. Stone[3], S. Hennig[4], and S. Moore[1], *[1]University of Alberta, Edmonton, Alberta, Canada, [2]Roslin Institute, Roslin, United Kingdom, [3]USDA, ARS, US Meat Animal Research Center, Clay Center, NE, [4]Max Planck Institut fuer Molekulare Genetik, Ihnestr. Berlin, German.*

Single nucleotide polymorphisms (SNP) have been considered as the next generation of genetic markers for construction of denser linkage maps and detection of quantitative trait loci (QTL) of complex traits. SNPs also allow the identification of causative genes of interest by association-based studies. In cattle, however, the application of SNPs has been hindered by the lack of novel and sufficient markers. This study reports a massive verification and mapping of bovine SNPs reported in literature and public sequence databases using the Illumina® BeadStation 500G genotyping system. In total, 800 SNP sequences were compiled, of which 594 (74.25%) were found to be designable for an OPA (Oligo Pool Assay) based on the sequence quality and oligo sequence compatibility. In order to verify the SNPs, a panel of DNA samples from a hybrid beef cattle population of various breeds (*Bos taurus*) were genotyped using the OPA of 594 SNPs and a SAM (Sentrix Array Matrix) as implemented by the Illumina ® BeadStation 500G genotyping system. To date 474 sequences have been amplified and genotyped. In addition, an OPA containing a subset of 1536 putative SNPs compiled from the Bovine Genome Sequence Project has been designed and the putative SNPs are verified. Verified SNP will be mapped using a bovine mapping reference panel from USDA and using the Roslin Institute 3000 rad bovine whole genome radiation hybrid panel.

Key Words: Single Nucleotide Polymorphisms, Verification, Mapping

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T24   Characterization of bovine functional genes from full-length cDNA libraries. M. Taniguchi*, L. L. Guan, Y. Meng, J. Yu, Z. Wang, and S. Moore, *University of Alberta, Edmonton, Alberta, Canada.*

Recent studies showed that the gathering of data pertinent to expressed genes (cDNA and full-length cDNA) will provide direct insight into the organization of bovine gene. As a part of Genome Canada's full-length cDNA sequencing project, the aim of this study is to generate full-length cDNA libraries for tissues of importance of beef production, quality and animal health and to characterize their related functional genes.

Animal tissues have been collected and used for mRNA extraction and synthesis of full-length of cDNA library using "cap-trapping" technology (Carninci 1999). The full-length cDNA was synthesized with reverse transcriptase, biotinylated and captured by magnetic beads system. The cDNA library was generated by using pCMV-SPORT 6 vector. Full-length of cDNAs was confirmed by the sequence analysis. Functional genes were identified by BLAST search.

Firstly we constructed full-length cDNA libraries from gastrointestinal (GI) tissues and analyzed the sequences of cDNA to investigate the relationships between their biological functions and the tissues. For example, libraries from Ileum and Peyer's Patch tissues have been analyzed due to association of those tissues with absorption of nutrients and with immune function. Based on the technology used, full-length cDNA sequences were successfully identified as functional genes and were deposited to GenBank. Our results will contribute to detect the genes which are associated with important traits for cattle industry such as disease resistance, meat quality, feed efficiency etc. Hence, the information from genes well-characterized can be used as genetic markers for animal estimation and selection.

Key Words: Full-Length cDNA, Functional Gene, Bovine

T25   Precision of estimated QTL positions in half-sib designs using combined haplotype sharing TDT and linkage analysis. D. Kolbehdari*[1,2] and L. R. Schaeffer[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]University of Tehran, Tehran, Iran.*

The aim of this study was to develop the linear haplotype sharing transmission disequilibrium test (LHS-TDT) method and combine this method with the simple regression method to estimate the precision of QTL positions in half-sib designs. The precision of estimated QTL positions was determined by Monte Carlo simulation in granddaughter designs. A single bi-allelic QTL at the midpoint of a linkage group and 26 markers with 1 cM intervals and with two alleles each were simulated. The heritability of the quantitative trait was assumed to be 0.3 and the ratio of QTL variance to total genetic variance is 0.1. The base population was generated by random mating for 100 generations with an effective population size equal to 100. Three linear models, (i.e. the simple regression model, the linear haplotype sharing TDT method and the combination of these two models) were compared. The mean of absolute differences (A) between the estimated and true QTL position of each method was considered for six different scenarios consisting of combinations of a number of markers and the most frequent haplotypes. The mean of A, using the simple regression method, was 4.38 centimorgan (cM). The means of A using the LHS-TDT method were less than the simple regression method in all scenarios and ranged from 1.86 to 3.82 cM depending on the scenario. The mean of A using the combined method was more than the LHS-TDT method and less than the simple regression method. The means of A using the combined method ranged from 2.32 to 4.36 cM. Therefore, for populations similar to those population simulated in this study, the LHS-TDT was better than the simple regression method and the combined method for precision of estimated QTL position in half-sib designs.

Key Words: Quantitative Trait Loci, QTL Position, Haplotype Sharing TDT

T26   QTL mapping in complex pedigrees: Focusing on inbreeding and overlapping generations. G. Freyer*[1] and N. Vukasinovic[2], [1]*Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany*, [2]*Monsanto Animal AG, St. Louis, MO*.

Mapping QTL in animal pedigrees faces various challenges due to complicated family structure, overlapping generations, and inbreeding. Daughter design or granddaughter design have been used to overcome these difficulties. These designs ignore other relationships within a pedigree, thus simplifying computations but also losing power of QTL detection. Here, we explore abilities of different QTL mapping methods to deal with complicated pedigree structures. A four-generational pedigree, containing 850 individuals in nine related halfsib families, has been simulated assuming simple pedigree structure, without inbreeding and overlapping generations, and complicated pedigree structure, containing highly inbred individuals and overlapping generations. Phenotype and marker information was generated for all individuals. A single QTL explaining 15% of the phenotypic variance was simulated. QTL mapping was considered within a chromosomal segment covered by 11 polymorphic markers. The length of the segment was either 120cM with approximately equidistant markers, or 55cM with greater marker density around the QTL position. QTL mapping was conducted using: granddaughter design (GDD), where each sire family was considered independent; general pedigree design (GPD), including all relationships; and combined linkage disequilibrium and linkage analysis (LDLA), considering all pedigree relationships, also historical generations. All analyses were performed by maximum likelihood techniques. Within a 55cM segment, GPD method located QTL precisely. Within a 120cM segment, GDD method was superior regarding precision of QTL location; GPD method produced slightly biased results. Complicated family structure caused increased computational time, convergence problems, and less accurate estimates of QTL position and parameters. LDLA method precisely located the correct marker bracket in all situations. However, LDLA method only calculates likelihood for middle points between two markers and mapping resolution may be insufficient with sparse maps. The results indicate that LDLA method may be best for mapping QTL in complex pedigrees, provided dense marker maps.

Key Words: QTL Mapping, General Pedigree Analysis, Inbreeding

T27   The incidence of programmed cell death after in vitro fertilization (IVF) with morphologically abnormal bovine spermatozoa. A. Walters*, R. Saacke, R. Pearson, and F . Gwazdauskas, *Virginia Polytechnic Institute and State University, Blacksburg*.

Normal embryonic development depends on the maintenance of a population of healthy cells within each embryo. The aim of this study was to assess the incidence of programmed cell death (apoptosis) in embryos after IVF with morphologically abnormal spermatozoa. Three different semen samples from four Holstein bulls, collected before and after a 48 h scrotal insulation period, were used: 1) semen collected prior to insulation (Control); 2) semen collected 2 wk post-insult (2 wk-PI); and 3) semen collected 3 wk-PI. Post-thawed morphological evaluation revealed a decrease (P < 0.01) in the percentage normal spermatozoa for the 3 wk-PI samples in comparison with the Control samples for Bulls I (74 to 22%) and Bull III (68 to 1%). For Bull II the percentage vacuolated spermatozoa increased, with no changes in the sperm populations for Bull IV. On d 8 of culture the embryos were subjected to either the terminal transferase dUTP-nick end labeling (TUNEL) or caspase assay. An apoptotic index and caspase intensity were recorded. No differences were found between the embryos generated from the semen samples for Bull I, but for Bull II the index was higher (P > 0.01) for the Control (46%) and 3 wk-PI (41%) embryos compared to the 2 wk-PI (29%) embryos. The opposite was found for Bull III, the 3 wk-PI index (35%) was lower (P > 0.01) than the indexes for the Control (43%) and 2 wk-PI embryos (41%). For Bull IV the index was highest for the 3 wk-PI (45.2%) embryos compared to the Control (38%) and the 2 wk-PI (37%) embryos. On Day 8 caspase intensity increased significantly for both Bull I (217 ± 147) and Bull III (229 ± 98) for the 3 wk-PI embryo groups compared to the equivalent embryo groups for Bull II (98 ± 115) and Bull IV (90 ± 111). In conclusion, the inability to consistently measure apoptosis in early stage embryos complicates the assessment of differences in embryo quality. Despite the discrepancies, our results clearly indicated a difference in the embryo quality

between embryos obtained after IVF with semen samples from bulls that had an intense response to scrotal insulation.

Key Words: Abnormal Spermatozoa, Scrotal Insult, Apoptosis

T28   X- and Y-chromosome bearing sperm ratio in individual bull ejaculates. J. Schenk, M. Meyers*, and E. Crichton, *XY, Inc., Fort Collins, CO*.

Small sample sizes often lead to erroneous conclusions about true sex ratios due to binomial statistical variation. DNA resort reanalysis, PCR and fluorescence in situ hybridization can be used to accurately determine sex ratios in a sample of semen. In this study we used a MoFlo[R] SX sperm sorter to determine proportions of X- and Y-chromosome bearing sperm in individual bull ejaculates. First and second ejaculates were collected weekly from each of 6 Holstein bulls for 3 consecutive weeks. Ejaculates were diluted with Tris sheath fluid, sonicated to remove sperm tails and centrifuged to pellet nuclei. The concentration of nuclei was adjusted to 200×10^6 sperm/ml and nuclei were stained (1 h, 34°C) with 72-99 µM H33342 dye. After staining, nuclei were diluted 1:1 with sodium azide (3.8 mM) and frozen at -160°C. Thawed nuclei were analyzed by flow cytometry into sperm populations encompassing all of the nuclei: properly oriented at 0-30°, nonoriented at 30-45°, and nonoriented at 45-90°, relative to the 0° photomultiplier tube detector. All sperm from each population were collected and the percent of total histogram events were recorded for X- and Y-chromosome bearing sperm for each population. Sperm from all 3 populations then were subjected to DNA resort analysis, and the percentage of X- and Y-chromosome bearing sperm was calculated after data were conformed to a pair of Gaussian distributions. Data were analyzed using a split plot ANOVA. There were no differences (P>0.05) from 50:50 between bulls or ejaculates within bulls. The largest observed deviation in an individual ejaculate was 46:54. Additionally, statistically identical (P>0.05) proportions of X- and Y-chromosome bearing sperm, 49 and 51% respectively, were found in the oriented and nonoriented populations. From analyzing 36 individual ejaculates, we conclude that there were no significant deviations from 50% X- or Y- chromosome bearing sperm due to bulls, ejaculates within bulls, or ejaculation frequency.

Key Words: DNA, Flow Cytometry, Sperm

T29   Karyological profile of bovine clones. S. C. Gupta*[1], N. Gupta[1], C. X. Tian[2], and X. Yang[2], [1]*National Bureau of Animal Genetic Resources, Karnal, Haryana, India*, [2]*University of Connecticut, Storrs*.

The success rate of nuclear transfer (NT) is very low and the production of viable clone is a complex phenomenon which may depend on the type of cell used, karyotype stability, reprogramming of cleavage activity and interaction between various cell or DNA functions. The aim of this study was to know the karyological profile of cloned calves in comparison to their donor mother's own genome and its skin fibroblast cells that donated the karyoplast to the recipient oocyte in NT procedure. Chromosomal profile of donor Aspin, a Holstein Freisian (HF) elite cow was having normal karyotype of 60, XX diploid chromosomal count in 95 % of blood lymphocytes. Aneuploidy with 59, XX diploid count was 8 % in skin fibroblast cells at 5-6 passage and increased to 15 % at 10-12 passages. The proportion of aneuploid cells increased further in later passages. Chromosomal profile of Amy, the first cloned calf in US from skin fibroblast cell showed aneuploidy only in 1 per cent of blood cells on day of birth. However, it showed high frequency (15.67 %) of myxoploidy of tetraploidy (4 N) and octaploidy (8N) in cultured blood lymphocyte cells. The percentage of these polyploid cells was however only 8 percent on day 7 and at later, the blood cells showed no polyploid cells. The placental cells of the mother also showed 40.65 % frequency of polyploid cells. From this data, it can be inferred that the increased frequency of polyploidy cells in new born clone could have been due to transfer of polyploid cells from surrogate mother's placenta and later on filtered out in peripheral blood by normal cell division process in their stem cells in the homopoitic tissue. The chromosomal profile of other clones in blood lymphocytes from the same donor was also normal (60, XX). It can be concluded that the high proportion of prenatal and perinatal deaths in clone pregnancies could

J. Anim. Sci. Vol. 83, Suppl. 1/J. Dairy Sci. Vol. 88, Suppl. 1

137

be due chromosomal abnormalities carried by the donor karyoplast before nuclear transfer and their screening in multiple passaging is warranted.

T30   Within breed selection of boars for a gene bank. H. Blackburn*[1], C. Welsh[1], and T. Stewart[2], [1]*USDA-ARS-NAGP*, *Ft Collins, CO*, [2]*Purdue University*, *West Lafayette, IN*.

A primary component of genetic conservation of livestock species is the development of cryopreserved collections. Approaches to prioritizing breeds for conservation and entry into gene banks have been developed; but little attention has been given to determining how to select individuals within a breed. We addressed this issue by utilizing breed association pedigree records for Hampshire, Yorkshire and Duroc breeds. From these records genetic relationships were computed and utilized in a cluster analysis. The Ward Method of clustering, from SAS, was selected after testing several different approaches. For all breeds approximately 2,800 young boars were clustered, litter mates were excluded from the analysis. The pseudo t-test was used to determine where significant breaks in the clusters occurred. In addition, a pre-determined collection target of 100 boars per breed had been set. Significant divisions in the clusters occurred when approximately 20 clusters had been formed. Once the number of clusters were determined, average relationships within and between clusters were computed and evaluated. Using the Yorkshire as an example, several approaches were evaluated for individual selection and compared to randomly selected boars (control). These approaches were: weighting the number of animals selected by the cluster size, and selecting 5 boars per cluster. Simulating selection for these three approaches resulted in average genetic relationships for the selected boars of: 0.08, 0.08, and 0.07 for control, weighted by cluster size and 5 boars/cluster. These results indicate the two approaches would enable the selection of individual boars for a gene bank with an average relationship at or below the population average.

Key Words: Genetic Conservation, Swine

T31   Association of a single nucleotide polymorphism in the leptin receptor gene with carcass and meat quality traits in beef cattle. F. Schenkel*[1], S. Miller[1], S. Moore[2], C. Li[2], A. Fu[2], S. Lobo[2], I. Mandell[1], and J. Wilton[1], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*University of Alberta*, *Edmonton, Ontario, Canada*.

The leptin receptor gene (LEPR) produces a high affinity receptor that mediates the regulation of the leptin gene, which has been implicated in the control of feed intake and body composition of mammals. This study investigated the association of genotypes for a single nucleotide polymorphism (SNP) in exon 20 of LEPR (Liefers et al. 2004. Animal Genetics 35: 138-141) with carcass and meat quality traits in beef cattle. The LEPR SNP was genotyped on a total of 800 heifers, steers, and bulls from commercial herds (399) and from the University of Guelph breeding project (401). These same animals were also genotyped for 4 SNP in the leptin gene (S1, S2, E2JW and E2FB) whose effects were previously reported. Animals were crossbreds with breed composition mainly formed by Angus, Limousin, Charolais, and Simmental. The measured carcass traits included fat (Fatyl), lean (Leanyl) and bone yield (by 4-rib dissection), grade fat (Gfat), longissimus dorsi muscle (LM) area, and hot carcass weight (Hcw). Meat quality traits included quality grade, LM intramuscular fat, tenderness evaluation (Warner-Bratzler shear force) of LM at 2, 7, 14 and 21 days postmortem, and tenderness evaluation of semitendinosus muscle at 7 days postmortem. A univariate mixed inheritance animal model (SNP genotypes for LEPR and leptin gene + polygenic effects) was used to evaluate the association of the LEPR SNP genotypes with the traits. The model also included the effects of sex, slaughter group, and breed composition. Association of LEPR polymorphism with Fatyl (P=0.03) and Gfat (P=0.005) was found, as well as a trend for association with Leanyl (P=0.09) and Hcw (P=0.06). The

heterozygote genotype CT decreased Fatyl and Gfat by 0.24 and 0.33 phenotypic SD and tended to increase Leanyl and Hcw by 0.21 and 0.20 phenotypic SD, respectively, compared to CC. The T allele, however, was quite rare in the population (4.1%). Only two TT genotypes were observed. Hence, the LEPR SNP was associated with fat yield and subcutaneous fat, but not with intramuscular fat, and tended to show association with lean yield and hot carcass weight.

Key Words: Beef Cattle, Carcass Traits, Leptin Receptor Gene

T32   Fat deposition in Angus cattle and its relation to animal age and body weight measures. A. Hassen*, D. E. Wilson, G. H. Rouse, R. G. Tait, Jr., and J. M. Reecy, *Iowa State University*, *Ames*.

The objective of the current study was to evaluate the relative influences of animal age and body weight measures on the rate of external and intramuscular fat deposition in young Angus bulls and heifers fed a medium energy diet. This study used data from 1,112 purebred Angus bulls and heifers born during 1998 and 2003 at the Rhodes beef research farm. Animals were ultrasonically scanned four to six times for 12-13th rib fat thickness (BKF), rump fat thickness (RMF), percentage of intramuscular fat (PFAT), and longissimus muscle area (LMA). Body weight (WT) and hip height (HT) measures were also recorded. Pooled data were analyzed using mixed linear models and allowing test of varying covariance structures for the between and within individual animal measures. There was a significant (P < .05) effect of sex on PFAT and BKF deposition. In addition, covariates of age and WT showed important (P<.05) influence on both traits. Plots of predicted PFAT trends showed that intramuscular fat deposition is more influenced by age than WT. At a constant mean WT of 382 kg, predicted PFAT values of bulls ranged from 2.68 % (age = 26 weeks) to 4.11 % (age = 64 weeks). Heifer PFAT values for the same range of ages increased by 3.55 % from the initial value of 3.00 % at 26 weeks. However, at a constant mean age of 46 weeks, the increase in PFAT values of bulls and heifers due to changes in WT (200 to 700 kg) was only 1.00%. External fat deposition was more associated with WT than age at measurement. At a constant mean age of 46 weeks, predicted BKF values of bulls increased from 0.18 cm (WT = 200 kg) to 1.27 cm (WT = 700 kg). The corresponding change for heifers was from 0.27 cm to 1.93 cm. At a constant weight of 382 kg, BKF measures of bulls and heifers showed no apparent change for ages ranging from 26 to 64 weeks. The present results confirm the suggestion that PFAT measures should be adjusted for age differences while yearling BKF measures need to be adjusted to a 365-day weight basis.

Key Words: Ultrasound, Beef Cattle, Body Composition

T33   Estimation of genetic parameters for image analysis traits on *M. longissimus dorsi* and *M. trapezius* of carcass cross section in Japanese Black steers. T. Osawa*[1], Y. Motohira[1], T. Sewaki[1], Y. Hirayama[1], K. Okamoto[1], K. Kuchida[1], and T. Kato[2], [1]*Obihiro University of Agriculture and Veterinary Medicine*, *Obihiro-shi, Hokkaido, Japan*, [2]*Tokachi Federation of Agricultural Cooperative*, *Obihiro-shi, Hokkaido, Japan*.

In Japan, *M. longissimus dorsi* (rib eye) has been evaluated in the beef meat grading process. However, size, shape and degree of marbling in other areas of muscle have also been important in determining the meat quality and carcass value. The purpose of this study was to estimate genetic parameters for the rib eye and *M. trapezius* of Japanese Black steers by computer image analysis. Digital images of the carcass cross section were taken between the 6-7th rib by photographing equipment. The numbers of records of Japanese Black steers and pedigree records were 2,418 and 9,293, respectively. Area, fat area ratio, overall coarseness of marbling and coarseness of the largest marbling particle in the rib eye and *M. trapezius* were calculated by image analysis. The ratio of minor and major axes for rib eye and the complexity of rib eye shape were also calculated. Genetic parameters for these traits were estimated with REMLF90 program using an animal model. Year-season and age at shipping as fixed effects and fattening farm and animal genetic effects as random effects were included in the model. For rib eye, heritability estimates were 0.42, 0.65, 0.49,

138

J. Anim. Sci. Vol. 83, Suppl. 1/J. Dairy Sci. Vol. 88, Suppl. 1

0.38 and 0.21 for area, fat area ratio, overall coarseness of marbling, minor and major axis ratio, and complexity of rib eye shape, respectively. For *M. trapezius*, heritability estimates were 0.41, 0.65 and 0.53 for area, fat area ratio and overall coarseness of marbling, respectively. Genetic correlation coefficients between subcutaneous fat thickness and fat area ratio for the rib eye and for *M. trapezius* were -0.18 and -0.16, respectively. Genetic correlation coefficients between rib eye and *M. trapezius* were 0.31, 0.58, 0.48 and 0.40 for area, fat area ratio, overall coarseness of marbling and coarseness of the largest marbling particle, respectively.

T34 Beef carcass characteristics and sex hormone levels in the longissimus dorsi and adipose tissue in Hanwoo. Y. H. Choy*[2], O. S. Han[1], S. K. Son[2], C. W. Lee[2], and M. G. Baik[1], [1]*Chonnam University*, *Kwangju, Republic of Korea*, [2]*National Livestock Research Institute*, *Suwon, Republic of Korea*.

Concentrations of sex hormones and their receptor gene expression levels in terms of mRNA's were analyzed to find out their relationship with carcass characteristics of Hanwoo especially the marbling scores (intra-muscular fat levels) and the effects of sexes on those characteristics. To take the loin eye samples for hormonal and gene expression analyses, carcasses of 10 steers, 10 bulls and 16 cows were taken from Namwon and Daekwanryung branches of National Livestock Research Institute, Korea. Correlation coefficients between marbling scores and crude fat contents in the rib eye were estimated to be around 0.7. Sex effect was a significant source of variation for estrogenic sex hormones in both muscle and adipose tissues while marbling was a significant source of variation for both estrogenic and androgenic sex hormone levels. Residual correlations showed that there were positive relationship between marbling scores and shear force or moisture content and negative relationship between marbling scores and cooking loss. Marbling scores were also positively correlated with pH or with water holding capacity. Significant positive relationships with estimated breeding values of body and carcass weights at slaughter or with rib eye area were found in the expression levels of androgen receptor genes. And estrogen receptor gene expression level in adipose tissues was positively and significantly related with marbling scores (r=0.61) in the loin eye area.

T35 Factors associated with ELISA likelihood s/p ratio scores for paratuberculosis in an Angus-Brahman multibreed herd of beef cattle. M. Elzo*, D. Rae, S. Lanhart, J. Wasdin, P. Dixon, and J. Jones, *University of Florida*, *Gainesville*.

Paratuberculosis is a chronic disease of ruminants that causes considerable economic losses in beef and dairy cattle due to diminished production and eventually death. The objective of this study was to identify factors that are associated with antibody response to the ELISA test in three year old and older cows from an Angus-Brahman multibreed herd. Blood samples were drawn from dams at the end of May each year. Outcomes of the ELISA test were represented by sample to standardized positive control (s/p) ratios. Data came from 245 dams and 359 calves born in the spring of 2003 and 2004. The mixed model included: 1) the fixed subclass effects of year and age of dam (3, 4, and 5 years and older), 2) the fixed regression effects of fraction of Angus (FA), dam heterosis (DH), birth weight of calf (BW), calf gain between birth and the date of the blood sample of their dams (CG), age of calf at date of dam blood sample (CA), dam change in weight between her last weight the previous year (late November) and her weight on the date of the blood sample (DG), dam condition score on the date of the blood sample (DS), and days pregnant at palpation (DP), and 3) the random effects of dam and residual. Dams were assumed to be unrelated. Procedure MIXED of SAS was used to carry out computations. Among subclass fixed effects, only year was important (P < 0.001). Assuming that the s/p ratio scores were a reflection of the impact of paratuberculosis on dams in this herd, estimates of fixed regression effects suggest that: 1) Brahman dams were more affected than Angus dams (FA = -0.610; P < 0.013), 2) sub-clinical paratuberculosis negatively affected calf birth weight (BW = -0.021; P < 0.021), pre-weaning calf gains (CG = -0.008; P < 0.002), and changes in dam weight between November and May of the following year (DG = -0.006; P < 0.002), and 3) dams that calved earlier in the season were more affected (CA = 0.005; P < 0.043). Variation due to dams yielded a repeatability estimate of 0.34 (SE = 0.01).

T36 Differential effects of dietary phosphorus levels on gene expression in two lines of pigs. L. Grapes*, A. Qu, L. Hittmeier, M. Rothschild, and C. Stahl, *Iowa State University*, *Ames*.

Despite the cost of phosphorous (P) supplementation in porcine diets, as well as public concern about the environmental effects of P in excreta, little research has focused on the genetic mechanisms controlling P utilization in pigs. Microarray analysis was conducted to explore the effects of dietary P levels on gene expression in pigs from two sire lines primarily selected for either growth performance or meat quality. Thirty-six total gilts (initial body weight 6.63 ± 0.78 kg) were allotted to a P adequate, P deficient or P repletion dietary treatment for two weeks. At the completion of the trial, liver and muscle RNA samples were obtained for microarray analysis using oligonucleotide arrays containing over 13,000 unique genes. The microarray study involved a loop design with all pair-wise treatment comparisons performed within litter. Mixed-model analysis was performed on normalized signal intensity data and included the fixed effects of sire line, dietary treatment and sire line by dietary treatment interaction. Significant changes in gene expression (P<0.01) in liver and muscle were found between sire lines (103 and 339 genes, respectively), dietary treatments (122 and 18 genes, respectively), and for the interaction of sire line by dietary treatment (88 and 31 genes respectively). Few genes differentially expressed in liver were also found to be differentially expressed in muscle. The large number of genes differentially expressed between sire lines in muscle as compared to liver may be related to inherent differences due to the selection goal for each line. For all combinations of sire line by dietary treatment, genes shown to have differential expression by microarray analysis have been validated using real-time quantitative PCR. Many of these genes are involved in energy metabolism and signal transduction. These results are a first step towards enhancing our understanding of P metabolism and eventually identifying pigs, based upon their genetics, that tolerate low dietary P levels while maintaining growth.

T37 Estimation of genetic parameters in Korean swine populations. S.-H. Oh*[1], D. H. Lee[2], and M. T. See[1], [1]*North Carolina State University*, *Raleigh*, [2]*Hankyong National University*, *Ansung, Kyeonggi-Do, Korea*.

The objective of this study was to estimate genetic parameters among reproductive and post weaning traits in swine. Reproductive traits analyzed included total pigs born (TB), number of pigs born alive (NBA), number of pigs weaned (NW), and litter weaning weight (LWT) for first parity females. Post weaning traits included average daily gain (ADG), backfat depth (BF) and loin muscle area (LMA). Numbers of records were 385 for TB, NBA, NW, ADG, BF, and LMA and 333 for LWT. Genetic parameters were estimated using the MTDFREML software program. The statistical model for reproductive traits included fixed effects of year-season(17), breed of sow(3), mate breed(3), and age(5) and random effect of animal(2,368). For NW and LWT, age at weaning was also included as a covariate. For post weaning traits the statistical model included fixed effects of year-season, breed, sex, parity of dam, age off test and weight off test and random effect of animal. Heritability estimates for TB, NBA, NW, LWT, ADG, BF, and LMA were 0.12, 0.16, 0.14, 0.07, 0.33, 0.49, and 0.18, respectively. High to moderate genetic correlations were observed be-

J. Anim. Sci. Vol. 83, Suppl. 1/J. Dairy Sci. Vol. 88, Suppl. 1

139

tween traits for number of pigs from first parity females (TB-NBA, 0.97; TB-NW, 0.40; NBA-NW, 0.61). Litter weight at weaning for first parity females showed low genetic correlations with TB, NBA and NW of 0.03, 0.09 and 0.00, respectively. Genetic correlations between ADG and BF and LMA were -0.03 and 0.13, respectively. The genetic correlation between BF and LMA was 0.06.

Key Words: Pigs, Heritability, Genetic Correlation

T38   Selection intensity for yield traits, somatic cell score, and days open when culling dairy cows. H. D. Norman*, J. L. Hutchison, M. T. Kuhn, J. R. Wright, and E. Hare, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

Traits emphasized when culling cows from the herd should be similar to those considered when selecting bulls for matings. Emphasis given by dairy producers to different yield and fitness traits when culling cows was documented, and trends since 1980 were determined. Least-square estimates for survivor groups provided first-parity differences for milk, fat, and protein yields; somatic cell score (SCS); and days open (DO) between cows that calved for additional lactations and those that were culled. Trait differences also were expressed on a standardized basis by dividing the least-square estimate by the phenotypic standard deviation for the trait. Cows with 2, 3, or ≥4 parities had an advantage of 900 to 1100 kg of first-parity milk over those culled before second parity; only a small advantage was found for cows with ≥3 parities compared with those with 2. Superiority of cows kept in recent years to culled cows has declined considerably, not only for milk yield but for fat and protein yields, SCS, and DO. On a standardized basis, the most intense selection from 1980 to 1995 was for protein and milk yields (0.80 to 0.90); selection intensity was lower for fat yield (0.54 to 0.75), SCS (0.29 to 0.53), and DO (0.29 to 0.45). Cows that survived ≥2 parities had lower first-parity SCS than those with only 1 parity. Likewise, those with ≥3 parities had lower first-parity SCS than those with only 2 parities, and those with ≥4 had lower SCS than those with only 3. Cows with only 2 parities had the highest mean DO during first parity followed by those with only 3, those with ≥4, and those with only 1; those with only 1 parity had 20 to 27 fewer DO than those with ≥2 parities. Knowledge of which traits dairy producers emphasize in culling cows can assist artificial-insemination organizations in determining which traits should be emphasized when choosing young bulls and graduating progeny-test bulls.

Key Words: Culling, Selection, Yield

T39   Effects of complex vertebral malformation gene on production and reproduction. M. Kuhn*, J. Hutchison, and C. Van Tassell, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

Approximately 3 million records from about 1.7 million daughters of sires with known genotype for complex vertebral malformation (CVM) were used to estimate the effect of the CVM allele on lactational milk, fat, and protein yield, SCS, and days open (DO). The linear model for analysis included the fixed effects of herd-year-season, parity, age-at-calving, CVM status of sire, and the random effects of animal, permanent environment, and error. With random mating, the difference between carrier and homozygous normal bulls estimates the quantity (true effect)/$[(q+1)*(q+2)]$ where q is the frequency of the CVM allele and true effect is the true difference between homozygous normal and carrier cows. Estimates of CVM gene frequency, based on random samples of the cow population, do not appear to be available. Thus, estimates from the linear model were doubled (corresponding to q = 0) which provides a lower limit for the estimate of the true effects. Using a gene frequency even as high as 0.1 had only a small effect on the estimates beyond doubling. For all traits, effects were minor. Lactational milk yield was 160 kg higher for carriers while lactational fat and protein were 4 and 5 kg higher, respectively, for cows from carrier sires. The difference in SCS between carriers and normals was only 0.03 and carriers averaged only 2 more DO than non-carriers. Given the lethal aspect of CVM, the small effect on DO may be a result of intentional avoidance of

inbreeding which, to date, may have led to avoidance of most carrier x carrier matings. Also, most CVM calves may be carried to term in which case DO would not be affected by carrier x carrier matings. Elimination of the CVM allele from the population would have little direct detriment for performance traits. Exclusion of cows whose sires have unknown genotype, as done in this study, could lead to bias. Further research will ascertain the potential magnitude of such a bias and possible methods to correct for such a bias, if it exits.

Key Words: Complex Vertebral Malformation

T40   Allele effect for calf survival estimated for US Holstein Population. H. N. Schlesser*[1], R. D. Shanks[1], P. J. Berger[2], and M. H. Healey[2], [1]*University of Illinois, Urbana*, [2]*Iowa State University, Ames*.

A bimodal pattern of inheritance for calf survival was identified in sons of Holstein bulls. One explanation of this pattern of inheritance is an allele effect for bulls heterozygous for a quantitative trait loci affecting calf survival. Data on predicted transmitting ability for Perinatal Survival from the first parity daughter records of 8,678 sons of 599 sires were collected during 1984 through 1997 from The National Association of Animal Breeders calving ease database. Sixteen of the thirty-nine bulls with at least 50 sons were identified with a potential bimodal pattern of inheritance, using Proc KDE in SAS. Six of the sixteen bimodal bulls had a common sire. Three other pairs from the sixteen bimodal bulls were brothers. Truncation point to define two groups from the bimodal distribution of each bull was based on equating the coefficients of variation between the two groups. The average allele effect for each bull was half the difference between the low and high group. Allele effects ranged from .29 to .41 with average allele effect of .35 (standard error of .03). An average allele effect represented just over one-third of a percent change in calf survival. Allele frequencies were estimated based on a one locus model with two alleles corresponding to 16 AA, 16 Aa and 7 aa bulls. The frequency of A for greater survival was .62, and the allele frequency of a for less survival was .38. Variation is sufficient to allow selection to move the average percent calf survival. Unfortunately, the bimodal bulls are younger than most of the other bulls suggesting that calf survival may be declining.

Key Words: Perinatal Survival, Allele Effect, Dairy Bulls

T41   Applying restricted maximum likelihood and bayesian methods to estimate variance components for milk yield in Brazil. A. Falcão*[1], E. Martins[2], C. Costa[3], E. Sakaguti[2], and J. Mazucheli[2], [1]*Pontifical Catholic University, Toledo, PR, Brazil*, [2]*Maringá State University, Maringá, PR, Brazil*, [3]*Brazilian Agricultural Research Corporation, Dairy Cattle, Juiz de Fora, MG, Brazil*.

Variance components for milk yield were estimated by REML and bayesian via Gibbs sampling (GS), using 40727 lactations of Holsteins cows, calving from 1981 to 1993 in 322 herds of Paraná state in Brazil. An animal model was applied and included the effects of herd-year, parity (five), genetics groups (PO and 31/32), and effects additive and permanent enviroment. There was no evidence of lack of convergence of the GS. Estimates and standard deviations of heritability using REML and GS were 0.26±0.001 and 0.28 ±0.014. Gibbs sampler allowed calculation point estiamtes and confidence interval.

Variance components and heritability and standard errors to milk yield, estimated using bayesian and REML methods

Method/Variance	Additive	Permanent	Residual	Phenotipic	Heritability
Bayesiano	355.1±20.2	257.2±16.4	663.3±7.5	1276±11.0	0.28±0.014
REML	331.6	268.2	664.8	1265.0	0.26±0.001

1 figures divided per 1000

Key Words: Dairy Cattle, Markov Chain, Variance Components

T42 The survey of Sistani cows dairy characteristics in rural production conditions. M. R. Birjandi*, *Agricultural and Natural Research Resources Center of Khorasan, Mashhad, Khorasan, Iran.*

The Sistani cattle is one of the most popular humped (Bos indicus) Iranian cattle spread in the Southern-East regions of Iran. This breed, with a population of about 100,000, is well adapted to the extreme hot and dry environmental conditions of the region and plays a major role in the country·s animal production. Two hundred and seventeen Sistani cows from 209 rural farms with similar production conditions were studied for one lactation period. Traits measured included total lactation yield, milk yield to 180 days, daily milk yield, amount of milk consumed by the calf, fat percentage, protein percentage, lactose percentage, total solid non-fat (SNF) percentage, total solid (TS) percentage, lactation length, days dry, calving interval, age at first calving, days open, peak yield, days to peak and weaning age. The effect of parity, calf feeding type, sex of the calf, calving season, management and lactation length were tested on the traits using the model: $Y_{ijklmn} = \mu + P_i + N_j + S_k + G_l + M_m + L_n + NS_{(jk)} + e_{ijklmn}$ in which Y_{ijklmn} is the observation, μ is mean, P_i is parity, N_j is calf feeding type, S_k is calving season, G_l is sex of the calf, M_m is management, L_n is lactation length, $NS_{(jk)}$ is feeding x calving season and e_{ijklmn} is the error.There were strong positive correlations (p < 0.01) between daily milk yield and lactation length (0.91), daily milk yield and calf milk consumption (0.77), Lactation yield and calf milk consumption (0.87), calving interval and days dry (0.70) and calving interval and days open (0.96). Lactation length and sex of the calf had significant effects on days to peak (p< 0.05). Lactation length also affected milk yield (p < 0.01), milk yield to 180 days (p < 0.05) and SNP % (p < 0.01). The interaction between calving season and feeding type was also significant (p < 0.01).The Relatively high coefficients of variations for many traits indicate potential for improvement by selective breeding within the population. This is important for the sustainable conservation-production of the Sistani population, given the danger of being crossed and (or) upgraded to exotic breeds for economical reasons.

Key Words: Sistani Cows, Dairy Characteristics, Rural Condition

T43 Crossbreed dairy cattle production in the tropical area in Bolivia. J. A. C. Pereira*[1], J. S. Romero[1], Z. B. Johnson[2], D. W. Kellogg[2], and A. H. Brown[2], [1]*Gabriel Rene Moreno University, Santa Cruz, Bolivia,* [2]*University of Arkansas, Fayetteville.*

The objective of this study was to determine the effects of birth (B), grade of crossing (G), calving season (S), parity (P) and its interactions on milk production, length of lactation, age at first calving and calving interval on different grades of Holstein (H), Zebu (Z) and Criollo (C) crosses in the tropical area of Bolivia. Records of 906 lactations of 356 cows collected from 1988 to 1999 were analyzed. The management of both systems of crossing (H x Z and H x C) was semi intensive: grazing with supplementation according to the level of production. The statistic analysis was performed independently for both crossing systems using the GLM procedure of SAS. The results determined that B, G, S and P have an influence (P< 0.05) for all the traits involved. The range of milk production (Standard Error in parenthesis) in 305 days of milking was 2870.1 (±121.1) to 3135.9 (±78.2) kg of milk yield for H x Z crosses and 3672.2 (±107.1) to 3920.8 (±64.3) kg of milk yield for H x C crosses. In the H x Z crosses significant differences (P< 0.01) were found for S and for the G X S interaction especially in the F1 animals. The study showed that the introduction of genes of specialized breeds increases significantly the milk yield production, and reproductive parameters were managed among acceptable ranges in tropical areas.

Key Words: Tropical, Crossbreeding Cattle

T44 Mature equivalent protein yield in daughters of Holstein sires selected for high and average fat plus protein yield. P. J. Berger, M. H. Healey, G. A. Gutierrez*, and A. E. Freeman, *Iowa State University, Ames.*

The objective of this analysis was to compare mature equivalent protein yield between two long-term selection lines. Sires were selected for high or average PTA fat plus protein (1988-2002). Data for cows (n = 978) were restricted to less than 7 parities. We analyzed the data using two models. Model 1: fixed model in SAS PROC GLM, fixed effects were generation of sire, lines, year-month, parity, and the interaction of parity by lines. Model 2: repeated-record sire model in SAS PROC MIXED, fixed effects were lines, year-month and parity; and random effects were sire, cow within sire. Random effects of cows within sire were modeled assuming compound symmetry (co)variance structure. Model 1 showed differences (P<0.001) among levels of year-month, and parities. Model 2 showed differences (P<0.001) between lines, and among levels of parity. Least square means were 303 ± 3.9 kg and 323 ± 3.7 kg for average and high lines, respectively. Implication of this research is that selection for fat plus protein yield increased protein yield in the high line.

Key Words: Selection, Protein Yield

T45 Estimation of genetic parameters and breeding values for persistency of lactation in Japanese Holsteins. Y. Masuda* and M. Suzuki, *Obihiro University of A & VM, Obihiro, Hokkaido, Japan.*

The objective of this study was to calculate genetic parameters and breeding values for persistency of milk and fat yield in the first three lactations using a random regression test day model for dairy cattle in Japan. Data included 11,562,034 (6,010,320 and 2,977,116) test day records from 1,149,474 (607,351 and 302,415) Holstein cows calving between 1975 and 2000 for 1st (2nd and 3rd) lactation. A single trait random regression model was employed for each lactation, and fourth order Legendre polynomial were fitted both animal genetic and permanent environmental effects. (Co)variance components were estimated with EM-REML using subsets sampled randomly from the whole data. Six different measures of persistency were investigated. Heritabilities and genetic correlations between persistency measures and 305-d yield were calculated as a function of (co)variances. Due to low genetic correlations of persistency with 305-d yield (-0.08 to 0.31) and due to high heritability (0.28 to 0.40) for both traits in all three lactations, the difference between test day yields at 60-d and 280-d was defined as persistency. Heritability estimates for persistency of milk (fat) in first lactation was 0.28 (0.24), lower than 0.36 and 0.40 (0.31 and 0.28) in two and three lactations. For bulls with more than 25 daughters, correlations between EBVs for persistency of milk and fat yields in the first three parities were 0.76, 0.86 and 0.87, respectively. Correlations between EBVs for those of milk (fat) in 1st-2nd, 1st-3rd and 2nd-3rd lactation were 0.59, 0.52 and 0.78 (0.54, 0.46 and 0.76), respectively. These results suggest that persistency of milk and fat yields can be improved genetically in Japan. Persistency in first parity may be a different trait from those in later lactations. Further studies should be conducted to investigate the genetic relationship by multiple trait analyses.

Key Words: Persistency, Genetic Evaluation, Test Day Model