

Breeding and Genetics - Livestock and Poultry I

M31 Effects of selection for post-weaning BW gain on carcass characteristics of *Bos indicus* and tropical adapted *Bos taurus* breeds. S. F. M. Bonilha*^{1,2}, L. O. Tedeschi¹, I. U. Packer², A. G. Razook³, G. F. Alleoni⁴, F. D. Resende⁵, R. F. Nardon⁴, and L. A. Figueiredo³, ¹Texas A&M University, College Station, ²ESALQ/USP, Piracicaba, SP, Brazil, ³Instituto de Zootecnia, Sertãozinho, SP, Brazil, ⁴Instituto de Zootecnia, Nova Odessa, SP, Brazil, ⁵APTA, Colina, SP, Brazil.

A genetic program for selecting post-weaning growth performance of *Bos indicus* and tropical adapted *Bos taurus* (Caracu) breeds was initiated in 1976 at Sertãozinho Experimental Station (São Paulo, Brazil). Several studies have found a significant effect of genetic selection on ADG and body size, but few studies have thoroughly evaluated the impact of this genetic selection on carcass characteristics and meat quality. Therefore, the objective of this work was to evaluate carcass characteristics of the selected progenies. Adjusted BW at 378 days of 414 bulls of genetic selected herds (Caracu, Ca; Nellore, NeS; Guzerah, GuS; and Gir, Gi) and unselected herd (Nellore, NeC), born from 1992 to 1999, were used. Animals across years were fed different diets (TRT) either under feedlot or grazing conditions and were slaughtered, on average, with 653 days of age. Data were analyzed using a random coefficients model, considering herd as fixed and TRT within year and year as random effects. Initial BW was used as a covariate. The table below shows the least-square means of ADG; empty BW (EBW); KPH; HCW, dressing percentage (DP), hindquarter percentage (HQP), rib-eye area (REA), fat thickness (FT), and Warner-Bratzler shear force (WBSF). We concluded that despite a greater ADG, EBW, HCW for Ca and NeS compared to NeC and Gi ($P < 0.05$), KPH and carcass characteristics (REA, FT, and WBSF) did not differ ($P > 0.05$). This indicated the genetic selection of Nellore increased HCW without affecting carcass deposition, composition and meat quality.

	Ca	NeS	NeC	GuS	Gi
ADG, g/d	798 ^a	785 ^a	661 ^b	760 ^{ab}	612 ^b
EBW, kg	444 ^a	438 ^a	414 ^b	429 ^{ab}	409 ^b
KPH, kg	7.44 ^a	7.50 ^a	7.96 ^a	7.33 ^a	7.38 ^a
HCW, kg	279 ^{ab}	285 ^a	269 ^b	268 ^b	266 ^b
DP, %	55.2 ^{bc}	57.2 ^a	57.0 ^{ab}	55.0 ^c	57.1 ^{ab}
HQP, %	45.8 ^b	46.6 ^a	46.3 ^{ab}	46.2 ^{ab}	46.3 ^{ab}
REA, cm ²	57.8 ^a	53.9 ^a	57.5 ^a	51.8 ^a	52.4 ^a
FT, mm	13.2 ^a	14.8 ^a	15.6 ^a	15.4 ^a	15.5 ^a
WBSF, kg	4.00 ^a	4.76 ^a	4.89 ^a	4.93 ^a	5.48 ^a

Within a row, means without a common superscript letter differ ($P < 0.05$) by least-square means adjusted for Tukey.

Key Words: Development, Growth, Composition

M32 Gene expression analysis of pig muscle associated to cholesterol and fat parameters. A. Cánovas¹, J. Casellas*¹, L. Varona¹, I. Díaz², R. Quintanilla¹, and R. N. Pena¹, ¹Genética i Millora Animal. IRTA-Lleida, Lleida, Spain, ²Tecnologia dels Aliments. IRTA-Monells, Monells, Spain.

The objective of this study is to detect and identify genes involved in lipid metabolism in pigs. With this purpose, we have used a microarray

approach over muscle samples. The animal material came from an experimental Duroc population of 370 castrated males distributed in five half-sib families. A total of 70 *Gluteus medius* (GM) muscle samples were processed, belonging to animals with the most extreme levels (HIGH and LOW lines; 35 animals per line) for cholesterol and fat parameters such as plasma lipoprotein and triglycerides concentration, percentage of intramuscular fat and fatty acid composition in muscle. Each sample was individually hybridized using *GeneChip Porcine Genome*[®] arrays (*Affymetrix*). After normalizing data with the RMA algorithm, comparison between lines was performed with two different analyses: a standard t-test and a Bayesian analysis by means of a mixed model with heterogeneous residual variances. The t-test results showed a total of 1,007 genes whose expression levels differed significantly (p -value $<10^{-7}$) between the HIGH and LOW lines. Among these significant genes, 140 had a ratio of expression between the two lines superior to 1.5. The mixed model analysis resulted in a total of 500 genes differently expressed at a significant level (p -value $<10^{-9}$), 158 of which showed a ratio between classes greater than 1.5. It is worth mentioning the high coincidence of genes detected with both analyses. The great majority of these 158 genes (95.5%) have a known human homonymous with biological functions related to a variety of processes such as: transcription factor, lipid metabolism and RNA processing.

Key Words: Cholesterol, Gene Expression, *Gluteus Medius*

M33 Positive association between porcine PTHLH gene and teat number in a F₂ Meishan and Iberian crossbreed. M. Martínez*¹, J.L. Noguera¹, O. Ramirez², E. Alves³, and R.N. Pena¹, ¹Genética i Millora Animal. IRTA-Lleida., Lleida, Spain, ²Departament de Ciència Animal i dels Aliments. UAB., Bellaterra, Spain, ³Departamento de Mejora Genética Animal. SGIT-INIA., Madrid, Spain.

The differentiation factor PTHLH (parathyroid hormone-like hormone) has an established role as a local modulator of epithelial-mesenchymal interactions such as those of bone, teeth, mammary gland and nipple development. PTHLH is expressed in placenta and in a variety of tissues at embryonic stages; however its role in adult tissue has not been well reported. PTHLH-knock out mice die at birth from complications of a chondrodysplastic syndrome, while reduction of PTHLH receptor expression decreased mammary gland and nipple development. A QTL was observed for teat number in chromosome 5, where the PTHLH gene is located. Based on this, we are investigating the PTHLH gene as a candidate gene for nipple development in a Meishan × Iberian (Ms×Ib) F₂ experimental intercross. These breeds differ substantially in teat number. A C>T non-synonymous polymorphism has been characterized in the coding region of pig PTHLH gene. An allelic discrimination assay was carried out in parental, F₁ and F₂ Ms×Ib animals. Statistical analysis was performed with a fixed effects model which included genotype (3 levels) and generation (2 levels). Iberian boars were all homozygous for allele C while the SNP was found to segregate in Meishan sows being allele C the most frequent. For the association study we have used the first two generations (F₁ and F₂) of the crossbred because we lack teat number information in parental generation. We observed significant differences between homozygous for allele C (13.40±0.08) and the other two genotypes: heterozygous (13.80±0.10; $P=0.0004$) and homozygous for allele T (14.21±0.36; $P=0.025$). This result must be confirmed with alternative statistical

models that included the information provided by neutral markers. This study has been financed by the project AGL2004-08368-C03/GAN.

Key Words: Swine, Teat Number, Parathyroid Hormone-Like Hormone

M34 Rapid characterization of radiation hybrid panel DNA by SYBR® Green I-based dissociation curve analysis and application for river buffalo gene mapping. K. J. Kochan¹, M. E. J. Amaral², and P. K. Riggs*¹, ¹Texas A&M University, College Station, ²IBILCE, UNESP, São José do Rio Preto, Brasil.

High quality genome maps are essential for identification of genes affecting economically important traits in domestic animals, yet genomic resources remain scarce for many agriculturally important livestock species, including the river buffalo (*Bubalus bubalis*). Meat and milk production from river buffalo is a valuable world commodity, but its genetic map has not been well characterized. Radiation hybrid DNA mapping panels are widely-used tools for the generation of gene maps in numerous vertebrate species. A radiation hybrid panel was recently developed for river buffalo, and a framework map is under construction. Efficient utilization of available resources is necessary for completion of this map, so the objective of this project was to reduce reagent and labor cost by adaptation of SYBR® Green-based real-time PCR and dissociation curve analysis methods for map construction. SYBR® Green I chemistry has been employed extensively in other real-time PCR applications, including quantification of gene expression, detection of mRNA splice variants and DNA sequence polymorphisms, and detection of bacterial and viral pathogens. Differences in fragment length or sequence composition of the PCR products can be distinguished by analysis of the dissociation curve. As an initial test of the application of this method, 30 bovine microsatellite markers were selected from the cattle genome map for analysis. These markers were tested by PCR amplification of DNA samples from a *Bos taurus* bull (positive control), river buffalo bull, and Chinese hamster A23 fibroblast cells. Of these markers, 26 (87%) amplified in river buffalo DNA and exhibited dissociation curves that were distinguishable between river buffalo and hamster, and were used to generate a map of chromosome 20 (BBU 20). Thus, this method can be used for fast and efficient mapping, and the necessity of gel electrophoresis and photodocumentation of gels has been eliminated, reducing overall cost. This technique can be employed for mapping of additional chromosomes to generate a whole genome river buffalo framework map.

Key Words: River Buffalo, Radiation Hybrid Mapping

M35 Comparison of ribosomal protein gene distribution between full-length enriched cDNA libraries from multiple stages of porcine early embryo. R. S. Wu*, E. -C. Lin, C. C. Hsu, and W. T. K. Cheng, *Department of Animal Science and Technology, National Taiwan University, Taipei, Taiwan.*

Preimplantation stage influences porcine early development. Ribosomal proteins are responsible for some basic functions to support the normality of embryogenesis during this period. In order to compare ribosomal protein gene expression between different stages of early embryo, the expressed sequence tags (ESTs) of ribosomal protein genes were extracted from porcine multiple embryonic stages: 4-cell,

8-cell, morula and early blastocyst. The strategy of the library construction is to generate full-length enriched cDNA library in early embryogenesis. Furthermore, the percentages of cDNA clones annotated were calculated as eighty ribosomal protein genes in the four libraries for statistical comparison of distribution for each ribosomal protein genes (4-cell vs. 8-cell; morula vs. early blastocyst). After cleaning those clones of low quality, short insertion and low complexity, the remaining sequences of high quality (N=31,339) were clustered into groups according to sequence similarity ($\geq 95\%$ identity and 90 bp minimum overlapping) to produce 1,378 clusters and 2,139 singletons. The ESTs of different ribosomal protein genes contained in the four libraries were different (4-cell: 10%, 8-cell: 6%, morula: 30% and early blastocyst: 63%). The ESTs frequency for 7 kinds of ribosomal protein genes were found to be significantly different between 4-cell and 8-cell embryos with R statistics from 12 to 47 (4-cell > 8-cell: 6 ; 8-cell > 4-cell: 1). As well, the ESTs frequency for 37 kinds of ribosomal protein genes were found to be significantly different between morula and early blastocyst with R statistics from 9 to 134 (morula > early blastocyst: 2 ; early blastocyst > morula: 35). The results described above showed that several ribosomal protein genes might be responsible for certain biological functions in the early embryogenesis in pigs.

Key Words: Ribosomal Protein, Early Embryogenesis, Pigs

M36 Use of random regression model in the milk yield analysis of water buffaloes. A. A. Ramos*¹, C. V. Araújo², S. I. Araújo², and D. C. P. Pereira², ¹Sao Paulo State University, Botucatu, SP, Brazil, ²Federal Rural University of Amazonia, Belém, PA, Brazil.

Data comprising 1,719 milk yield controls of 357 females (predominantly Murrah breed) daughters of 110 sires, with births from 1974 to 2004, obtained from the Programa de Melhoramento Genético de Bubalinos (PROMEBUL) and also from records of EMBRAPA Amazônia Oriental - EAO herd, located in Belém, Pará State, were used to compare random regression models, for estimating variance components and predicting breeding values of the sires. Data of milk yield were analyzed by different random regression models using the Legendre's orthogonal polynomials functions of second, third and fourth orders. The random regression models included the effects of herd-year, month of parity date of the control; regression coefficients for age of females (in order to describe the fixed part of the lactation curve) and random regression coefficients related to the direct genetic effects and the permanent environment. The comparisons among the models were based on the Akaike Criteria Information. The random regression model that used the third order Legendre's polynomials and four class of the environmental effect was the one which better described the additive genetic variation of milk yield. The heritability estimates varied from 0.08 to 0.40. The genetic correlation between milk yields in younger ages was close to the unit, but in older ages was low.

Key Words: Genetic Evaluation, Murrah Breed, Milk Yield

M37 Effects of cytoplasmic line on scrotal circumference and semen quality traits in Angus bulls. A. G. Garmyn* and D. W. Moser, *Kansas State University, Manhattan.*

The purpose of this study was to estimate the heritability of semen traits, genetic correlations between scrotal circumference (SC) and

semen quality parameters, and the effect of cytoplasmic line on semen traits. Breeding soundness exam (BSE) data was collected on registered Angus bulls at four ranches over seven years. The American Angus Association provided historical pedigree information to estimate the effect of cytoplasmic line on SC and semen quality traits. After editing, the evaluated dataset contained 1,281 bulls with BSE data that traced to 100 founder dams. Data were analyzed using a two-trait animal model to obtain heritability, genetic correlation between SC and semen quality traits, as well as the effect of cytoplasmic line as a random effect for SC, percent motility (MOT), percent primary abnormalities (PRIM), percent secondary abnormalities (SEC), and percent total abnormalities (TOT) using MTDFREML. Fixed effects included source ranch and birth year, and test age was used as a covariate. Estimates of heritability for SC, MOT, PRIM, SEC and TOT were 0.46, 0.05, 0.27, 0.24, and 0.25, respectively. Genetic correlations between SC and MOT, PRIM, SEC, and TOT were 0.37, -0.20, -0.13, and -0.25, respectively. The proportions of phenotypic variance accounted for by cytoplasmic line for SC, MOT, PRIM, SEC, and TOT were <0.001, 0.013, 0.022, 0.0023, and <0.001, respectively. Genetic correlations between SC and semen quality traits were low to moderate and favorable. Cytoplasmic line may have a marginal effect on MOT and PRIM, but is likely not a significant source of variation for SC, SEC, or TOT.

Key Words: Bulls, Cytoplasmic Line, Semen

M38 Effect of temperature and humidity on gestation length.

H. D. Norman, J. R. Wright*, and J. B. Cole, *Agricultural Research Service, USDA, Beltsville, MD.*

High temperature and humidity have been shown to suppress daily milk and component yields of dairy cows, but their effects on most other performance traits have not been investigated. To determine if monthly differences in GL are caused by temperature and humidity, meteorological data since 1997 recorded at 238 weather stations was used in conjunction with national data for nearly 7 million calvings from 1999 through 2005. Temperature and relative humidity recorded at the weather station closest to the herd were combined into temperature-humidity indexes (THI): $THI = (1.8T + 32) - (0.55 - 0.0055H)(1.8T - 28)$, where T is temperature in °C and H is relative humidity expressed as a percentage, for the week prior to calving and for calving day. Effect of weekly and calving-day THI on GL were compared with a model that accounted for THI, calving day, calving year, calving herd-year, calving month, age-parity, calf birth code (gender and multiple-birth status), lactation length, milk yield, service sire, sire, and cow. All effects were fixed except service sire, sire, and cow. Effect of THI on GL without calving month in the model also was examined. When weekly THI was 36 to 40, 56 to 60, and 76 to 80 with calving month in the model, GL was 279.7, 279.5, and 279.1 d, respectively; without calving month in the model, GL was 280.2, 279.8, and 278.6 d. Excluding calving month from the model resulted in greater variation in GL, which became shorter at an accelerated rate as THI increased. Calving-day THI were less effective than weekly THI in accounting for GL differences. Although the benefit of including THI in the model was rather limited if calving month was already considered, GL still became noticeably shorter when THI was >70. Either calving month or THI can be effective in helping to predict calving dates.

Key Words: Gestation Length, Heat stress, Temperature-Humidity Index

M39 Relationship of gestation length to stillbirth. R. L. Powell*, H. D. Norman, and J. R. Wright, *Agricultural Research Service, USDA, Beltsville, MD.*

Gestation length (GL) has economic and management effects, but its relationship to stillbirth (SB) has not been well documented. Mean Holstein SB rate by GL was examined using >800,000 Holstein calvings with SB data from 1999 through 2005. Data were limited to calvings with a GL of 260 to 295 d from herds with ≥15 calvings with SB data that included ≥3 reported SB. The SB rate was 17.8% for GL of <270 d, 5.0% for GL of 278 to 282 d, and 8.1% for GL of >290 d. Genetic parameters for SB were estimated with a linear model that included fixed effects for calving year, calving herd-year, age-parity, calf birth code (gender and multiple-birth status), lactation length, and milk yield and random effects for service sire, sire, and cow. Effect of calving year on SB rate was small. The SB rate was 1.5% higher for calvings in December and January compared with April to June, 2% higher for lactations of >500 d compared with <250 d, and 2% higher for milk yield of <6,000 kg compared with >16,000 kg. Multiple birth tripled SB rate. Heritability estimates for SB were 0.6% for service sire and 1.2% for sire (2.3% and 4.6%, respectively, when transformed to an assumed underlying scale); heritabilities for February 2007 USDA SB evaluations, which are calculated with a threshold model, were 3.0% for service sire and 5.8% for sire. Correlations of calculated service-sire and sire SB predicted transmitting abilities (PTA) with corresponding February 2007 USDA SB PTA were 0.77 and 0.82 for bulls with >100 daughters with SB data. Correlations of GL PTA, which accounted for the same effects as for SB PTA, with February 2007 USDA SB PTA were 0.20 for service-sire traits and 0.03 for sire traits for bulls with ≥100 observations for each trait (1,613 service sires; 1,040 sires). Of those bulls that were in active artificial-insemination service (132 service sires; 109 sires), corresponding correlations were 0.38 and 0.09. Linear regression of SB PTA on GL PTA showed a 0.07% increase in service sire SB PTA ($P > 0.05$) and a 0.14% increase in sire SB PTA ($P < 0.0001$) for each 1-d increase in corresponding GL PTA.

Key Words: Genetic Evaluation, Stillbirth, Gestation Length

M40 Genomic structure and polymorphisms of the bovine c21orf66 gene. K. R. Wunderlich*, C. A. Abbey, and C. A. Gill, *Texas A&M University, College Station.*

The c21orf66 gene is a putative transcription factor with no known function that lies within the polled interval on BTA1. In humans, this gene spans approximately 37,000 bp and alternative splicing results in at least 4 variant isoforms. The objective of this study was to evaluate this gene as a positional candidate for polled and characterize the genomic structure of this gene in bovine. In order to characterize c21orf66, we assembled bovine whole-genome shotgun, bacterial artificial chromosome, expressed sequence tag, and in-house sequence data into a contig spanning over 50,000 bases to include c21orf66, its promoter, and its 3' end. As in humans and mice, and based on this sequence information, this gene has 18 exons. The contig also served as a reference sequence for SNP discovery through the sequencing of 93 animals from within a breed panel consisting of Angus, horned Hereford, polled Hereford, Ankole, Brahman, Nelore, and Simmental. Single nucleotide polymorphisms within breeds were identified using polyPHRED followed by manual verification in Consed, and then consensus sequences were compared between breeds. The number of confirmed SNPs within c21orf66 for each individual breed varied from

29 to 98 with a total of 145 SNPs discovered across all breeds. The average spacing between SNPs was 363 bp and the average ratio for transitions vs. transversions was 1:2.6. Additionally, 7 indels were also discovered. However, no single SNP or insertion/deletion discovered is consistently different between the horned and polled consensus sequences and thus cannot be attributed as the causative mutation for polled.

Key Words: c21orf66, Bovine, SNP

M41 Application of the Sleeping Beauty transposon system to avian cells. B-W. Kong^{*1}, L. K. Foster², and D. N. Foster², ¹University of Arkansas, Fayetteville, ²University of Minnesota, St. Paul.

The Sleeping Beauty (SB) transposon system is a member of the Tc1/mariner superfamily of DNA transposable elements which have been reconstructed from inactive elements found in salmonids fish. The SB system was developed for gene therapy and mutagenesis in human and mouse species, and until now, has not been shown to function in chicken and turkey cells as a molecular tool for avian transgenesis and chromosome engineering. The transposon construct was generated using the antibiotic (puromycin) selectable marker flanked by the Sleeping Beauty repeat sequences in the improved transposon vector, pT2 (pT2/Puro). To test the ability of SB-mediated transposition in avian species, immortal DF-1 chicken embryo fibroblast (CEF), breast-derived CEF (BCEF) and turkey turbinata-derived (TT-1) cell lines were transfected with a selectable transposon (pT2/puro) vector with or without the transposase (pCMV/SB) vector. Following antibiotic selection, resistant foci were stained and counted to determine relative transposition frequencies. DF-1 CEF cells co-transfected with the transposon and SB vector (pT2/puro + pCMV/SB) showed an approximate 1300-fold increase in the number of foci, compared to the non-transposon vector control (pCMV/puro). When SB mediated transposition was compared to non-SB mediated transposition, the SB co-transfected immortal TT-1, BCEF, and DF-1 CEF cells showed approximately 15-, 20-, and 40-fold increases in the number of puromycin resistant colonies, respectively. This suggests that the "cut and paste" manner of foreign gene insertion into genomic DNA using SB system possibly could be more effective than the nicking mechanism for the incorporation of a non-transposable expression vector. Of interest, primary CEF cells did not show significant increased SB-mediated transfection or transposition efficiencies, suggesting that a more efficient transfection method is needed in order to apply SB-mediated transposition in primary avian cells. In conclusion, we have demonstrated that the SB transposon system can be utilized for the mutagenesis of avian cultured cells.

Key Words: Sleeping Beauty Transposon, Mutagenesis, Avian Cell Lines

M42 Evaluation of growth traits of Brazilian herefords using multivariate analysis. J. C. Souza^{*1,2}, L. T. Campos³, J. A. Freitas², R. Weaber⁴, and W. R. Lamberson⁴, ¹Scholarship of CNPq, Brazil, ²Parana Federal University, Palantina, Brazil, ³Engenheiro Agrônomo, Brazil, ⁴University of Missouri, Columbia.

The objective was to evaluate growth and conformation of Brazilian Herefords using principal component (PC) analysis. Traits analyzed

included birth weight (BW); weaning weight (WWT); weight adjusted to 205 d (W205); daily and total gain birth to weaning (DGBW, TGBW); observed yearling weight (OW365); weight adjusted to 365 d (W365); daily and total gain weaning to yearling (DGWY, TGWY) and scores of conformation (CS); maturity (MAT); muscle (MS); and frame (FS). Eigenvalues of the first three PC were 5.33 (41%), 3.75 (29%) and 2.03 (16%). The correlations among W205, DGWY and W365 were high and positive as were those among CS, MAT, MS, and FS, but were near zero between these sets of traits. Traits contributing most to the first PC were W365 (0.40) and W205 (0.38), to the second PC were CS (0.48), MAT, MS and FS (0.47). Genetic parameters for W205, W365 and PC1 were estimated with MTDFREML using a univariate animal model fitting contemporary group (year, herd, management, season and sex) and age of dam (linear and quadratic covariate) as fixed effects and direct and maternal genetic, their covariance, and uncorrelated maternal permanent environment (c^2) as random effects. For W205, W365 and PC1, respectively, estimates of direct h^2 were 0.22 ± 0.14 ; 0.50 ± 0.02 ; 0.44 ± 0.03 ; of maternal h^2 were 0.13 ± 0.02 ; 0.13 ± 0.02 ; 0.14 ± 0.04 ; and c^2 were 0.07 ± 0.10 ; 0.07 ± 0.01 ; 0.09 ± 0.02 and correlations between direct and maternal genetic effects were -0.67 ± 0.04 ; -0.80 ± 0.03 ; -0.64 ± 0.06 . Both direct and maternal heritabilities were of expected magnitude as was the negative direct-maternal correlation. The first principal component, weighted heavily toward growth traits, had similar estimates of genetic parameters. Principal components can be used to consolidate correlated traits into a simpler set of groupings.

Key Words: Beef Cattle, Growth, Heritability

M43 Molecular evidence that turkey varieties belong to a single breed. E. Smith*, J. Xu, X. Guan, T. Geng, and D. Kamara, Virginia Polytechnic Institute and State University, Blacksburg.

Using a total of 250 birds from seven varieties, we investigated the relatedness among and within different populations of the domestic turkey, *Meleagris gallopavo*. The molecular markers used in the investigation were obtained from both nuclear and mitochondrial genome. From the nuclear genome, the markers used were microsatellite, SNP, and RAPD-based. The mitochondrial-based markers, developed from the whole genome sequence obtained for this work and submitted to GenBank (Accession number assigned is EF_153719) were d-loop and 16S rRNA-based. In addition to variants in the mitochondria, a total of 15 markers formed the basis of the analyses. Together, the analyses suggest that except for the Royal Palm, the turkey varieties are very closely related with a higher genetic variation within than among the populations. The Royal Palm appears to be distant from all the varieties including the commercial turkey as alleles of several distinct markers and marker-types were absent in other varieties but fixed in the Royal Palm populations. The Royal Palm appears to be distant from all the varieties including the commercial turkey, as alleles of several distinct markers and marker-types were absent in other varieties but fixed in the Royal Palm populations. However, consistent with morphological reports, results suggest that turkey varieties originated from a single breed.

Key Words: Turkey, Varieties, Molecular Phylogeny

M44 Evaluation of nucleolar proliferating protein 1 as a candidate gene for beef carcass characteristics. J. H. Bosques-Méndez*¹, M. Pagan¹, E. Casas², A. Casas¹, and D. Cianzio¹, ¹University of Puerto Rico, Mayagüez, Puerto Rico, ²Roman L. Hruska USDA MARC, Clay Center, NE.

Single nucleotide polymorphisms (SNP) identified in four regions of nucleolar proliferating protein 1 (Nol1: A, B, C and D) were evaluated for associations with carcass traits. Genotyping was performed in a group of 42 Senepol x Charolais and Angus x Charolais crossbred bulls grazing tropical grass from weaning to harvest. Nol1-A was associated ($P < 0.05$) with shrinkage percentage (SH), Oblique muscle weight (OM; kg), trimmed fat (TF; kg), and dressing percentage (DP). Animals inheriting the TT and CT genotype had greater SH, OM and DP than those inheriting the CC genotype. Nol1-B was associated ($P < 0.05$) with SH, left hindquarter weight (LHQ; kg), OM, hindquarter percentage (HQP), frontquarter percentage (FQP), total muscle weight (TMW; kg), and slaughter weight (SW; kg). Animals with the CC and CT genotypes were heavier than those inheriting the TT genotype. Associations ($P < 0.05$) between Nol1-C and SH, Gastrocnemius muscle weight (GM; kg), TF, LHQ and TMW were detected. Animals having the AA genotype had greater values for SH and GM compared with animals with the AG and GG genotypes. Animals inheriting the GG genotype had greater TF than the other genotypic groups. For Nol1-D, associations were ascertained for HQP, FQP, LHQ, TMW. No animals inherited the AA genotype, but AG animals had greater values for HQP, LHQ and TMW. Although larger studies need to be conducted, results from this study indicate that markers at the nuclear proliferating protein 1 gene are associated with important carcass traits for beef cattle in the tropics.

Key Words: Nol1, SNP, Carcass

M45 Application of Wilmink's function to Bayesian inference of heritability for monthly test day milk yields in Iranian Holsteins. H. Farhangfar*, Birjand University, Birjand, Iran.

To estimate heritability of individual monthly test day milk yields in Iranian Holstein heifers, a total of 32854 test day records collected from 3842 first lactation Holsteins (progeny of 466 sires) calving from 2001 to 2005 and distributed in 125 herds of Razavi Khorasan province of Iran was used. Bayesian statistical method via Gibbs sampling technique in a random regression test day animal model was applied. In the random regression model, fixed environmental effect of herd-year-month of test-milking times (as contemporary group with 1359 levels), covariables (linear and quadratic) of cow age at calving, linear covariable of Holstein gene as well as random effects of direct additive genetic and permanent environment were included. Wilmink's function ($y = a + bt + c(\text{Exp}(-0.05t))$) was also included in the random regression test day model as a sub-model to take account of milk yield variation over the course of the lactation at two genetic and environmental levels. Heterogeneous environmental variance was assumed over the course of lactation. The analysis was undertaken using RRGIBBS software in which Bayesian heritability estimates of test day milk yields were obtained through 50000 rounds Gibbs sampling from which the first 10000 chains was considered as burn-in period. The lowest and greatest heritabilities were obtained for months 2 (0.236) and 10 (0.361) of the lactation period respectively. The results of the present research also showed that permanent environmental variance as a proportion of the phenotypic variance were maximum

(0.625) and minimum (0.337) for the first and fourth month of the lactation course.

Key Words: Wilmink's Function, Bayesian Estimate, Iranian Holstein

M46 Bivariate genetic analysis of monthly test day milk yield and protein percentage for Holstein heifers in Khorasan province of Iran. H. Farhangfar*, R. Lotfi, and H. Naeemipour, Birjand University, Birjand, Iran.

In this study a bivariate animal model was used to estimate genetic parameters of monthly test day milk yield and protein percentage for Holstein heifers in Khorasan province of Iran. The data was 27673 monthly test day records obtained from 4125 first lactation cows (representing 430 sires and 3744 dams) calving between 2002 and 2005 in 113 herds. The average milk yield and protein percentage over the course of the lactation were 28.69 Kg and 3.27% respectively. In the repeatability test day model, the environmental factors were the combined effect of herd-year-season of production (as contemporary group), stage of lactation, milking times, covariables of Holstein gene (linear) and age of cow at recording (linear and quadratic). Random effects of direct additive genetic as well as permanent environment were also included in the model. Genetic and environmental variance and covariance components were estimated by AI-REML algorithm implemented in DMU package. The results obtained in the present study showed that the heritabilities of milk yield and protein percentage were 0.100 and 0.048 respectively. Additive genetic, permanent and temporary environment correlations between the traits were -0.147, -0.713 and -0.069 respectively. Repeatability estimate of monthly test day milk yield was found to be 0.601 while the corresponding estimate for monthly test day protein percentage was 0.092.

Key Words: Animal Model, Heritability, Iranian Holstein

M47 Insemination of Holstein cows with sexed sperm. J. L. Schenk*¹ and R. W. Everett², ¹XY, Inc., Fort Collins, CO, ²Cornell University, Ithaca, NY.

Most research with sex-sorted sperm has been limited to heifers. The objective of this field trial was to determine pregnancy rates in lactating dairy cows following AI of frozen-thawed X-chromosome-bearing sperm. Sperm were sorted with a MoFlo[®] SX flow cytometer on the basis of DNA content, targeting 90% purity of X-sperm. Holstein cows (N=2197), lactations 1 - 4 and 20 - 140 DIM were inseminated 12 or 24 h after synchronized (PGF_{2α} or Ovsynch) or natural estrus. Three experimental treatments, unsorted control (20 x 10⁶ sperm/dose) in 0.25 mL straws and sex-sorted (2 x 10⁶ sperm/dose) in 0.25 mL or 0.5 mL straws, were balanced over 3 Holstein bulls. Equal numbers of straws of each treatment x bull combination were distributed to 7 commercial dairies. AI services were limited to two per cow and performed by multiple technicians. Pregnancy was determined via rectal palpation at ~60 d after insemination. Data were analyzed with a mixed model ANOVA that included environmental and biological variables known to influence pregnancy rates in cows. Pregnancy rates from sexed sperm were similar ($P > .05$) for 0.25 mL (25.0%) and 0.5 mL (24.4%) straws, but different ($P < .001$) from controls (37.7%). Pregnancy rates with sexed sperm were >12 percentage points lower than those for unsexed sperm (64% of controls). Pregnancy rates for

sexed sperm after 84 - 98 DIM were 7.9 percentage points higher than earlier in lactation and >6 percentage points lower in 3rd and 4th lactation cows compared to 2nd lactation cows. The range of differences between bulls (6.7 percentage points; $P < .001$) was consistent across treatments. Pregnancy rates were similar between cows synchronized with PGF_{2α} or Ovsynch ($P > .05$), but 15 percentage points higher for natural estrus compared to Ovsynch ($P < .001$). Use of sexed sperm will reduce pregnancy rates ~12 percentage points compared to unsexed sperm in lactating cows. Limiting use of sexed sperm to 1st and 2nd lactation cows after an elective postpartum waiting period of >100 DIM will yield the highest pregnancy rates with sexed and unsexed sperm.

Key Words: Dairy Cows, Pregnancy, Sexed Sperm

M48 Genetic trends for dairy traits in the Holstein x Other Breeds multibreed dairy cattle population in tropical central Thailand. S. Koonawootrittriron¹, M. A. Elzo*², and T. Tongprapi³, ¹Kasetsart University, Bangkok, Thailand, ²University of Florida, Gainesville, ³Dairy Farming Promotion Organization, Saraburi, Thailand.

There has been a concerted effort to increase milk production in Thailand over the past 35 years. This effort has been a combination of government policies, importation and widespread use of Holstein semen, and extensive use of high percent Holstein sires generated in Thailand. This mating strategy has resulted in a multibreed dairy population where 90% of animals are 75% Holstein or greater. Central Thailand is the most important dairy region. The objective of this research was to assess genetic variability and genetic trends for 305-d milk yield (MY), 305-d fat yield (FY), and average 305-d fat percent (FP) in Central Thailand from 1991 to 2005. Data consisted of 15,260 monthly test-day records from 1,377 first-lactation cows collected in 92 farms from 1991 to 2005. Dairies in Thailand maintain cows in open barns, and less than 10% use fans to reduce heat stress. Estimates of variance and covariance components and breeding values (EBV) were obtained using a multiple-trait animal model. Fixed effects were contemporary group (herd-year-season), calving age, and additive genetic group as a function of Holstein fraction. Random effects were animal and residual. Program ASREML was used to perform computations. Estimates of heritabilities were 0.39 ± 0.10 for MY, 0.26 ± 0.10 for FY, and 0.21 ± 0.11 for FP. Although the difference between the mean MY for cows in 2005 and 1991 was 79.3 kg, the regression of mean cow EBV for MY on year was only 0.9 kg/yr. Differences between mean cow EBV for FY and FP in 1991 and 2005 and their corresponding regressions of mean FY and FP on year were all near zero. Similarly, mean EBV for sires and dams of cows also showed near zero trends during these years. The absence of genetic trends suggests that high percent Holstein cows are not reaching their production potential under the management, nutrition, and hot and humid climatic conditions in this tropical region.

Key Words: Multibreed, Cattle, Tropical

M49 Multi-trait evaluation for calving ease and stillbirth with separate genetic effects by parity. G. R. Wiggans, J. C. Cole, and L. L. M. Thornton*, *Agricultural Research Service, USDA, Beltsville, MD.*

Genetic evaluations for calving ease and stillbirth were calculated with Holstein and Brown Swiss data from 14,164,522 calving reports in the USDA national dairy database. Calving ease was measured on a scale of 1 (no difficulty) to 5 (difficult birth); stillbirth status was designated as live or dead within 48 hr. Calving-ease scores were transformed separately for first and later parities and calf gender. The score used in the analysis was on a unit standard deviation scale in the middle of the range for each score. Stillbirth status was present for 53% of calving-ease observations. Variance components were estimated from a 103,909-record Holstein sample with no missing observations, which represented the 2,999 bulls with the most data. For calving ease and stillbirth in first and later parities, a multitrait sire-maternal grandsire (MGS) linear model included fixed effects for year-season, gender, sire birth year, and MGS birth year and random effects for herd-year interaction, sire, and MGS was applied. For later parities, gender effects were separated by parity. The correlation between first and later parities was 0.69 for sire and 0.19 for MGS solutions for calving ease and 0.84 for sire and 0.78 for MGS solutions for stillbirth. For first-parity, the correlation between calving ease and stillbirth was 0.86 for sire and 0.34 for MGS solutions. To calculate national evaluations for Holstein and Brown Swiss, a fixed effect for breed was added to the model. Correlations between solutions on the underlying scale from the current evaluation with those from this analysis averaged 0.85 for sire and 0.80 for MGS for calving ease and 0.67 for sire and 0.70 for MGS for stillbirth. The multitrait analysis provided stillbirth evaluations for bulls with missing observations based on correlated calving-ease data and accounted for genetic differences in calving performance between first and later parities. Evaluation stability should be improved as the portion of observations from different parities changes. Accuracy of the net merit index can be improved by adjusting weights to use evaluations for separate parities optimally.

Key Words: Calving Traits, Dystocia, Stillbirth

M50 Estimation of genetic parameters for milk and fat yields in Holstein cattle of Khorasan province of Iran. H. Naemipour*¹, H. Farhangfar¹, H. Moravej², M. Rokoei³, and M. B. Sayyadnejad⁴, ¹Birjand University, Birjand, Khorasan, Iran, ²Tehran University, Tehran, Tehran, Iran, ³Zabol University, Zabol, Sistan va Bluchestan, Iran, ⁴Animal Breeding Center, Karaj, Tehran, Iran.

In order to estimate genetic parameters for milk and fat yields in Holsteins of Khorasan province of Iran, a total of 17791 records belonging to 26078 cows calving from 1990 to 2003 and distributed in 133 herds was used. The data was recorded by animal breeding center of Iran. Two separate analyses consisting of bi-variate (first lactation milk and fat yields) and four-variate (first and second lactation milk and fat yields) animal models were undertaken. In the models, fixed effect of herd-year-season of calving, age at first calving (linear and quadratic covariates) as well as the random effect of additive genetic were included. Additive genetic and environmental (co)variance components were estimated for the traits under consideration applying restricted maximum likelihood method based upon derivative-free algorithm. The results obtained in the present study indicated that heritability estimates of milk and fat yields were 0.28 and 0.23 respectively in bi-variate model. In four-variate model, the heritability estimates of milk yield were 0.29 (at first lactation) and 0.23 (at second lactation) while the corresponding figures for fat yield were found to be 0.24 and 0.21 respectively.

Key Words: Genetic Parameters, Holstein, Khorasan Province of Iran

M51 REML heritability and repeatability estimates of net energy for lactation trait for Holstein heifers in Khorasan province of Iran. H. Farhangfar*¹, H. Naeemipour¹, R. Lotfi¹, and M. Pajaz², ¹*Birjand University, Birjand, Iran*, ²*Jihade Agriculture of Razavi Khorasan, Mashhad, Iran*.

In this study, a total of 24473 monthly test day records of net energy for lactation (NEL in terms of Mcal/kg) obtained from 3805 Iranian Holstein heifers (representing 423 sires and 3474 dams) calving between 2002 and 2005 and distributed in 112 herds was used to estimate heritability and repeatability. A repeatability fixed regression test day animal model was fitted to the data. In the model, fixed environmental effects of herd-year-season of calving-milking times-stage of lactation, age at calving (linear and quadratic covariates), Holstein genes (linear and quadratic covariates) and daily milk yield (linear and quadratic covariates), and random direct additive genetic and permanent environmental effects were included. Restricted maximum likelihood (REML) estimates of heritability and repeatability of NEL were obtained by DFREML software. The results showed that NEL had a heritability of 0.05 indicating that there was low direct genetic variation among cows to be selected in a genetic evaluation. For this trait the same figure was also observed for repeatability suggesting that non-significant permanent environmental variation was found during the course of lactation.

Key Words: Net Energy for Lactation, Genetic Parameters, Iranian Holsteins

M52 Genetic evaluation of lactation persistency estimated by best prediction for Ayrshire, Brown Swiss, Guernsey, and Milking Shorthorn dairy cattle. J. B. Cole and D. J. Null*, *Animal Improvement Programs Laboratory, USDA, Beltsville, MD*.

The objectives of this study were to calculate (co)variance components and breeding values for best predictions of persistency of milk (M), fat (F), protein (P), and SCS in Ayrshire (AY), Brown Swiss (BS), Guernsey (GU), and Milking Shorthorn (MS) dairy cattle. Cows with high persistency tend to milk less than expected at the beginning of lactation and more than expected at the end. Persistency was calculated as a function of a trait-specific standard lactation curve and the linear regression of a cow's test day deviations on days in milk. Heritabilities represent the additive genetic variance of persistency that is independent of yield and defined to have a phenotypic variance of 1. Available data ranged from 27,964 (MS) to 159,898 (BS) records for cows calving since 1997. The number of active AI sires receiving evaluations for persistency ranged from 4 (MS) to 39 (BS). Results from the four breeds were similar; only BS results are presented (Table 1). Sire EBV for persistency of M, F, and P were similar and ranged from -0.36 to 0.67 for M; EBV for persistency of SCS ranged from -0.40 to 0.42. Regressions of sire EBV on birth year were near zero ($P < 0.0001$) but in favorable directions for all breeds and traits. Genetic correlations of persistency of M, F, and P with SCS were moderate and negative for all breeds, indicating that persistency of SCS decreases as persistency of yield increases. Genetic correlations among yield and persistency were low to moderate and ranged from 0.01 (SCS) to

0.08 (F). As expected, selection for improved yield has not affected persistency of yield. Heritabilities and repeatabilities were similar to those previously reported for US Holsteins with the exception of SCS, which were larger in the colored breeds.

Table 1. Heritabilities, repeatabilities, and genetic and phenotypic correlations among persistency traits in Brown Swiss.

Trait	M ¹	F	P	S
M	0.10 (0.19)	0.84	0.88	-0.52
F	0.76	0.08 (0.17)	0.80	-0.50
P	0.91	0.79	0.08 (0.17)	-0.44
S	-0.21	-0.15	-0.17	0.06 (0.12)

¹Heritabilities (repeatabilities) on diagonal, genetic correlations above diagonal, and phenotypic correlations below the diagonal.

Key Words: Best Prediction, Persistency, Test Day Model

M53 Phenotypic and genetic analysis of days open for Japanese Holstein cows. H. Abe*, M. Suzuki, and Y. Masuda, *Obihiro University of A & VM., Obihiro, Japan*.

The objectives of this study were to analyze phenotypic change and to estimate genetic parameters of days open for Japanese Holstein cows. Days open for cows that calved between 1990 and 2002 were calculated from reproduction records obtained from Hokkaido Dairy Milk Recording & Testing Association. Phenotypic change of records from first to fifth parities was investigated. Descriptive statistics were calculated by categories of herd size and average yield of herd. Days open of first and second parities were analyzed by a two-trait animal model. The model included the fixed effects of herd-year, month of calving and age of calving, and random additive genetic effect of animal. The numbers of records were 592,294 and 494,944 for the first and second parities, respectively. Records with less than 22 d or greater than 500 d were deleted. At least 5 records were required per herd-year. The numbers of edited records were 338,440 and 249,702 for the first and second parities, respectively. Five subsets of records were extracted by random sampling of herds, and means of estimates on each subset were used as final estimates. Genetic parameters were estimated by the AIREMLF90 program. The mode on days open was nearly 75 d for each year. However, over the years, the average increased from 120 d to nearly 140 d. For all the categories of the herd size and average yield of herd, the modes were nearly constant, whereas the averages and standard deviations increased every year. As the average yield of herd increased, the averages and standard deviations for days open decreased. Moreover, as the herd size increased, the averages, standard deviations, and modes decreased. Estimates of heritability were 0.056 and 0.049 for the first and second parities, respectively. Estimates of phenotypic, genetic and environmental correlation were 0.11, 0.93 and 0.062, respectively.

Key Words: Days Open, Genetic Parameters, Japanese Holstein Cows