1396 Differential effect of dexamethasone on lymphocyte proliferation and immunoglobin production *in vitro*. M.R. Rogers*[1], S.C. Lozano[1], K.M. Kammlah[1], T.H. Welsh, Jr.[2], and J.C. Laurenz[1], [1]*Texas A&M University-Kingsville,* [2]*Texas A&M University-College Station*.

The present study investigated the effect of the synthetic glucocorticoid, dexamethasone (DEX), on concanavalin (ConA)-induced lymphoproliferation and immunoglobin M (IgM) production by pig lymphocytes *in vitro*. Blood was obtained from male, crossbred pigs (n=3-6 pigs/experiment; 40-45 days of age) and lymphocytes obtained by density gradient centrifugation over Lymphoprep (Nycomed, Oslo, Norway). Lymphocytes were plated in 96-well plates at 1 X 10^5 cells/well in DME/F12 containing 10% fetal bovine serum, 2 mM L-glutamine, 10 uM 2-mercaptoethanol, ConA (0 to 10 ug/ml) and/or DEX (0 to 10^{-6} M). Cultures were incubated for 96 h and lymphoproliferation determined using the CellTiter proliferation assay (Promega, Madison, WI). In replicate cultures, supernatants were removed and IgM production determined using an ELISA specific for pig IgM. As expected, ConA induced a dose-dependent increase ($P < .01$) in lymphoproliferation and IgM production with maximal effects occurring at .6 and 1.25 ug/ml, respectively. Although not effecting basal lymphoproliferation, DEX dose-dependently inhibited ($P < .01$) ConA-induced (0.3 and 1.25 ug/ml) lymphoproliferation with maximal effects occurring at 1 x 10^{-8} M. However, the suppressive effects of DEX (1 x 10^{-8} M) on lymphoproliferation could be overcome ($P < .05$) with the addition of higher concentrations of ConA (5 to 10 ug/ml). Similarly, when cells were stimulated with low concentrations of ConA (.3 ug/ml), DEX dose-dependently inhibited ($P < 0.01$) IgM production with maximal effects occurring at 10^{-8} M. In contrast, in cultures treated with 1.25 ug/ml ConA, low concentrations of DEX (10^{-10} to 10^{-9} M) actually augmented ($P < .05$) IgM production. Furthermore, DEX (10^{-8} M) induced additional 1.7 to 1.9 fold increases ($P < .05$) in IgM production by lymphocyte cultures treated with higher concentrations of ConA (2.5 to 10 ug/ml, respectively). Collectively, these results demonstrate that glucocorticoids have primarily a suppressive effect on lymphocyte proliferation, but can augment immunoglobin production depending on both the degree of lymphocyte stimulation and the concentration of glucocorticoid.

Key Words: Pigs, Glucocorticoid, Lymphocyte

1397 Effect of oral administration of dehydroepiandosterone-sulfate (DHEAS) on pig lymphocyte function *in vitro*. S.C. Lozano*[1], T.H. Welsh, Jr.[2], and J.C. Laurenz[1], [1]*Texas A&M University-Kingsville,* [2]*Texas A&M University-College Station*.

The present study investigated the effect of chronic, oral administration of DHEAS on lymphoproliferation and immunoglobin (IgM) production by isolated lymphocytes *in vitro*. Crossbred, female pigs (n = 12; initial weight 9.3 .5 kg) were assigned by weight to one of two treatments (n = 6 pigs/treatment) and were fed either 0 or 1 mg DHEAS/kg body weight twice daily for 100 days. At the end of the treatment period, blood was obtained via jugular venipuncture and lymphocytes isolated by density gradient centrifugation over Lymphoprep (Nycomed, Oslo, Norway). Lymphocytes were plated in 96-well plates at 1 x 10^5 cells/well in DME/F12 containing 10% FBS, 2mM glutamine, 10 uM 2-merceptoethanol, ConA (0 to 2.5 ug/ml), or ConA (.3 or 1.25 ug/ml) in the presence of DEX (0 to 10^6 M). Cultures were incubated for 96 h and lymphoproliferation determined using the Celltiter proliferation assay (Promega, Madison, WI). In replicate cultures, supernatants were removed and immunoglobin M (IgM) production determined using an ELISA specific for pig IgM. As expected, ConA induced dose-dependent increases ($P < .01$) in lymphoproliferation and IgM production with initial increases apparent at .3 ug/ml and maximal effects occurring at 1.25ug/ml ConA. Although not effecting ($P > .05$) the response of lymphocytes to low concentrations of ConA (< .3 ug/ml), feeding of DHEAS to pigs increased ($P < .05$) the extent of lymphoproliferation and tended to increase ($P = .06$) IgM production by lymphocytes at higher concentrations of ConA (.6 to 2.5 ug/ml). In both treatment groups, DEX dose-dependently inhibited ($P < .01$) ConA-induced (0.3 and 1.25 ug/ml) lymphoproliferation with maximal effects occurring at 10^{-8} M. Similarly, when cells were stimulated with low concentrations of ConA (.3 ug/ml), DEX dose-dependently ($P < .01$) inhibited IgM production with maximal effects occurring at 10^{-8} M. In contrast, in cultures treated with 1.25 ug/ml ConA, DEX (10^{-10} to 10^{-8} M) augmented ($P < .05$) IgM production and the effect of glucocorticoid treatment was increased ($P < .01$) in pigs fed DHEAS. Collectively, these results indicate that oral administration of DHEAS can enhance the responsiveness of lymphocytes to antigenic challenge and suggest that DHEAS may be beneficial to enhance immune function in domestic livestock species.

Key Words: pigs, dehydroepiandosterone, glucocorticoid

ASAS/ADSA Breeding and Genetics: Gene Mapping, QTL, and Statistical Methods

1398 A novel and highly effective method to generate transgenic mice and chickens: linker-based sperm-mediated gene transfer. Jin Qian*[1], Yi-Hsin Liu[2], Mason Jiang[3], Tsehay Mekonnen[1], and Ken Wang[1], [1]*BioAgri Corp.,* [2]*Center for Craniofacial Molecular Biology, USC,* [3]*Dept. of Anesthesiology, UCLA*.

Genetic modification of domestic animal traits can be used to improve productivity and quality or to produce bioreactors for modern medicine. DNA microinjection, the current method to produce transgenic livestock, is time consuming and requires extensive training and special equipment. More importantly, except in mice, microinjection has reported only limited success in larger or higher species. Sperm-mediated gene transfer has been recognized as a potentially powerful alternative method, but has been questioned by many laboratories around the world since the original results were difficult to duplicate. We have developed a linker (mAb C) to bind with sperm and DNA. Using flow cytometry, it has shown cross-reactivity with sperm cells from all tested species including mouse, pig, cow, sheep, goat, chicken, and human. mAb C has been characterized as a basic protein and has been shown to bind DNA through ionic interaction. We report here the use of this novel linker with the sperm-mediated gene transfer method to successfully generate transgenic mice and chickens. Sperm from FVB/N mice were treated first with mAb C and then combined with a linearized DNA fragment, pGL3-control (Promega). After *in vitro* fertilization, fertilized eggs at the two-cell stage were implanted into pseudopregnant mice. 12 offspring were born and used to mate with wild type mice. 2 (16.7%) transmitted transgenic mouse lines (F1) were identified by Southern blot. Furthermore, this novel technology was also tested in the chicken through artificial insemination. The transgene was detected in 10 out of 88 (11.4%) chicken embryos by PCR. Combined with our high success rate in making transgenic pigs (58.3%) through surgical oviduct fertilization, our data strongly suggests that this novel linker-based sperm-mediated gene transfer method is both universal and effective and could be of great value to modern agriculture and medicine.

Key Words: Linker-based sperm-mediated gene transfer, Transgenic chicken, Transgenic mice

1399 Generation of transgenic pigs by sperm-mediated gene transfer using a linker protein (mAb C). Keejong Chang[2,3], Jin Qian[1], Mason Jiang[4], Ming-Che Wu[5], Chidar Chen[2], Hin-Lung Lo[3], Meng-Chun Hu[2], Wen-Wen Lin[2], Iris Ho[2], and Ken Wang*[1], [1]*BioAgri Corp.,* [2]*BioAgri Corp., Taiwan Division,* [3]*Dept. of Chemistry, Soochow University,* [4]*Dept. of Physiology, Taiwan Livestock Research Center,* [5]*Dept. of Anesthesiology, UCLA*.

Sperm-mediated gene transfer (SMGT) has been recognized as a potentially powerful method to make transgenic animals for many years. The current method of gene transfer, microinjection, used widely in transgenic mouse production, has had only limited success in producing transgenic animals from larger or higher species. We report here a sperm-mediated gene transfer method that uses a linker protein to vastly improve the efficiency of large transgenic animal production. A monoclonal antibody (mAb C) that could be used as a linker was identified after screening hybridomas immunized with mouse sperm cells. mAb C is reactive to a surface antigen on mouse sperm cells and is also cross-reactive with sperm cells from many different species such as pig, cow, sheep, goat, chicken, and human. mAb C has been characterized

as a basic protein that binds to DNA through ionic interaction. Therefore exogenous DNA can specifically bind to the sperm surface via mAb C and has been shown to successfully integrate into the chromosome of mouse, pig and chicken offspring. Furthermore, expressed foreign proteins can be detected in the serum of transgenic pigs. Diluted pig sperm cells were mixed with mAb C to form a sperm-mAb complex and then pSEAP-2 reporter gene DNA (Clontech) was added to react with the sperm-mAb complex. In group I and II animals, one half-million treated sperm cells were injected into each side of the oviduct in ovulating pigs by surgical oviduct fertilization. In group I, forty-three pig offspring (F0 founders) were analyzed and 30.2% (13/43) of piglets' tails were shown to contain exogenous DNA integration into the host genome by Southern blot analysis. 58.3% (21/36) of these offspring were found to express SEAP secreted into the serum. In group II, thirty-two pig offspring (F0 founders) were analyzed. Results of Southern blot and SEAP analysis show similar findings as those in group I. In a subsequent study, seventeen F0 founders were randomly selected to mate with wild type pigs. Seven (41.2%) transmitted transgenic lines (F1 generation) were identified by Southern blot analysis. These results demonstrate that transgenic pigs can be generated with a remarkably improved efficiency by sperm-mediated gene transfer using the linker protein, mAb C.

Key Words: Linker-based sperm-mediated gene transfer, Transgenic pigs

1400 Macroarray analyses of differential gene expression in porcine fetal and postnatal skeletal muscle RNA. S. Zhao*[1,3], C. Fitzsimmons[1], C. Ernst[2], and C. Tuggle[1], [1]*Iowa State.University, Ames, IA,* [2]*Michigan State Univeristy, East Lansing, MI,* [3]*Huanzhong Agricultural University, Wuhan, PRC.*

High-throughput analysis of transcript abundance holds great promise to identify genes controlling biological traits important in animal agriculture. To test the utility of such transcriptional profiling for porcine muscle gene expression studies, a cDNA macroarray comprising 327 cDNAs spotted in duplicate onto nylon membrane filters was developed. Total RNA from two muscle samples, 75-day fetal hind limb muscles (including gluteus, semitendinosus and semimembranosus) and 7-week postnatal semitendinosus muscle, were used to make radiolabeled targets for filter hybridization. To test reproducibility, two identical membranes were hybridized to each target in two separate incubations. The intensity of expression at each spot was determined by phosphor imager scanning and evaluated by ImageQuant software. Values for each probe spot were normalized to signal at the beta-actin probe spot and to signal from a complex probe consisting of a mixture of cDNA from spleen, muscle, liver and lung tissues. Correlation coefficients of signal intensity between duplicate spots was greater than 0.98 and normalized signal intensity between two identical membranes was greater than 0.96 (Pearson test), indicating the reproducibility between duplicate spots and identical membranes was very good. Differences in gene expression between the two developmental stages for each gene were then determined by making all possible pair-wise comparisons of the four membranes. This analysis showed that 78 genes displayed increased expression (greater than 3 fold) in fetal over post-natal muscle, and that zero and one gene showed greater than 3 fold expression differences in fetal-fetal and postnatal-postnatal comparisons, respectively. Three genes were up-regulated in postnatal semitendinosus muscle, including alpha-actin, muscle alpha 7-integrin, and one muscle EST with no database match. These experiments show that cDNA macroarrays can identify differentially expressed genes in a cost-effective and rapid manner. Additional time points and Northern analyses will be required to confirm these predicted expression differences.

Key Words: Pig, Transcriptional profiling, Muscle

1401 Production of 17 cDNA libraries and successful EST sequencing of 10,124 clones from porcine female reproductive tissues. C.K. Tuggle*[1], J.A. Green[2], C. Fitzsimmons[1], R. Woods[2], R. Prather[2], S. Malchenko[3], M.B. Soares[3], C.A. Roberts[4], K. Pedretti[4], and T. Casavant[4], [1]*Iowa State University, Ames, IA,* [2]*University of Missouri-Columbia, Columbia, MO,* [3]*Pediatrics-University of Iowa, Iowa City, IA ,* [4]*ECE-University of Iowa, Iowa City, IA.*

Sequencing of cDNAs expressed in reproductive tissues will provide useful information in identifying specific genes involved in quantitative traits for pig reproduction. We have produced a total of 17 libraries from the following tissues: whole embryo (day 14, 20 and 45 of gestation); term placenta, anterior pituitary (day 0, 5 and 12 of estrus), hypothalamus (day 0, 5 and 12 of estrus) ovary (day 0, 5 and 12 of estrus) and uterus (day 12 and 14 of gestation). To determine the quality of these libraries, we have sequenced randomly selected clones from each library. A total of 10,124 sequences has been produced and will be submitted to Genbank (7,932 submitted to date). The average sequence read length across this dataset is 424 base pairs, with less than 22% shorter than 300 base pairs. As assessed by cluster analysis of 9,911 sequences, these data represent 6,655 different genes for a novelty rate of 67.2%. A sequence similarity analysis using the BLAST program and publicly available data within Genbank (ca. 53,660 porcine genes and ESTs as of December 20, 2000) indicates that 3,939 (59 %) of these clusters are unique relative to existing porcine Genbank entries (BLAST score <50). Further, over 900 (14%) have a significant match with human sequences (BLAST score >400). Thus, these sequences are highly useful for comparative mapping with the human genome. To facilitate selection of genes for such mapping, we have developed software to predict the pig cytogenetic location based on human cytogenetic and RH mapping data. Preliminary testing of the IMpRH panel indicates no technical problems; over 15 loci have been mapped using both the SCHP and the RH panel at this point. A WWW site has been established for public access to these sequences and the analysis data (http://pigest.genome.iastate.edu). In summary, this EST project has currently identified over 10,124 pig reproduction ESTs, representing over 3,939 new genes, toward a project goal of 20,000 submissions to Genbank.

Key Words: Pig, Expressed sequence tag, Reproduction

1402 Development of a physical map of bovine chromosome 4 that contains the gene responsible for Bovine Progressive Degenerative Myeloencephalopathy (PDME). Mheni Ben Abdallah*, Scott Speidel, Emily Oberg, and Sue DeNise, *University of Arizona, Tucson, AZ, USA.*

Bovine Progressive Degenerative Myeloencephalopathy (PDME) or Weaver Syndrome is recessively-inherited neurological disease found in the Brown Swiss breed. It has been reported that sires that are heterozygous for PDME had significantly higher genetic merit for milk and fat yield than normal homozygotes due to linkage with a major gene or a pleiotropic effect. To identify candidate genes for PDME, we intend to develop a bovine BAC-contig in the region containing the gene, and use comparative genomics to identify candidate genes and orient the contig. A recombination event in the region near BM1224 indicates that PDME is located telomeric of this microsatellite marker. Initial screening of a bovine BAC library (RPCI-42, BACPAC Resources) using BM1224 and the next mapped marker, BM6437, provided 5 positive BAC clones. We have begun constructing a BAC contig that physically spans the region by end- sequencing these clones and then shotgun sequencing the BACs that comprise the shortest tiling distance. Our rationale is to stablish BAC-based contigs by using the human map for orientation and walking toward the center of the contig. The homologous human region is 7p14-13 region. Bovine sequence from the BAC clones are aligned onto human BAC sequences in the region. New EST and STS sequences identified from the human map are amplified in bovine and mapped in the 12000 rad radiation-hybrid panel to determine relative location in the bovine. Using the combined strategy of the bovine physical map and comparative genomics, we hope to identify likely candidates for PDME that can be sequenced and studied in affected and normal animals.

Key Words: Dairy cattle, Genetic diseases, Physical mapping

1403 Comparative mapping and linkage analysis to identify the genetic region responsible for Bovine Spinal Muscular Atrophy (SMA). E.A. Oberg*[1], N. Vukasinovic[2], and S.K. DeNise[1], [1]*University of Arizona,* [2]*Utah State University.*

Spinal Muscular Atrophy (SMA) is a recessively-inherited neurological disease found in the Brown Swiss breed. Clinical signs of SMA can be observed as early as 3 to 4 weeks of age and result in death of the calf by 12 weeks. Bovine SMA has symptoms similar to several human diseases that have already been chromosomally localized; thus, a search for homologous diseases/symptoms between humans and cattle was performed in order to obtain potential candidate regions to begin a logically organized genome scan in affected families. A resource population of sixty carrier and non-carrier animals was identified through progeny testing and DNA samples collected. Depending on the size of

the candidate regions and the heterozygosity of the chosen markers, approximately 10 microsatellite markers per chromosome are used in the analysis. Microsatellite marker linkage analysis will be performed on the genotypes obtained from animals in the resource population to identify the putative regions where the disease gene resides. The ultimate goal is to create a genetically based test that can easily identify SMA carrier animals so as to eliminate high-risk matings.

Key Words: Gene Mapping, Dairy Cattle, Genetic Diseases

1404 Genetic analysis of candidate genes for Weaver Syndrome in Brown Swiss cattle. Scott Speidel*, Emily Oberg, Mheni Ben Abdallah, and Sue DeNise, *University of Arizona, Tucson, AZ/USA*.

Weaver Syndrome or Bovine Progressive Degenerative Myeloencephalopathy (PDME) is a recessively inherited neurological disease described in Brown Swiss Cattle that has been mapped to bovine chromosome 4 (BTA4). To locate the PDME causative gene, human and murine candidate loci have been identified that map to homologous regions on BTA4. The reelin gene (RELN) has been shown to control neuronal migration in the developing brain in mice; and mutations in the gene have shown similar symptoms to PDME. It maps to the long arm of human chromosome 7, which is homologous to BTA4. Primers developed from human studies were used to amplify a 159-bp fragment, which encompasses positions 1136-1295 of the human RELN sequence. After initial sequencing of direct PCR product, the fragment had a 90.06% homology score with human RELN. Mapping RELN using the 5,000 (5K) rad radiation hybrid panel placed the RELN gene outside the area of interest on BTA 4, telomeric to the microsatellite TGLA 116. A recently discovered recombination event narrowed our focus down to an 8 cM region on BTA 4. Human BAC clones in the homologous region of HSA 7 have been identified to contain genes, which would aid in fine mapping the region. Two EST's discovered on HSA 7 in the homologous human BAC will be mapped in cattle to provide a framework for the bovine BAC contig development. The first is annotated as a neuronal precursor to neuroepithelial cells (Accession #AA218986). The second EST has an unknown function and is labeled KIAA0087 gene product (Accession # D42038). These two gene products have been amplified in bovine genomic DNA. The next step is to sequence the product to verify homology, and then they will be mapped using the 12,000 rad radiation hybrid panel.

Key Words: Gene Mapping, Dairy Cattle, Genetic Diseases

1405 Evaluation of genetic relativeness and diversity in five goat breeds using randomly amplified polymorphic DNA (RAPD) analysis. J. Luo*[1], Z. G. Liu[2], G. S. Yang[2], and X. M. Zhen[3], [1]*E(Kika) de la Garza Institute for Goat Research, Langston University, Langston, OK,* [2]*Northwest Agricultural University, Yangling, Shaanxi, China,* [3]*Biotechnology Laboratory of Hubei Agricultural Science Academy, Wuhan, Hubei, China*.

The primary objective of this study was to apply randomly amplified polymorphic DNA technique to evaluate genetic relativeness and diversity among five goat breeds, namely Boer, Saanen, Angora, Shaannan white, and Guanzhong dairy goat. They were meat, dairy, fiber, and indigenous dual-purpose breed, respectively. The analysis was based on band-sharing frequency, genetic distance, and Shannon diversity index. Blood samples were collected from 17 Boer, 14 Saanen, 13 Angora, 11 Shaannan white, and 5 Guanzhong dairy goats via jagular venipuncture for each individual DNA isolation. DNA pools were formed for 7 individuals from each breed except 5 of Guanzhong dairy goats. A total of 20 arbitrary 10mer primers with GC content of either 40, 50, 60, or 70%, designed according to references and manufacturer's recommendations and synthesized by Dalian Biotechnology company of China thereafter, were employed in RAPD analysis. Seventeen of 20 primers detected an amplified pattern with 2 to 11 bands, 4 of which had amplified polymorphic fragments in each breed; the between-breed average band sharing frequency was from 0.91 to 0.98. Neils standard genetic distance was in the range of 0.02 to 0.09, and a dendrogram based on Neils distance from amplification patterns of four random primers in five goat breeds was constructed. As expected, the estimate of distance between Saanen and Guanzhong dairy goat was lowest among goat breeds. The Shannon diversity index of each goat breed was 0.54, 0.19, 0.12, 0.35 and 0.34, respectively, which indicated a large genetic diversity in Boer, Shaannan white, and Guanzhong dairy goat populations in the sampling region. It was confirmed that RAPD marker analysis can be used to determine genetic diversity and relativeness among and within goat breeds.

Key Words: RAPD, Genetic Diversity, Goat Breed

1406 PIT-1 gene sequencing and mutation analysis in sheep. E Bastos*[1], I Parmentier[2], I Santos[3], A Cravador[4], H Guedes-Pinto[1], and R Renaville[2], [1]*University of Tras-os-Montes e Alto Douro, Vila Real, Portugal,* [2]*Gembloux Agricultural University, Gembloux, Belgium,* [3]*National Zootechnical Station, Santarem, Portugal,* [4]*University of Algarve, Faro, Portugal*.

The pituitary-specific transcription factor Pit-1/GHF1 is a member of the POU domain family of regulatory proteins. It is required for activation of the growth hormone, prolactin, and thyroid stimulating-β genes in somatotrope, lactotrope, and thyrotrope cell types, respectively. In humans, mutations in Pit-1 have been associated with pituitary dwarfism and it has been proposed that this transcription factor can have a contribution in the pathogenesis of pituitary adenomas. In farm animals, there is a strong correlation between a mutation on exon 6 of this gene and milk production in bovine. The aims of the present study were to sequence the Pit-1 gene in sheep and optimize a methodology for the detection of mutations in the coding region. Specific primers were designed for the amplification of the sequence between two subsequent exons, based on the comparation of the gene sequence in human and the mRNA sequence in ovine. Five different clones were obtained, using the Invitrogen PCR cloning kit. The sequencing result was used to design primers near the exons in order to screen possible mutations, by the methodology BESS T/G scan. As the Pit-1 gene can play an important role in lactation and growth, the identification of mutations in this gene can contribute to the explanation of the differences in production and open new prospects for marker assisted selection.

Key Words: Pit-1, Sequence, Polymorphisms

1407 The pairwise relatedness between relatives conditional on genetic markers. Yuefu Liu*[1], Gerald Jansen[1], and Ching Lin[2], [1]*University of Guelph, Guelph, Canada,* [2]*Agriculture and Agri-Food Canada, Lennoxville, Canada*.

The development of molecular genotyping techniques makes it possible to analyze a quantitative trait on the basis of individual loci. With marker information, the classical theory of estimating the covariance between relatives has to be reformulated to improve the accuracy of estimation. This study derived an algorithm for computing the covariance between relatives conditional on a single marker or two flanking markers, and provided procedures for calculating the conditional relationship coefficients due to allelic effects, additive effects, dominance effects, and epistatic interactions including additive by additive, additive by dominance, dominance by additive and dominance by dominance. The relationship coefficients were computed based on conditional transmission probabilities of QTL alleles, which are, in turn, inferred from the transmission probabilities of marker alleles. An example data set with pedigree and marker genotypes of two linkage groups was used to demonstrate the procedure developed. Although this study dealt with two QTLs coupled with linked markers, the same principle can be easily extended to a multiple QTL situation.

Key Words: Covariances between relatives, Additive and non-additive relationship matrices, Genetic markers

1408 Marker assisted selection for first calving age at embryo level: a simulation study. A. J. M. Rosa*[1], R. B. Lobo[1], P. Bijma[2], M. Rutten[2], H. N. Oliveira[3], and J. van Arendonk[2], [1]*USP - Ribeirao Preto,SP/Brazil,* [2]*Wageningen Institute of Animal Science, Wageningen, Holland,* [3]*UNESP - Botucatu,SP/Brazil*.

Potential genetic benefits of marker assisted selection (MAS) at the embryo level to improve first calving age were evaluated by simulation of a MOET closed nucleus, with discrete generations, multi-stage selection (with or without embryo pre-selection) and QTL information. The QTLFCA were included in the selection index as a correlated trait with total substitution effect ranging from .00 to .95 of the additive genetic variance ($\sigma_a{}^2$). In the first simulated situation, MAS at 2 years of age resulted in higher response to QTLFCA corresponding to higher proportion of the $\sigma_a{}^2$ due to the increase in accuracy. Genetic response was increased to .68, 1.76 and 3.70% for QTLFCA with .02, .05 and .1 $\sigma_a{}^2$

reaching 55.76% for QTLFCA of .95 $\sigma_a{}^2$, while the accuracy increased from .513 and .543 to .981 and .955, respectively for sires and dams. Response to MAS, with QTLFCA effect corresponding to .1, .3 and .5 $\sigma_a{}^2$, at embryo level and different pre-selection rates was evaluated resulting in lower genetic gains when compared to MAS with one-stage selection due to the lower intensity at 2 years old (when more information is available: own performance for cows, full and half sibs) resulting in smaller total accuracy. Therefore, it is possible to obtain responses larger than 98% of the total response using embryo selection rates of .6, .3 and .2 for QTLFCA substitution effects of .1, .3 and .5 respectively. The production of 3 times more embryos allow to increase the genetic gain approximately 23%, due to the increase in selection intensity. When 13 of the 40 embryos were transferred, even markers with small effect (.02, .05 $\sigma_a{}^2$) could be used in MAS resulting in satisfactory response: 9.0% and 12.6%, respectively. Considering that most of the total cost in a MOET nucleus breeding program is due to maintenance of recipients and feeding growing animals until selection age the MAS utilization on embryo pre-selection can lead to a substantial improvement in the genetic response, even with markers with small substitution effect, without relevant increase in costs.

Key Words: Marker assisted selection, Embryo pre-selection, Beef cattle

1409 A heterogeneity model for estimating the number of QTL alleles in a segregating population.

Jean Xu* and Yang Da, *Department of Animal Science, University of Minnesota*.

A frequently observed phenomenon in data analysis for the detection of a quantitative trait locus in a segregating population is the genetic heterogeneity of a quantitative trait among different families. This heterogeneity could be due to the following situations: 1) some families do not have segregating alleles so that marker effects tend to be zero for those families, 2) families with segregating QTL alleles in fact have multiple QTL alleles, 3) different families have the same QTL effect but different marker-QTL recombination frequencies, and 4) different families have multiple QTL alleles and different marker-QTL recombination frequencies. Assuming situation 2), families with similar QTL effects can be placed in the same group using a cluster analysis and a heterogeneity model can be used to estimate the QTL effects of different family groups. Then, the number of QTL alleles can be estimated under the assumption of equal difference between two adjacent QTL alleles when QTL alleles are ordered according to the sizes of their effects. Let k = the number of QTL alleles, α_m = the average of QTL effects of different family groups, and α_d = the largest QTL distance obtained as the difference between the largest and smallest QTL effects. Then, the number of QTL alleles can be estimated as $k = [2 + (3\alpha_m/\alpha_d - 1)]/(3\alpha_m/\alpha_d - 1)$.

Key Words: Heterogeneity model, QTL alleles, segregating populaton

1410 Evidence of paternally imprinted QTL around *IGF2* in a Berkshire-Yorkshire cross.

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A paternally imprinted QTL with major effect on muscle mass and fat deposition near *IGF2* on SSC2 has been reported for crosses of the Large White with Pietrain and Wild Boar breeds. Our objective was to confirm the presence of an imprinted QTL on SSC2 in an F2 cross between the Berkshire and Yorkshire breeds. Data on average backfat (ABF) and loineye area (LEA) from 512 F2 animals and genotypic data for eight markers on SSC2 were used. Breed cross regression interval mapping was implemented using the following QTL models: Mendelian (additive and dominance effects), full imprinting (allowing for different maternal and paternal allele effects plus dominance), paternal imprinting (only paternal expression), and maternal imprinting (only maternal expression). Tests of each model against the no-QTL model and tests of full imprinting against the Mendelian, paternal and maternal imprinting models were used in a decision tree to determine presence and mode of inheritance of QTL. Chromosome-wise significance thresholds were determined by permutation. Tests of the Mendelian against the no-QTL model showed no evidence of QTL for ABF and LEA (P>0.05) but tests of the full imprinting against the no-QTL model detected a QTL for both traits at the same position on the distal end of SSC2p (P<.01 for LEA and P<.02 for ABF), near *IGF2*. Further testing for mode of inheritance showed that the full imprinting model was not significant over paternal imprinting (P>.10) but highly significant over maternal imprinting (P<.01), indicating evidence for exclusive paternal expression. The final analysis of paternal imprinting against the no QTL model was highly significant (P<.01). Favorable alleles originated from the Yorkshire and, when transmitted through the sire, reduced average backfat by .1 cm and increased LEA by 1.0 cm2, compared to Berkshire alleles. Evidence of these QTL, which were not detected based on a Mendelian model, confirms that the *IGF2* region is imprinted in pigs and harbors important QTL for muscularity and fat deposition. Supported by USDA CSREES # 00-52100-9610

Key Words: QTL detection, Imprinting, *IGF2*

1411 Combined interval mapping of QTL using mixed models in reference families with complex pedigrees and its application to chromosome 13 of swine.

X. L. Wu and C. Lee*, *Hallym University, Chuncheon, Korea*.

A method for mapping quantitative trait loci (QTL) was introduced incorporating information from various types of progeny and from multiple generations. Effects and positions of QTL were obtained by a joint estimation using the joint QTL-marker distribution of mixed populations or by a weighted least square method. Interval mapping was used to illustrate the theory based on a mixed model. Analysis of variance using multi-point analysis suggested that a Danish pig family carried a QTL on chromosome 13 which significantly affected slaughter weight (SWT) and average daily gain to slaughter (ADSG) (P<0.05), but QTL effect on backfat depth (BFDP) was inconsistently observed. This QTL was located between loci SW1898 and SW398 (ρ = 0.520.36). This was a region which flanked the PIT1 gene, an essential transcriptional regulatory factor of growth hormone, prolactin and thyrotropin β subunit. This result agreed with previous results that suggested a QTL for other growth traits at the estimated PIT1 position. Variance contributed by this QTL was 9.37% for SWT and 9.45 % for ADSG.

Key Words: Linkage Maps, Segregation Families, QTL

1412 PIT-1, a candidate gene for mass assisted selection in dairy bulls.

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Pit-1 is a protein important for pituitary cell differentiation and proliferation. It acts as a transactivator that regulates growth hormone and prolactin, TSH-b genes. In a previous study (Renaville et al. 1997, J. Dairy Sci. 80, 3431-3438), we have reported that the polymorphism associated to a transition A to G in the exon 6 of the gene could be associated to milk performances. The aim of this study was to search for eventual associations between Pit-1 polymorphism and dairy production traits by using a representative population of dairy sires. DNA was extracted from 1100 A.I. Holstein bulls using in A.I. scheme by Semex-Alliance (Guelph, Canada). A primer-specific PCR test has been developed to reveal the two alleles of Pit-1 gene which are called A and B. A mixed linear animal model including milk data of 2,400,000 lactations from 1,100,000 daughters of tested bulls was developed. The allelic frequencies were 53% and 47% for A and B respectively. Allelic frequencies were introduced as regression into the mixed linear animal model. The results showed an a value of +46,3 kg, + 1,9 kg and + 1,5 kg for milk, protein and fat yield, respectively. This a value represents the effect, on the trait, of the substitution of a B allele by a A allele. In conclusion, this study showed an significant relationship between the A allele of Pit-1 and dairy production traits of Holstein bulls. This gene could be considered as an interesting tools for marker assisted selection of dairy bulls. (Supported by the Belgian Ministry of Small Enterprises, Traders and Agriculture (grant 5983S), Semex-Alliance (Guelph, Canada) and Tomen Corp. (Tokyo, Japan))

Key Words: Pit-1, Marker, Lactation

1413 Composite interval mapping analysis of milk production and health traits in US Holsteins. A. B. Kurtz*, S. L. Rodriguez-Zas, H. A. Lewin, and D. W. Heyen, *University of Illinios at Urbana-Champaign, Urbana, IL.*

Identification of quantitative trait loci (QTLs) affecting milk, fat and protein yield, and somatic cell score was performed using composite interval mapping (CIM). Daughter yield deviations and predicted transmitting abilities from eight US Holstein families in a granddaughter design were analyzed. Sons were screened for 174 microsatellite markers distributed across 29 autosomes. Family sizes ranged from 72 to 203 sons and the average number of informative markers per chromosome was three. Interval mapping (IM) model was combined with significant ($P < 0.05$) regressors representing markers at least 10 cM from either side of the interval studied to account for other loci. Univariate and multivariate CIM analyses were implemented within each family using QTL Cartographer. Univariate genome-wise critical P-values were calculated using permutation tests and chromosome-wise critical P-values were calculated using a Bonferroni correction. On chromosome six, results from univariate and multivariate IM ($P < 0.05$) and CIM ($P < 0.025$) models identified a QTL located at 80 cM affecting protein yield in family two. Single-marker model findings suggested similar associations ($P < 0.025$) between protein yield and consecutive informative markers, BMS518 (69 cM) and ILSTS97 (80.3 cM). On chromosome 14, univariate CIM identified a QTL at 1.5 cM affecting milk yield in family four. This finding was supported by multivariate IM, which located a QTL ($P < 0.001$) at 0 cM in family four, and by multivariate CIM that located a QTL at 3.5 cM in family four ($P < 0.01$) and at 5.5 cM in family five ($P < 0.001$). The multivariate CIM approach identified a QTL at 26.3 cM on chromosome 14 for family four ($P < 0.001$), which is consistent with single marker results that identified a marker (BM1508) at 30.5 cM with a significant ($P < 0.05$) effect on somatic cell score. Our study confirmed that the comprehensive multivariate CIM model provided precise QTL estimates while accounting for QTL outside the interval under study.

Key Words: Quantitative Trait Loci, Maximum Likelihood, Permutation

1414 Interval mapping of quantitative trait loci affecting yield and health traits in dairy cattle. A. B. Kurtz*, S. L. Rodriguez-Zas, H. A. Lewin, and D. W. Heyen, *University of Illinois at Urbana-Champaign, Urbana, IL.*

Phenotypic records for milk, fat and protein yield, and somatic cell score were combined with genetic data from eight US Holstein families in a granddaughter design. The phenotypes were regressed on the conditional probabilities of inheriting a quantitative trait locus (QTL) allele at 1-cM intervals along the chromosome, using an interval mapping (IM) model. A total of 1065 sons were screened for 174 microsatellite markers across all autosomes. The number of informative markers per chromosome ranged from one to eight. A weighted least squares analysis was performed within and across families with weights equal to the variance of the trait. The impact of the use of two different phenotypic measures, daughter yield deviations (DYD) and predicting transmitting abilities (PTA), was compared. Genome-wise critical P-values were calculated using a Bonferroni correction to account for multiple testing. Small differences were observed between the estimates obtained for PTA and DYD. A significant effect ($P < 0.001$) for somatic cell score was detected in family four on chromosome 23 (3 cM). This autosome includes the bovine major histocompatibility complex. On chromosome three, significant effects for milk and protein yield were found. For family one, a potential QTL with significant effect ($P < 0.001$) on milk yield was located at 46 cM and supported by single marker findings. Both DYD and PTA models for protein yield estimated the same position (26 cM) using within and across family analyses. The estimates of the effects were similar, meeting suggestive significance levels ($P < 0.0001$). These results support those obtained with single marker models that detected effects of nominal significance ($P < 0.05$) on protein yield in the same family (five) for the two markers flanking the 16-cM interval containing the effect at 26 cM. The IM model provided an estimate of QTL position in proximity of the center of an interval that was not clearly resolved using single marker models.

Key Words: Least Squares, Protein , Somatic Cell Score

1415 Identification of genome positions associated to monthly production and health records using a single-marker model. S. L. Rodriguez-Zas*, B. R. Southey, H. A. Lewin, and D. W. Heyen, *University of Illinois, Urbana, IL.*

Many traits of agricultural importance such as monthly dairy records are measured repeatedly over time. Current methods of detection of quantitative trait loci (QTL) use single (average or cumulative) phenotypic measurements thereby ignoring the pattern that these traits exhibit. The objective was to identify genome positions expressed at specific stages of lactation or influencing the shape and scale of the lactation curve. A nonlinear single-marker model was used to describe monthly milk yield, fat and protein percentage, and somatic cell score (SCS) records from daughters of 475 sons across three Holstein families. A total of 46 markers along six chromosomes were fitted. Six percent of the hypothesis tests across families, traits, markers, and parameters were significant ($P<0.0001$) after adjustment for multiple tests. Some positions had significant effects on all parameters describing the lactation curve (chromosome 3, marker at 41 cM affecting the shape and scale of the SCS curve) meanwhile other markers were associated with a significant variation on a specific descriptor of the lactation curve (chromosome 6, marker at 64 cM, only affecting the shape of the protein curve). These results suggest the presence of putative QTL in the proximity of the significant positions that influence not only the magnitude but also the profile of the lactation curve. Identified positions can be incorporated into selection decisions to alter the persistency of production or the somatic cell score fluctuations during lactation.

Key Words: Lactation curve, Longitudinal data, Non-linear model

1416 Random regression models to estimate genetic growth parameters of young zebu beef cattle. E. S. Sakaguti*[1], R. L. Quaas[2], M. A. Silva[3], E. N. Martins[1], P. S. Lopes[4], and L. O. C. Silva[5], [1]*Universidade Estadual de Maringa, Maringa, Brazil,* [2]*Cornell University, Ithaca, New York,* [3]*Universidade Federal de Minas Gerais, Belo Horizonte, Brazil,* [4]*Universidade Federal de Vicosa, Vicosa, Brazil,* [5]*EMBRAPA - Gado de Corte, Campo Grande, Brazil.*

A total of 66,430 body weights measured at ages ranging from 365 to 650 days on 28,234 Tabapua beef cattle born from 1975 to 1997 and raised under Brazilian pasture conditions were used to evaluate the application of random regression models (RRM). Linear Legendre polynomials were used to describe random effects. Likelihood ratio test was used to compare the animal models. A simple repeatability model was inappropriate to evaluate the current data file because additive genetic and permanent environmental effects were dependent of the age of animal. Therefore the model that used continuous functions to describe these two effects had the most adequate fit. Growth rate estimated by the linear random regression coefficient had heritability equal 0.54 and genetic correlation with live weight at 507.5 days of age equal 0.47. The heritabilities for the live weight ranged from 0.3 to 0.4 within the age interval considered.

Key Words: Random regression, Genetic parameters, Beef cattle

1417 Inversion-free method for variance component estimation under the animal model. Jean Xu* and Yang Da, *Department of Animal Science, University of Minnesota.*

Estimation of variance components using maximum likelihood (ML) or restricted maximum likelihood estimation (REML) under the animal model requires the inversion of the coefficient matrix of the mixed model equations. Matrix inversion is computationally intensive and is a limiting factor for the number of animals that can be analyzed jointly. Under the assumption of constant relationships among family members and independent families, an inversion-free method for variance components is available to estimate three variance components. These three variance components can be additive, dominance, and residual variance components, or additive, permanent environment, and residual variance components. Formulae of this inversion-free method were developed for both ML and REML.

Key Words: Inversion free method, Variance component, Animal model

1418 Incorporating external information in multi-breed genetic evaluation. R. L. Quaas* and Z. Zhang, *Cornell University, Ithaca, NY.*

Some sires in multi-breed genetic evaluation have highly accurate genetic evaluations based on data not included in the multi-breed evaluation. In some cases, the external information is much greater than the internal. It is dissatisfying to breeders that sires rank differently, especially when the multiple breed evaluations are based on relatively limited data. Application of Bayesian principles with some simplifying assumptions provides a framework for incorporating external information. The external information is assumed to be contained in the animals' external Expected Progeny Differences (EPD) and their accuracies. Parameters are included to account for base differences. Effects of incorporating external EPD were investigated with data drawn from the American Simmental Association database. The data set included herds with both Simmental- and Angus-sired calves plus a sample of large Simmental herds. It contained 40680 records of calves sired by 1047 bulls. Data were analyzed with and without incorporating external information. The external information consisted of 64 American Angus Association (AAA) EPD and 51 Red Angus Association of America (RAAA) EPD. Average accuracies of external EPD were 0.91, 0.89, 0.87 and 0.82 for BWT, WWT, YWT and milk from AAA, and 0.78, 0.72, 0.70 and 0.64 for RAAA. Without external information rank correlations between internal EPD and AAA EPD were 0.49, 0.50, 0.47, 0.27 for BWT, WWT, YWT and milk. The corresponding values were 0.64,0.68, 0.59, 0.20 for RAAA bulls. Following incorporation of external information the rank correlation between internal EPD incorporating external information and external EPD from AAA were 0.87, 0.91, 0.90, 0.91 for BWT, WWT, YWT and milk. For RAAA sires the corresponding values were 0.91,0.93, 0.95, and 0.90. In contrast the changes for purebred Simmental sires were small; all rank correlations were $>$ .999. The procedure succeeded in ranking Angus bulls similarly to their external EPD but did not effect the ranking of Simmental sires.

Key Words: Expected Progeny Difference, Bayesian Analysis, Beef Cattle

1419 Bayesian linear mixed models employing the contaminated normal distribution: a simulation study in animal breeding. I. G. Pereira*, G. J. M. Rosa, and H. N. Oliveira, *UNESP - Botucatu, SP/Brazil.*

The Gaussian distribution is often assumed in applications of linear mixed model for quantitative traits in animal breeding. This assumption, however, makes inferences vulnerable to the presence of discrepant observations, such as those originated from preferential treatment or error in measurements. Thick-tailed distributions such as the Student-t process have been suggested for robust estimation. Here, the contaminated normal distribution is assumed for the residuals of linear mixed models in beef cattle evaluation. A simulation study is used to compare the performance of the Gaussian model and this robust alternative. Fifty data sets were simulated, considering two levels of fixed effects and five generations with 200 animals each, without selection. Different levels of contamination were studied. A Bayesian framework was adopted, and the Gibbs sampler and the Metropolis-Hastings algorithm were used to carry out the posterior analyses. Single chains were run for each model and data set, with 250,000 iterations, after burn-in. Except for data sets without contaminants, the robust model presented better estimates of residual variance. Estimates of heritability were similar for all models, but predict genetic values obtained by the robust model were closer to the real breeding values, as assessed by correlation analysis. The results suggest that the contaminated normal linear mixed model offers a flexible alternative for robust estimation in animal breeding.

Key Words: Contaminated normal distribution, Linear mixed models, MCMC

1420 Effect of reducing the frequency of milk recording on accuracy of genetic evaluation using a random regression model. J.J. Tosh[1], J.A.B. Robinson*[1], G.B. Jansen[1], and C.Y. Lin[2], [1]*Centre for Genetic Improvement of Livestock, University of Guelph, Ontario, Canada,* [2]*Dairy and Swine Research and Development Centre, Agriculture & Agri-Food Canada, Lennoxville, Quebec.*

Accuracy of national dairy cattle genetic evaluation programs that use a random regression model was studied to determine the effect of reducing monthly milk recording to less frequent schemes. A large dynamic population of dairy cattle was stochastically simulated. The population consisted of 1000 herds of 45 cows on average each and heifers, as well as young (n = 160) and proven (n = 40) bulls at an AI stud. Selection and mating mimicked a progeny test with weak to moderate selection on first lactation production (phenotype). All cows left the herd upon completion of their third lactation. Test day records for monthly farm visits were generated for milk, fat, and protein yield, and somatic cell score using a multiple-trait random regression model analogous to that used for genetic evaluation of dairy cattle in Canada. The simulation ran for a period of 20 years, and created more than 6.2 million records. Genetic evaluation was done using the records and industry software. Correlations between estimated breeding values and known true values (i.e., accuracies) were calculated. Accuracies for cows (n = 318680) and bulls (n = 590) were 0.773 and 0.940, 0.772 and 0.935, 0.758 and 0. 934, 0.669 and 0.912, and 0.720 and 0.943 for milk, fat, and protein yield, somatic cell score, and lactation persistency, respectively. As expected, accuracy increased for cows with more lactations, and bulls with more daughters (mean = 451; range 1 to 2991). Genetic evaluation was also done after editing the data set to randomly eliminate test days, mirroring reduced milk recording. Halving the frequency of milk recording to every second month did not notably affect accuracy, which decreased by no more than 0.02 for any trait in cows; in bulls the effect was even smaller. Results indicated an average of ten records per cow would suffice as well as twenty. Corresponding reductions in the cost of milk recording could be great. Conducting on-farm milk recording every second month rather than monthly appears justified when a random regression model is used for genetic evaluation of large dairy cattle populations.

Key Words: Dairy Cattle, Milk Recording, Test Day Model

1421 Bayesian analysis of multiple-linear and categorical traits with varying number of categories. D.H. Lee*[1], I. Misztal[1], J.K. Bertrand[1], and R. Rekaya[2], [1]*University of Georgia, Athens, Georgia,* [2]*University of Wisconsin, Madison, Wisconsin.*

The purpose of this study was to determine properties of a Bayesian method for joint analysis of multiple linear and categorical traits. Data sets with 10,630 records were simulated for to 3-trait linear models, with effects of sex, 50 contemporary groups, and 14,400 animals in 5 generations using BLUP selection. Selected traits were categorized with a binary and 4-categories. Bayesian analyses used Gibbs sampling. Residual variances for the categorical traits were assumed to be 1. The first threshold was set to 0, and the remaining thresholds were estimated. Sampling of the residual variances was from 1) the inverted Wishart (IW) distribution with rescaling (RS-IW), 2) IW distribution conditioned to residual variances of 1 for categorical traits by extending the methodology of Korsgaard et al. (1999, GSE 29:177) (RT-IW). Estimates were posterior means. Consistent estimates in models involving binary traits were obtained only after location parameters were reparameterized by weights resulting from conversion from samples of IW to RS-IW or RT-IW. This modification also increased the mixing rate several times in other models without affecting the estimates. No bias was observed with one categorical and several linear traits. In several models, biases were the same with RS-IW and RT-IW. In a model with three traits each with four categories, maximum biases were 0.01 for heritabilities and 0.14 for correlation. In a model with one binary and two linear traits, biases were 0.02 and 0.03 for heritabilities and correlations, respectively. In a model with two binary and one 4-category traits, these biases were 0.05 and 0.57 with RS-IW, and 0.04 and 0.30 with RT-IW. Analysis of multiple linear and categorical traits using a Bayesian method via Gibbs sampling is possible but biases can be expected especially for covariances and with binary traits. Differences when using samples of residual variance from RT-IW and RS-IW are small except with binary traits.

Key Words: Bayesian analysis, Threshold model, Reparameterization

1422 Analyses of sequential weights of Brazilian Zebu cattle using a multiple trait model by REML and Bayesian method. P. R. C. Nobre*[1], I. Misztal[1], S. Tsuruta[1], D. Lee[1], J. K. Bertrand[1], L. O. C. Silva[2], and P. S. Lopes[3], [1]*University of Georgia,* [2]*CNPGC/Embrapa, Brazil,* [3]*UFV, Brazil.*

The purpose of this study was to estimate parameters of birth weight and sequential weights of Nellore cattle. Data collected by the Brazilian Zebu Breeders Association consisted of 620,528 records collected from 1975 to 1999. Weights were recorded at 10-110 days, 102-202

days, 193-293 days, 283-383 days, 376-476 days, 467-567 days, 551-651 days and 633-733 days, respectively. Two sample data sets with all known ancestors with genetic ties were created. The number of animals from all herds was 18,889 and 16,161 from herds with no missing traits. Records preadjusted to fixed age were analyzed by a multiple trait model, which included the effects of contemporary group, class of age of dam, and direct, maternal and permanent environmental effects. Analyses by REML were conducted five traits at a time, and analyses by the Bayesian method using block Gibbs sampling involved all nine traits. For REML and the first data set, the range of estimated direct genetic correlations for each pair of traits was 0.43 to 0.99, with higher values between weights at higher ages. Direct heritability varied from 0.17 to 0.33, and was highest for weight at 551-651 days; however, maternal and permanent environmental variance decreased after an age of 193-293 days. Additive and residual estimated variance increased from birth weight through weight at 551-651 days, however maternal and permanent environmental variance decreased after age of 193-293 days. Heritabilities with the complete data set were slightly lower. With the Bayesian method, chain length of 50,000 was insufficient to obtain consistent maternal and permanent environment estimates, especially for weights over 476 days. This is most likely due to extreme correlations between these traits. The parameter estimates will be used to validate parameter estimates obtained from random regression models.

Key Words: Beef cattle , Covariance components, Longitudinal data

PSA Genetics

1423 Influence of genetics on phytate phosphorus utilization by chickens. T. N. Smith, S. E. Aggrey*, R. I. Bakalli, and G. M. Pesti, *University of Georgia*.

An experiment was conducted to determine whether there is a genetic basis for selection for phytate phosphorus (P) utilization in chickens. Fifty-eight Athens-Canadian random bred chickens were fed a phosphorus deficient diet and the phytate P levels in their excreta was determined by Near Infra-red Spectrophotometry. Five roosters categorized as High sire excreta phytate P (SEPP) (1.17±0.002) and Low SEPP (1.09±0.002) were selected to sire progeny. The SEPP values were significantly different (P<0.0001) between the two sire groups. One hundred and seventy chicks from Low SEPP and 180 chicks from the High SEPP were hatched and fed a P deficient diet (.53% P). The chicks were sacrificed at 16 d by carbon dioxide asphyxiation and body weight (BWT) was recorded. The left tibia were collected for ash determination on a fat-free basis. There was a negative correlation (r=-0.15; P=0.0053) between sire excreta phytate P and 16 d BWT. The correlation between SEPP and tibia ash was also negative but not significant (r=-0.01; P>0.05). Progeny from Low SEPP had higher BWT (152.7±1.5 g) than progeny from High SEPP (146.8±1.4 g) (P=0.0042). Similarly, progeny from Low SEPP had higher tibia ash (36.57±0.31%) than progeny from High SEPP (35.55±0.03%) (P=0.0187). This implies that sires that excrete low phytate P, that is, those that are better able to utilize phytate P, produced progeny that were significantly heavier at d 16 and had better bone mineralization than progeny sired by poor phytate P utilizers.

Key Words: Broilers, Phytase, Phosphorus

1424 Inheritance of Alkaline Phosphates in Local Iraqi Chicken and its association with Production. Ali Al-Hillali[1] and Khalid Al-Soudi*[2], [1]*Iraqi Atomic Energy Commission, Baghdad. Iraq,* [2]*Animal Production Department. Agriculture College, Baghdad University. Baghdad, Iraq*.

Ninety eight dams and twenty one sires representing the parent stock 0f local Iraqi cl,ickei, and their progeny (305 pullets) were typed for alkaline phosphates isozymes and activity in order to assess the effect of sex, age and genotype. Genetic analysis revealed three types of electrophoretic isozymes. namely fast, slow and a mixture of a fast and slow band. Gene ftequencies of the fast band were 0.41 and 0.39 and that for the slow band were 059 and 0.61 for dams and progeny flocks, respectively. Furthermore, age, sex and type of enzyme were found to have significant effects on enzyme activity. and birds of fast isozyme type had higher egg weight, lower age at sexual maturity and higher body weight at sexual maturity. Heritabilities of plasma alkaline phosphatase at different ages and economic traits ranged from moderate to high. Phenotypic, genotypic and environmental correlations between level of plasma alkaline phosphatase and growth rate and production characters indicated that the high activity of alkaline phosphatase was associated with higher growth rate at early stages, earlier sexual maturity and production of heavier but fewer eggs. Genetic and pheaotypic correlations among enzyme activities at three ages were positive and high and expected genetic response after one generation of individual selection for alkaline phosphntase activity leads to improved production characters.

Key Words: Alkaline phosphates, Electrophoresis, Enzymes

1425 Multisource Multitrait Selection Indices For Genetic Improvement In Poultry Breeding Programs For Laying Hens. 2. Construction And Evaluation Of Various Indices. A. A. Enab[1], N. Kolstad[2], and F.H. Abdou[1], [1]*Fac. Of Agric., Minufyia Univ., Shebin El-Kom, EGYPT,* [2]*Agricultural Univ. Of Norway*.

Records on 11689 pullets progeny of 326 sires and 1546 dams produced in two hatches of four strains of White Leghorn hens raised under Norwegian conditions were utilized to construct and evaluate general, reduced and restricted selection indices. Eight indices were constructed using five traits and three sources of information for each trait in different combinations. The studied traits were age at sexual maturity (SM); egg number up to 260 days of age (EN); egg weight (EW); body weight (BW) and egg specific gravity (SG). The sources of information used in different combinations for each trait were individual's own phenotypic value (OP) and its full (FS) and half sister's (HS) average. It was noticed that the female general index which included all of the five traits and all of the three sources of information was found to be the most efficient index (rTI = 0.76, 0.65, 0.69 and 0.61) in the four lines, respectively. The general index for males which included only two sources of information (FS&HS) for each of the five traits was found to be less efficient (rTI = 0.60, 0.54, 0.55 and 0.51) in the four lines, respectively. The restricted index for both EW&BW in line 1 was the lowest efficient index (rT I = 0.50). Expected and actual genetic progress (G) achieved in each trait was also maximum for female general index, for most traits in the four lines. It was noticed that the multisource index considering all of the five traits was superior to the multisource index involving only three or four traits. It was concluded that an index based on five traits and three sources of information could be applied to improve egg production and specific gravity traits.

Key Words: Genetic improvement, Multisource selection indices, Layers.

1426 A comparative genomic approach to identifying QTL's for growth in chickens. J. Funk-Keenan and G. F. Barbato, *The Pennsylvania State University, University Park, PA* .

It has long been surmised that different genes must influence different aspects of the growth curve. Unsurprisingly, different sets of QTLs influencing either early or late growth have been identified in mice and pigs. Using data from Vaughn et al (2000), we performed a modified candidate gene approach to identify QTLs influencing early growth in an F2 cross of chickens divergently selected for 14-day exponential growth rate (EGR). By aligning the mouse QTL's with the murine physical map; we targeted QTL's having syntenous genes in both the mouse and chicken genome. We selected the three to five microsatellite markers from the chicken linkage map based on their proximity to the locations of the murine syntenous genes in the chicken genome. Twenty-four microsatellite markers corresponding to six murine QTL's on six chicken chromosomes (1,3,4,5,6 and Z) were targeted for investigation. We chose the top and bottom 3% of chicks from the 14-day EGR distribution from the F2 cross. We then tested whether the microsatellite marker allele frequencies differed between the two tails of the distribution. Of the twenty-four microsatellite markers genotyped, eight markers (representing 5 putative QTL's) exhibited significantly different marker allele frequencies between birds having high or low 14-day EGR. The significant markers were located on chicken chromosomes 3,4,5,6 and Z. Notably, the putative QTL located on chromosom 4 is located at 148cM,