785 Biosecurity measures of spray-dried plasma protein in weanling pigs. J.M. Campbell*[1], B.S. Borg[1], L.E. Russell[1], J. Polo[1], and J. Pujols[2], [1]*APC, Inc., Ames, IA,* [2]*CRESA, Barcelona, Spain.*

The experimental objective was to evaluate safety of spray-dried plasma protein after oral administration in weanling pigs by monitoring clinical, serological, and performance results. Thirty-six pigs (13.6 kg body weight) were randomly assigned to dietary treatments consisting of control (soybean meal) or 8% plasma. Diets were formulated to contain 1.20% lysine due to continuous administration for 2 months after weaning. Individual body weights and feed intake were determined on d 0, 21, 42, and 63 post-weaning. Clinical observations were monitored daily. Blood samples were obtained on d -14, 0, 21, 42, and 63 post-weaning for serological testing. Average daily gain was improved ($P < 0.10$) from d 22-42 and 0-42 due to plasma consumption compared to control pigs. Average daily feed intake and feed efficiency tended towards ($P > 0.10$) improvement. During the experiment, no clinical signs were associated with oral plasma consumption; however, control pigs had mild clinical symptoms and one death. Serological results of all blood samples from control and plasma treated pigs were negative for antibody presence against the following viruses: porcine parvovirus (PPV), Aujeszky's disease virus (PRV), porcine respiratory and reproductive syndrome virus (PRRS), and bovine viral diarrhea virus (BVD). The plasma used in the study was devoid of titers for PRV, PRRS, and BVD, but positive for PPV. In summary, results indicate that oral administration of plasma had no adverse effects on clinical or performance parameters. Serological results indicate no transmission of disease from plasma for the period from a 14 to 63 kg pig.

Key Words: pigs, spray-dried plasma protein

ASAS/ADSA Breeding and Genetics: QTL Detection and Mapping

786 Fine scale mapping of QTL using of linkage and linkage disequilibrium. T.H.E. Meuwissen*[1] and M.E. Goddard[2,3], [1]*Institute fo Animal Science & Health, Lelystad, The Netherlands,* [2]*University of Melbourne, Melbourne, Australia,* [3]*Victoria Institute of Animal Science, Melbourne, Australia.*

Genome wide scans for QTL in livestock populations have revealed many QTL carrying chromosomal regions. However, the size of these regions is rather large: > 30cM. Linkage disequilibrium has proven useful for the fine mapping of mono-factorial diseases in humans. A Quantitative Trait Loci (QTL) mapping method is presented that combines the information from linkage analysis and linkage disequilibrium mapping. The method is based on predicting an Identity By Descent (IBD) probability matrix between all haplotypes of the animals at the putative QTL position. By using this IBD-matrix as a correlation matrix between haplotypes, the variance associated with the putative QTL and the likelihood of the data can be estimated using REML variance component estimation. This likelihood can be maximised over all putative QTL positions in order to find the maximum likelihood position of the QTL. The matrix of IBD probabilities is predicted using 1) the identities of marker alleles in the region surrounding the QTL (linkage disequilibrium information); 2) recombinations within the marker haplotypes that occurred in the genotyped and pedigreed animals (linkage analysis information). The information on the IBD probabilities comes from two parts of the pedigree: 1) say 100 early generations where no pedigree and no genotyping information is available (but effective population size was assumed known); 2) say 2-5 generations where pedigree and genotypes are available. Background genes are accounted for by including a polygenic term in the REML variance component estimation.

Key Words: fine scale mapping, linkage analysis, linkage disequilibrium

787 Evaluation of statistical models and permutation tests for detecting gametic imprinting in QTL scans. H. K. Lee[1], J. C. M. Dekkers*[2], R. L. Fernando[2], and M. F. Rothschild[2], [1]*National Livestock Research Institute, Korea,* [2]*Iowa State University, Ames, IA.*

Recently, De Koning et al. (PNAS, 2000) detected imprinted QTL in an F2 swine breed cross based on significance of paternal and maternal imprinting effects against a no-QTL model. They did, however, not test for deviations from Mendelian inheritance. Our objective was to develop and evaluate such tests. Breed cross regression interval mapping was implemented using the following QTL models: Mendelian (additive and dominance effects), full imprinting (separate maternal and paternal allele effects plus dominance), paternal imprinting (only paternal expression), and maternal imprinting. Tests of each model against the no-QTL model and tests of full imprinting against the Mendelian (Full/Mend), paternal and maternal imprinting models were used in a decision tree to determine presence and mode of inheritance of QTL. Chromosome-wise significance levels were derived by permutation (20,000 replicates). For the Full/Mend test, data were permutated by shuffling paternal against maternal coefficients within individual. Permutation test thresholds were compared to true values obtained from replicate (10,000) simulation of data under the null hypotheses (512 progeny from 8 F1 sires and 32 dams). The QTL was either fixed in alternate breeds or segregating at different frequencies (.7 and .3). The Full/Mend test had higher F-value significance thresholds than tests against the no-QTL model. For fixed QTL, thresholds for Full/Mend derived by permutation underestimated simulated 10, 5, and 1% chromosome-wise type I error rates, but by less than 1.5, 0.6, and 0.3%. Simulation thresholds were slightly more stringent for segregating QTL. As a result, the permutation test underestimated simulated type I error rates slightly more (<1%). Similar work is ongoing to validate tests of full against paternal or maternal imprinting. In conclusion, statistical models and permutation tests can be used to determine presence and mode of inheritance of QTL, although true type I error rates may deviate slightly from desired rates. Supported by USDA CSREES # 00-52100-9610.

Key Words: QTL detection, Imprinting, Permutation test

788 A Bayesian approach for constructing genetic maps when genotypes are miscoded. G. J. M. Rosa*[1,2], B. S. Yandell[2], and D. Gianola[2], [1]*UNESP - Botucatu, SP/Brazil,* [2]*UW - Madison, WI.*

The increased availability of information on genetic markers has created opportunities for understanding quantitative inheritance and for developing novel strategies for genetic improvement in agriculture, such as exploitation of quantitative trait loci (QTL). A QTL analysis relies on having accurate genetic marker maps. At present, however, statistical methods for map construction ignore the possibility that molecular data are read with error. Often, there is ambiguity about at least some genotypes, and ignoring this phenomenon can affect inferences adversely. Here, a Markov chain Monte Carlo Bayesian approach is presented for constructing genetic maps (gene ordering and genetic distances) when there is some random miscoding of genotypes. A probability of miscoding is incorporated in the calculation of recombination events, assuming Haldane's mapping function. Samples from the joint (conditional) posterior distributions of recombination rates and gene order are obtained with the Metropolis-Hastings algorithm. Missing marker genotypes are imputed from Bernoulli distributions. Backcross data sets were simulated, with 100 or 300 individuals, genotyped for 5 loci (including some missing data), and with recombination rates between adjacent loci ranging from .02 to .18. Miscoding probabilities were 0, 2, 4 and 5%. Analyses were conducted ignoring or contemplating miscoding in the model. Results indicate that unless there is certainty that genotypes are coded correctly, it may be safer to use our alternative, robust, procedure, as it provides more reliable inferences about genetic maps. An analysis of *Brassica napus* is presented to illustrate how the procedure works in practice.

Key Words: Genetic map, Miscoding genotype, Bayesian inference

789 The extention of mixed model equations to finite normal mixture models for marker assisted analysis of quantitative traits. Yuefu Liu*, *University of Guelph, Guelph, Canada.*

The marker-based analysis of quantitative traits, such as marker assisted genetic evaluation, is characterized by the mixture model since the QTL genotypes are not observable. It is, therefore, important to develop a general statistical procedure for mixture model analysis. In this study, a set of mixture model equations was derived based on the normal

mixture model and the EM algorithm to analyze the data with mixture distributions. The derived equations are a generalization of Henderson's mixed model equations for mixture models. The mixture model equations were applied to marker assisted genetic evaluation with different parameterizations of QTL effects. The sire-QTL-effect model and the founder-QTL-effect model were introduced to illustrate the utilization of the mixture model equations. The potential advantages of the mixture model equations for marker assisted genetic evaluation were discussed. Comparing with mixed model equations, the mixed effect mixture model equations are flexible in modeling and shows desirable properties in estimating QTL effects.

Key Words: Normal mixture model equations, EM algorithm, Marker assisted genetic evaluation

790 Parameter estimation of epistasis effects using orthogonal marker contrasts. Yang Da*, *Department of Animal Science, University of Minnesota*.

The epistasis effects of two QTLs can be detected and mapped through their linked markers. Assuming marker A is linked to QTL 1 and marker B is linked to QTL 2, the marker genotypic effects can be obtained from the following model, $\mathbf{y} = \mathbf{X}\beta + \mathbf{Zm} + \epsilon$, where $\mathbf{X}\beta$ represents fixed non-genetic effects, $\mathbf{Z}$ = nx9 model matrix, $\mathbf{m}$ = (AABB, AABb, AAbb, AaBB, AaBb, Aabb, aaBB, aaBb, aabb) = 9x1 column vector of the genotypic effects of two-marker genotypes, and ϵ = random residuals including recombination residuals of the QTL value. Then, a QTL effect can be tested using an orthogoal amrker contrast of $\mathbf{c}_i\mathbf{m}$, where $\mathbf{c}_i$ is one of the following eight contrasts: $\mathbf{c}_1$ = (1, 1, 1, 0, 0, 0, -1, -1, -1) = additive contrast for QTL 1, $\mathbf{c}_2$ = (-1/2, -1/2, -1/2, 1, 1, 1, -1/2, -1/2, -1/2) = dominance contrast for QTL 1, $\mathbf{c}_3$ = (1, 0, -1, 1, 0, -1, 1, 0, -1) = additive contrast for QTL 2, $\mathbf{c}_4$ = (-1/2, 1,-1/2, -1/2, 1, -1/2, -/2, 1, -1/2) = dominance contrast for QTL 1, $\mathbf{c}_5$ =(1, 0, -1, 0, 0, 0, -1, 0, 1) = additive additive contrast, $\mathbf{c}_6$ =(-1/2, 1, -1/2, 0, 0, 0, 1/2, -1, 1/2) = additive dominance contrast, $\mathbf{c}_7$ =(-1/2, 0, 1/2, 1, 0, -1, -1/2, 0, 1/2) = dominance additive contrast, $\mathbf{c}_8$ =(1/4, -1/2, 1/4, -1/2, 1, -1/2, 1/4, -1/2, 1/4) = dominance dominance contrast. Based on the above contrasts, analytical formulae are derived for estimating QTL locations and the size of each epistasis effect.

Key Words: Epistasis effect, Orthogonal marker contrast, QTL parameters

791 The effect of the number of loci on genetic evaluations in finite locus models. L.R. Totir*, R.L. Fernando, and S.A. Fernandez, *Iowa State University,Ames,IA*.

Several traits of interest are known to have low heritability, suggesting a non-additive gene action. Best linear unbiased prediction (BLUP) methods, although extremely efficient under additive gene action, have computational problems for large pedigrees under non-additive gene action. Multibreed data further increases the complexity of this problem. Finite locus models have been investigated recently as an alternative to infinitesimal models for genetic evaluation. A finite locus model can easily accommodate non-additive gene action even for multibreed data. Given a finite locus model, Markov Chain Monte Carlo (MCMC) methods can be used to estimate the posterior mean of genotypic values. Successful application of MCMC methods for genetic evaluation depends, among other factors, on the number of loci assumed in the model. In order to investigate the effect of the number of loci on genetic evaluations obtained with finite locus models, purebred as well as multibreed data were simulated for a 20-locus model. For a small pedigree, genetic evaluations obtained by best linear prediction (BLP) were compared to those from 1,2, and 3-locus models. For BLP evaluations, the required parameters are the first and second moments of the joint distribution of the genotypic and phenotypic values. These moments were calculated from the gene frequencies and genotypic effects used in the simulation. For finite locus evaluations, the required parameters are the gene frequencies and effects for each locus in the analysis model. These were defined such that they yield the same first and second moments as the 20 locus model. For the 1, 2, and 3-locus models, exact posterior means were calculated using SALP, a segregation and linkage analysis computer program. As the number of loci increased, the finite locus genetic evaluations were closer to the BLP evaluations. Evaluations from the 2-locus model provided a good approximation to those from BLP. The improvement brought by the use of 3 loci was limited. So far only up to 3-locus models have been considered, which is the upper limit for SALP. An MCMC sampler, known as ESIP will be used to investigate models with more than 3 loci in order to find the model that yields robust results and is still computationally efficient.

Key Words: Finite locus model, Markov Chain Monte Carlo, Best linear unbiased prediction

792 Accuracy of marker assisted selection using a mixed model method. Mathew A Chrystal*, Yang Da, Leslie B Hansen, and Antony J Seykora, *Department of Animal Science, University of Minnesota*.

The accuracy of marker assisted selection (MAS) was evaluated using a mixed model method and simulated data with known true QTL effects and marker-QTL distances. Correlation between the predicted marker effects and the true QTL values (r_1) was compared with the correlation between the phenotypic value and the true QTL values (r_2) for heritabilities (h^2) ranging 5% 30%. Also, the frequency of the favorable QTL allele in the selected population based on MAS is compared to that based on phenotypic selection for heritabilities ranging 5% 30% and for percentage of selected individuals (PSI) ranging 5% 30%. The correlation between the predicted marker effects and the true QTL values were substantially higher than that between the phenotypic and true QTL values, particularly when heritability is low. For example, for h^2 = 30%, r_1 = 0.726, r_2 = 0.548; for h^2 = 5%, r_1 = 0.718, r_2 = 0.224. Furthermore, MAS results in higher frequency of the favorable QTL allele in the selected population than phenotypic selection. Let p_1 = frequency of individuals with the favorable QTL allele using MAS, and p_2 = frequency of individuals with the favorable QTL allele using phenotypic selection. For the same PSI value of 5%, p_1 = 0.996 and p_2 = 0.961 if h^2 = 30%, and p_1 = 0.973 and p_2 = 0.728 if h^2 = 5%. For the same heritability of 5%, p_1 = 0.973 and p_2 = 0.728 if PSI = 5%, and p_1 = 0.948 and p_2 = 0.630 if PSI = 30%. In summary, MAS is most helpful when phenotypic selection is least effective, i.e., when heritability is low and the percentage of selected individuals is high.

Key Words: Marker assisted seletion, QTL, Mixed model

793 Improved resolution of the porcine-human comparative genetic map. G. A. Rohrer*, S. C. Fahrenkrug, E. M. Campbell, J. W. Keele, and B. A. Freking, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, USA*.

The last comprehensive porcine genetic map published by the MARC contained 1,042 loci and spanned an estimated 98.6% of the genome. Unfortunately, development of a high resolution human-swine comparative map was not possible as only 46 loci were associated with protein coding sequences (genes). Since that time, most marker development at MARC have been focused on increasing the number of genes represented on the porcine genetic map. Many of these markers were developed by screening porcine genomic libraries for specific genes and then identifying microsatellite markers within the identified clones. Our recent research emphasis has been to map genetic markers associated with porcine expressed sequence tagged (EST) sequences developed at MARC. Some ESTs were mapped using informative microsatellite markers identified within the sequences. Most ESTs have been mapped by identification of single nucleotide polymorphism (SNP) markers. In total more than 200 gene associated loci have been genotyped across the MARC reference population since the last published map, increasing the number of comparative anchor loci to nearly 250. Based on these gene assignments inferences about the conservation of synteny and gene order during the evolution of man and pigs can begin to be developed. In general, the predicted chromosome location of a gene has agreed with bi-directional ZOO-FISH results. The degree of conserved gene order varies widely across different chromosomes. In particular, SSC X appears to have an identical gene order as HSA X, while the gene orders within the conserved syntenic segments of SSC 5 and HSA 12 are quite different. Some ESTs have not mapped to the predicted porcine chromosomes which may be caused by incorrect determination of the human orthologue or previously undetected chromosomal rearrangements. Our efforts in mapping porcine genes has increased the marker density of the porcine genetic map as well as significantly improved the resolution of the porcine-human comparative map. The improved comparative map facilitates use of the human map to select positional candidate genes in QTL studies.

Key Words: Pig, Gene mapping, Comparative map

794 Effects of the Porcine Melanocortin 4 Receptor gene on growth rate, feed conversion and carcass composition of pigs sired by PIC337 or PIC408 boars. S. Jungst*[1], E. Wilson[1], M. Rothschild[2], C. Booher[1], T. Pastor[1], B. Fields[1], and G. Plastow[1], [1]*PIC USA Franklin, KY,* [2]*Iowa State University, Ames.*

Camborough 22 and 24 sows were inseminated with semen from PIC337 (N=9) or PIC408 (N=10) boars to produce pigs to examine the effects of the Melanocortin 4 Receptor (*MC4R*) gene. Boars were randomly selected within line and their *MC4R* genotypes were unknown. Fifteen pigs were allotted to pens with either 13.4 or 8.4 m^2 of floor space during the growing - finishing period. Pigs were allotted to pens so each sire line and *MC4R* genotype was represented in the finisher pens. A total of 718 pigs from 102 litters were started on test. Objectives were to: 1) estimate *MC4R* additive effects, 2) determine if the marker effect was the same in each sire line and 3) determine if the gene effects were different for the two floor space allowances. SAS PROC MIXED was used to complete the analyses. Fixed effects for sire line, dam line, sire line x dam line, *MC4R* genotype, floor space and sex were included in all models. Boars nested within sire line and sows nested within dam line were included as random effects. Average daily gain, feed intake and feed conversion were adjusted for on-test weight. Carcass traits were adjusted for carcass weight. Sire line x *MC4R* and floor space x *MC4R* interactions were not detected for any trait (P>.10). The *MC4R* genotype that reduced fat thickness was deemed the favorable genotype. *MC4R* additive effects were -13 g/d for average daily gain (P<.10), -.07 kg/d for feed intake (P<.05), -.6 mm for real-time backfat (P<.05) and .7 mm for real-time loin depth (P<.10). Additive effects were .11 kg (P<.05), .09 kg (P<.05), .04 kg (P<.10) and -.06 kg (P<.10) for ham, loin, shoulder and belly weight, respectively. *MC4R* additive effects were -.5 mm for carcass backfat thickness and .2% for primal percentage (P<.05). These results confirm and extend the initial findings of Kim *et al.*(2000 Mamm. Gen. 10 p131-135). This gene can be used to produce leaner and more efficient pigs.

Key Words: Pigs, *MC4R*, Growth

795 Genetic relationships between insulin-like growth factor-I and performance traits in two lines of purebred swine. K.G. Lahti*[1], K. Bunter[2], J. Mercer[1], and S. Clearkin[3], [1]*Bell Farms, Wahpeton, North Dakota,* [2]*University of New England, Armidale, NSW,* [3]*PrimeGRO Pty. Ltd., Thebarton, South Australia.*

Insulin-like growth factor-I (IGF-I) measured in the blood of weanling piglets is a suggested predictor of feed efficiency and carcass performance. Blood card samples were collected for IGF-I analysis in the nursery of a breeding company nucleus from 606 Landrace (LA) and 600 Large White (LW) piglets at 27 to 36 days of age. Samples were from 377 boars and 829 gilts, weaned at an average of 17 days. IGF-I assays were performed by PrimeGRO Pty. Ltd. Some pre-selection of boars for castration and feeder pigs for sale occurred before pigs began performance testing at 90 to 101 days of age. Valid daily feed intakes were measured on 124 boars with Osborne Industries Feed Intake Recording Equipment (FIRE feeders) and used to calculate feed conversion ratios (FCR). Pigs completed testing at 160-183 days of age, with weights and real-time ultrasound measurements of last-rib backfat (BF) and muscle depth collected on all pigs to compute gains and lean tissue growth rate (LTGR). Data were analyzed using SAS PROC GLM and ASREML. For LA and LW, univariate estimates of heritability were respectively, .09(.04) and .13(.04) for FCR, .44(.12) and .59(.11) for IGF-I, .38(.02) and .37(.02) for BF, and .26(.02) and .24 (.02) for LTGR. Genetic correlations obtained with bivariate analyses of IGF-I with BF were .49(.15) and .54(.14), with FCR were .50(.38) and .59(.40), and with LTGR were -.25(.18) and -.20(.18) for LA and LW. The large, positive genetic correlations between IGF-I and BF indicate that animals with high IGF-I at weaning are more likely to be fatter at finishing. This is consistent with the strong positive genetic correlations found between IGF-I and FCR, and moderate negative genetic correlations between IGF-I and LTGR. Despite low numbers of feed records, results correspond in size and magnitude with previous studies. IGF-I may be a useful tool for early selection of boars and for obtaining increased accuracy of breeding values for feed intake and efficiency.

Key Words: Insulin-like Growth Factor-I, Swine

796 Interval mapping detection of QTL influencing lactation patterns in Holstein cattle. S. L. Rodriguez-Zas*, B. R. Southey, H. A. Lewin, and D. W. Heyen, *University of Illinois, Urbana, IL.*

Quantitative trait loci (QTL) affecting the shape and scale of the lactation curve of production and health indicators in dairy cattle were located using microsatellite marker data. Information on 46 genetic markers distributed across bovine chromosomes 3, 6, 7, 14, 21 and 22 was available from a total of 475 sons in three Holstein families. This information was combined with protein and somatic cell score (SCS) monthly records following a granddaughter design. A nonlinear mixed effects model was used to portrait the lactation curve patterns. The probability of receiving either QTL allele from the grandsire was computed at 1cM intervals using an interval-mapping approach. Estimates of the putative QTL effect were obtained at the most likely position and significance values were adjusted for multiple testing. The implemented approach uncovered QTL associated with considerable variation of the lactation patterns. Some positions were associated with significant variation of various descriptors of the lactation curve. For example, a QTL located 69-79 cM on chromosome 6 was associated with variation on both the shape and scale of the protein lactation curve in one family. Other QTL exerted their effect on one or two curve parameters, such as a QTL located 61 to 71 cM on chromosome 3. Detected QTL can be used in marker assisted selection schemes to modify lactation patterns for more efficient production. This innovative approach enhances the understanding on the genetic control of the different aspects of the lactation curve and can be applied to other longitudinal traits.

Key Words: Monthly records, Non-linear model, Repeated measurements

797 A genome scan to identify quantitative trait loci affecting economically important traits in an elite US Holstein population. M.S. Ashwell*, C.P. Van Tassell, and T.S. Sonstegard, *USDA, ARS Gene Evaluation and Mapping Laboratory.*

Quantitative trait loci (QTL) affecting economically important traits were studied for eight Dairy Bull DNA Repository large US Holstein grandsire families using the granddaughter design. A total of 155 microsatellite markers located throughout the bovine genome were selected for the scan. Effects of marker alleles were analyzed for 22 traits including traits for milk production, somatic cell score, productive life, conformation and calving ease. Permutation tests were used to calculate empirical trait-wise error rates. A trait-wise critical value of P = 0.1 was used to determine significance. Twelve chromosomes (BTA) had significant marker-trait associations identified from within- and across-family analyses. Two chromosomes (BTA6 and 14) had significant effects on milk composition traits and BTA7 had a significant effect on somatic cell score. Significant effects on conformation traits, especially rump angle, were found on 8 bovine chromosomes (BTA4, 9, 12, 14, 16, 18, 22 and 27). The QTL identified in this genome scan may be useful for marker-assisted selection to increase the rate of genetic improvement on traits such as disease resistance and conformation traits associated with fitness while maintaining or accelerating genetic improvement for production. Before incorporation in marker-assisted selection programs, these potential QTL must be validated in other populations or newer generations of the original families. Validation studies are underway for QTL affecting dairy form and protein percentage on BTA27 and 6, respectively.

Key Words: Quantitative Trait Loci, Conformation traits, Dairy cattle

798 Detection of quantitative trait loci for functional and conformation traits in a whole genome scan in dairy cattle. H Thomsen*[1], N Reinsch[2], M Schwerin[3], G Erhardt[4], and E Kalm[2], [1]*Department of Animal Science, Iowa State University, Ames,* [2]*Institut fuer Tierzucht und Tierhaltung, D-24098 Kiel,* [3]*Forschungsinstitut fuer die Biologie landwirtschaftlicher Nutztiere, D-18196 Dummerstorf,* [4]*Institut fuer Tierzucht und Haustiergenetik, D-35390 Giessen.*

A granddaughter design, consisting of 16 German Holstein grandsires and 872 sons, was used to locate quantitative trait loci (QTL) that affect functional and conformation traits in dairy cattle. The data was part of the granddaughter design of the joint German QTL research effort of AI organisations, breeding organisations and several institutions of animal breeding. Grandsires and sons were genotyped for 247 microsatellite

markers, 8 SSCP polymorphisms, 4 protein polymorphisms, and 5 erythrocyte antigen loci covering the whole genome. De-regressed breeding values were available for 29 traits, including 20 conformation, 2 fertility, 4 birth, 2 workability, and 1 longevity trait. After determining the most likely marker haplotypes for all grandsires based on the genotypes of their sons, multi-marker regression analysis of the trait data was used to scan the genome for QTL. Chromosome-wise and experiment-wise significance thresholds were determined by permutation test. The test statistic exceeded the genome-wise significance threshold with a type I error of less then 10% for the following traits and chromosomes: rump width on chromosome 1; feet and legs, foot angle, teat placement, udder, and udder depth on chromosome 6; calving difficulties on chromosome 8; teat length on chromosome 13; rate of stillbirth on chromosome 18, and milking speed and temperament on chromosome 29. All QTL on chromosome 6, that exceeded the genome-wise significance threshold, were located around 88 cM. QTL for rump width on chromosome 1 may have an effect on calving difficulties. QTL for udder traits on chromosome 6 and 13 may affect somatic cell score and mastitis resistance. If there are no unfavorable correlations with other economic traits, marker assisted selection using markers associated with these QTL can be applied.

Key Words: whole genome scan, quantitative trait loci, conformation and functional traits

ASAS/ADSA Growth and Development: Conjugated Linoleic Acid (CLA) in Milk Production, Growth, and Health

799 Conjugated linoleic acid (CLA) and lipid metabolism in lactating cows. D. E. Bauman*[1], L. H. Baumgard, B. A. Corl, E. Matitashvili, D. G. Peterson, J. W. Perfield II, and M. A. Madron, [1]*Cornell University*.

The uniqueness of CLA in ruminant fat relates to biohydrogenation of unsaturated fatty acids by rumen bacteria. The major CLA isomer is *cis*-9, *trans*-11 and recent work with animal models has established that this isomer is anticarcinogenic when provided as a natural component of food. Although some CLA is of rumen origin, the major source in lactating cows is endogenous synthesis via Δ^9-desaturase from *trans*-11 C18:1, another biohydrogenation intermediate. Thus, fat content of CLA is a function of rumen outflow of CLA and *trans*-11 C18:1, plus tissue activity of Δ^9-desaturase. Investigations of these aspects have identified dietary manipulations, regulatory processes and animal differences that can impact the CLA content of ruminant fat. Under certain conditions, the initial step in linoleic acid biohydrogenation is altered so the isomerization results in production of *trans*-10, *cis*-12 CLA. This CLA isomer affects lipid metabolism during growth and lactation. Across a range of diets a curvilinear relationship exists between the increase in milk fat content of *trans*-10, *cis*-12 CLA and the reduction in milk fat yield. Thus, rumen biohydrogenation can result in the formation of *trans*-10, *cis*-12 CLA, and possibly other unique biohydrogenation intermediates that are potent inhibitors of milk fat synthesis; we refer to this as the "biohydrogenation theory" of milk fat depression. *Trans*-10, *cis*-12 CLA is a potent inhibitor of milk fat synthesis with 3.5 g/d (0.016% dietary dry matter) resulting in a 25% reduction. Yields of all milk fatty acids are reduced, but effects are especially pronounced on those fatty acids originating from de novo synthesis and Δ^9-desaturase activity. Although specific mechanisms are not well defined, recent investigations indicate that exogenous *trans*-10, *cis*-12 CLA causes substantial reductions in mammary tissue mRNA abundance for key enzymes associated with de novo fatty acid synthesis, uptake of preformed fatty acids, fatty acid transport and esterification, and plasticity of milk fat.

Key Words: CLA, fat, milk fat

800 The use of rumen-protected conjugated linoleic acid to reduce milk fat percentage in lactating dairy cattle. M.A. Sippel*[1], J.P. Cant[1], and R. Spratt[2], [1]*University of Guelph, Guelph, Ontario,* [2]*Agribrands Purina Canada, Woodstock, Ontario*.

The use of conjugated linoleic acid (CLA) has been shown to reduce milk fat secretion in dairy cattle. A rumen-protected source of CLA is required for commercial feed applications. To test the ability of different rumen-protected CLA sources to induce milk fat depression, four Holstein cows (avg. 77 DIM, 40.9 kg/d milk, parity 2.25) were randomly assigned to treatments in a 4 x 4 Latin Square design. Treatments were a control diet (0 g CLA/d), CaCLA salt providing 50 g CLA/d, GRAS-coated providing 50 g CLA/d, and liquid CLA oil providing 50 g CLA/d. Periods were 3 weeks of adjustment and 1 week of sampling. The CaCLA and liquid CLA oil caused 23.4 and 23.9% depressions in milk fat content, respectively, without affecting milk, protein or lactose yields, or dry matter intake. In a second experiment, CaCLA was fed to provide 0, 25, 50, 75 or 200 g CLA/d. Ten Holstein cows were divided into two 5 x 5 Latin Squares by parity number; square 1 multiparous (avg. 110 DIM, milk yield 35.9kg/d, parity 2.3), square two primiparous (avg. 103 DIM, milk yield 29.3kg/d). Periods were 3 weeks of adjustment, followed by 1 week of sampling. Milk fat content averaged 3.48, 2.84, 2.53, 2.47 and 2.19 % as CaCLA intake increased from 0 to 200 g CLA/d. Milk yield was reduced by 2.19 kg/d on the 200g CLA/d treatment relative to the control. There was no effect of treatment on dry matter intakes or milk protein and lactose percentages. There was no significant difference in response due to parity. Feeding the CaCLA salt source to provide 25 to 75 g CLA/d was effective in decreasing milk fat percentage without affecting other production variables.

Key Words: conjugated linoleic acid, milk fat, rumen protection

801 Milk fat synthesis in dairy cows is progressively reduced by increasing amounts of *trans*-10, *cis*-12 conjugated linoleic acid (CLA). Lance H. Baumgard*, Jodi K. Sangster, and Dale E. Bauman, *Cornell University*.

CLA supplements containing a variety of isomers reduce milk fat yield in a number of species. We have recently identified *trans*-10, *cis*-12 as the CLA isomer responsible for inhibiting milk fat synthesis in dairy cows (Baumgard et al. Am. J. Phys. 278:R179). Our objectives were to establish a dose-response relationship between *trans*-10, *cis*-12 CLA and milk fat synthesis, and relate effects on milk fatty acid composition to the potential mechanism of action. Multiparous Holstein cows in late lactation were used in a 4 x 4 Latin square design where treatments consisted of four doses of *trans*-10, *cis*-12 CLA: 1) 0.0 g/d, 2) 3.5 g/d, 3) 7.0 g/d, and 4) 14.0 g/d. Over the 5d treatment intervals doses were continuously infused into the abomasum as a convenient experimental means to avoid possible alterations by rumen microbes. Milk fat yield was decreased 25, 33, and 50%, and milk fat concentration was reduced 24, 37 and 46% when cows received 3.5, 7.0 and 14.0 g/d of *trans*-10, *cis*-12 CLA, respectively. Feed intake, milk yield and milk protein content and yield were unaffected by treatment. Milk fat content of *trans*-10, *cis*-12 CLA averaged < 0.1, 1.5, 3.2 and 7.0 mg/g from cows receiving 0.0, 3.5, 7.0 and 14.0 g/d of *trans*-10, *cis*-12 CLA. Comparison of milk fat composition and synthesis revealed that reductions were most extensive for *de novo* synthesized fatty acids (short and medium chain) when cows received the two highest doses, but at the low dose (3.5 g/d) decreases in *de novo* synthesized fatty acids and preformed fatty acids were similar. Changes in milk fatty acid composition also indicated that Δ^9-desaturase was inhibited at the two high doses of *trans*-10, *cis*-12 CLA, but relatively unaffected by the low dose. Overall, results indicate that *trans*-10, *cis*-12 CLA is a potent inhibitor of milk fat synthesis. A hyperbolic dose response curve was observed and even the low dose of *trans*-10, *cis*-12 CLA (0.016% of dietary intake) dramatically inhibited milk fat synthesis (25%).

Key Words: CLA

802 Mechanisms for conjugated linoleic acid-mediated reduction in fat deposition. Harry Mersmann*, *USDA/ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine*.

Potential mechanisms for the decreased fat deposition observed after oral administration of conjugated linoleic acids (CLAs) to mice, rats, hamsters, humans, and pigs will be reviewed. Most mechanisms are based on experiments with rodents or rodent-derived cells. In intact mice, there is an increased metabolic rate, but not in rats or sows. There is a decreased respiratory quotient in mice and rats, suggesting increased fat oxidation. Bovine milk-fat synthesis is decreased. Rat adipocyte size is smaller, but cell number is unchanged. In mice, there is increased adipocyte apoptosis. In 3T3-L1 preadipocytes, a clonal cell line derived from rodents, CLAs decrease proliferation. Differentiation