

Blood samples were drawn from the jugular vein 1-2 wk before the expected day of parturition as well as on days 0, 7, 14, and 21 after parturition and plasma concentrations of serum amyloid A (SAA) and haptoglobin (Hp) were measured by ELISA. Concentrations of SAA and Hp in plasma of control cows increased on the day of parturition as well as at 7 days postpartum and declined thereafter. Cows infused with 212 g/d of L-glutamine had greater concentrations of SAA and lower concentrations of Hp on days 7 ($P<0.05$) and 21 ($P<0.05$) postpartum compared to controls. Cows infused with 106 g/d of L-glutamine also had greater concentrations of SAA in plasma on day 21 ($P<0.05$) postpartum compared to controls. In conclusion our data indicate that parenteral administration of glutamine modulates acute phase response in dairy cows immediately after parturition. Further research is warranted to understand the mechanism by which glutamine affects immune response in transition dairy cows.

Key Words: Glutamine, Acute Phase Response, Dairy Cows

M13 Evaluation of two simple tests for the detection of cryptosporidium parvum oocysts in calf feces. L. Trotz-Williams¹, S. Martin¹, D. Martin², T. Duffield¹, K. Leslie^{*1}, D. Nydam³, and A. Peregrine⁴, ¹University of Guelph, Guelph, ON, Canada, ²Ontario Ministry of Health and Long-Term Care, Etobicoke, ON, Canada, ³Cornell University, Ithaca, NY, ⁴University of Guelph, Guelph, ON, Canada.

A sucrose wet mount test developed at the Ontario Veterinary College (OVC) for the detection of *Cryptosporidium parvum* oocysts in calf feces, and a lateral immunochromatography test (BioX Diagnostics, Jemelle, Belgium) for *C. parvum* in feces, were evaluated in terms of epidemiological sensitivity and

specificity, cost, and utility. Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) targeting the *Cryptosporidium* oocyst wall protein (COWP) gene locus was used as the gold standard for evaluation of the tests.

One hundred and ninety-nine fecal samples from naturally infected Holstein calves under 21 days old were used for the study. All samples were analyzed in a blinded manner. Cohen's kappa statistic of agreement (κ) between the OVC sucrose wet mount test and COWP PCR-RFLP was 0.82, showing good agreement, and the sensitivity and specificity of the OVC sucrose wet mount test were 88.6% and 93.8%, respectively. The sensitivity and specificity of the lateral immunochromatography test were 78.3% and 93.3% respectively, and agreement between this test and PCR-RFLP was also good ($\kappa=0.73$). There was also substantial agreement between the OVC sucrose wet mount test and the lateral immunochromatography test ($\kappa=0.84$). Both tests were inexpensive and easy to use. However, the lateral immunochromatography test was faster and simpler to perform than the sucrose wet mount test, and was generally more user-friendly. Both of these tests provide practitioners and researchers with cheap, quick and accurate methods of detecting *C. parvum* infection in young calves.

Acknowledgements: Thanks to Grazyna Adamska-Jarecka for diagnostic support, and to Dr. Frances Jamieson and Billy Yu, Laboratories Branch of the Ontario Ministry of Health and Long-Term Care, for collaborative assistance with this research. The lateral immunochromatography test kits used for this project were kindly supplied by BioX Diagnostics.

This study was funded by the Ontario Ministry of Agriculture and Food, the National Sciences and Engineering Research Council of Canada, Dairy Farmers of Ontario and Dairy Farmers of Canada.

Key Words: *Cryptosporidium parvum*, Diagnostic tests, Calves

Breeding and Genetics I

M14 Estimatives of heritability to time in different distances of race in Quarter Horse. S. Oliveira, M. Correa, and M. Mota*, *Unesp, Botucatu, SP, Brazil*.

The Quarter Horse are known by their versatility, they can be used for conformation, work and race modalities. This way, this work objected to estimate the heritabilities to race time in distances of 301m (2,770 observations), 320m (2,039), 365m (3,739) and 402m (5,366), in Quarter horse races. The components of variance needed to the obtation of the heritabilities were estimated by MTGSAM program, under animal model. The Gibbs sampling considered 2,005,000 samples, excluding the first 5,000 and after these, one in each 1,000 samples were stored for inference, totalizing 2,000 samples for studying. The linear model used to information analyse included the random effects of animal and permanent environment and the fixed effects of age (2, 3 and 4 years-old or more), sex (male and female) and race. The estimatives of heritability were, in average, 0.26, 0.15, 0.40 and 0.35, respectively to the distances of 301, 320, 365 and 402m. The biggest density intermission "a posteriori", with 90% of probability, following the previous presentation order were 0.25 to 0.34, 0.09 to 0.33, 0.33 to 0.58 and 0.34 to 0.38. The results indicate that longer distances present bigger heritability and, in consequence, they shall possible good replies to the masal selection.

Key Words: Heritability, Quarter horse, Race

M15 Estimatives of repeatability to time in different distances of race in Quarter horse. M. Correa, S. Oliveira, and M. Mota*, *Unesp, Botucatu, SP, Brazil*.

The Quarter horse are admired by their versatility, they can be used for conformation, work and race modalities. Based on this, this work objected to estimate the repeatabilities to race time in distances of 301m (2,770 observations), 320m

(2,039), 365m (3,739) and 402m (5,366) in Quarter horse races. The components of variance needed to obtain the repeatabilities were estimated by MTGSAM program, under the animal model. The Gibbs sampling considered 2,005,000 samples, excluding the first 5,000 and after them, one in each 1,000 samples were stored for inference, totalizing 2,000 samples for studying. The linear model used to information analyse included the random effects of animal and permanent environment and the fixed effects of age (2, 3 and 4 years-old or more), sex (male and female) and race. The setimatives of repeatability were, for 301m, in average, 0.36, with 90% of probability of the information appear between 0.29 and 0.36, for 320m, 0.27, with the informatinos between 0.19 and 0.45, for 365m, 0.48, between 0.43 and 0.61, and for 402m, 0.68, between 0.65 and 0.68. The estimated results suggest that for longer distances, just a result of performance can be enough to rule out the animal, while for shorter distances, more than one result of performance shall be done.

Key Words: Repeatability, Quarter horse, Race

M16 Simulation model of cashmere goat production system: I. A dynamic herd simulation model & breeding strategies for fiber quality. B. Tseveenjav^{*1,2}, D. J. Garrick¹, S. LeValley¹, and Z. Yondon², ¹Colorado State University, Fort Collins, ²Cashmere Goat Association of Mongolia, Ulaanbaatar, Mongolia.

Fiber diameter is the most important factor determining the value per unit weight of cashmere fleece. The need to consider fiber diameter in selection programs in addition to cashmere fleece weight has increased in the last decade, because fiber diameter in many Cashmere populations has deteriorated as a result of intensive selection on fleece weight. The objective of this study was to quantify the superiority of an economic selection index applied to simultaneously decrease fiber diameter and increase cashmere fleece weight in indigenous Cashmere goats. Throughout computer modeling the effects of different breeding

schemes applied to a hierarchical integrated cashmere production system, involving purebred goats, were investigated. The study simulated cashmere production based on traditional cashmere herd management practices in Mongolia and utilized the published genetic parameters with heritabilities of .28 for cashmere fleece weight (CFWT), .10 for live weight (LWT), .32 for fiber diameter (FD) and .23 for fiber length FL. Simulation program of cashmere production was developed using AWK and JAVA programming languages. Using multi-trait animal model, individual animal breeding values were predicted and deterministic procedures were applied to develop a model for cashmere production system. Using different selection criteria and their combinations of FD, CFWT, FL and LWT effects were tested for 20 years and the accuracy of prediction and economic responses each of breeding schemes in long term were compared. Genetic trends for each economically relevant trait were calculated for 20 years. Using economic selection indexes likely to be the most profitable in an integrated cashmere production system. The main conclusion of this study were (i) new estimated breeding values (EBV) should be developed for FD, a major determinant of cashmere price, for every breeding does and bucks in those indigenous goats (ii) economic selection indexes could simultaneously improve genetically antagonistic two economically relevant traits- FD and CFWT.

Key Words: Economic Selection Index, Cashmere Goats, Fiber Characteristics

M17 Bayesian inference of the genetic trend for litter size in the Ripollesa breed of sheep in Spain. J. Casellas*, G. Caja, A. Ferret, and J. Piedrafita, *Universitat Autònoma de Barcelona, Bellaterra, Spain.*

The Ripollesa is an autochthonous sheep breed managed under semi-intensive conditions for the production of light lambs (24 kg BW at slaughter) in Catalonia (Spain). The ewes used (n = 365) came from a flock naturally mated for fall lambing (Christmas harvesting) and selected under a phenotypic breeding program for litter size since 19 yr ago. Replacement ewes and rams were chosen from the progeny of the most prolific ewes which have had at least three recorded lambings. A total of 1,590 litter sizes (single, 54.0%; twins, 44.2%; triplets, 1.8%; and quadruplets, 0.1%) were recorded from 1986 to 2004 for which annual litter size ranged between 1.23 and 1.70 lambs/ewe, showing a positive phenotypic trend. The dataset was analyzed using the Bayesian threshold methodology. The model included the additive genetic effect, as well as age of the ewe, year of lambing and ewe's permanent environmental effect, as the non-genetic sources of variation. Response to selection was analyzed as the change in average breeding value (ABV) per year of the replacement ewe-lambs and as the ABV of all ewes present in the flock. Estimated heritability was 0.13, with the highest posterior density at 95% ranging between 0.05 and 0.37. The ABV values was 0.01 in 1986, and peaked to 0.39 (1997) and 0.29 (2004) residual variance units (RVU) for ewe-lambs and ewes, respectively. A significant increase of multiple lambing (≥ 2 lambs) was observed with a mode of approximately 10 percentage units. Litter size also varied according to year of lambing (estimates ranging from 0 to 0.85 RVU, for 1986 and 2000, respectively) although there was no significant trend. Despite the small population size, our results show that litter size was effectively improved through phenotypic selection, with a low amount of triplets and quadruplets.

Acknowledgements: Conveni DARP-ANCRU-UAB

Key Words: Bayesian Inference, Litter Size, Ripollesa Breed

M18 Estimation of genetic parameters for body weight in Rambouillet and Targhee lambs. J. M. Rumph*, K. C. Davis, P. G. Hatfield, and R. W. Kott, *Montana State University, Bozeman.*

Weights were analyzed using records from 8055 Rambouillet and 6604 Targhee lambs collected at Montana State University's Red Bluff Research Ranch from 1970 through 2004. Records included birth weight (BW), turnout weight (TW) when lambs were turned out to summer range at an average age of 50 d, and weaning weight (WW) at an average age of 125 d. All traits were analyzed with fixed effects of year, line, age of dam, number born, and sex. BW and TW were analyzed in a multiple trait model. Analyses of BW with WW and TW with WW

could not reach convergence, so WW was analyzed in a single trait analysis. Estimates of heritability for BW were 0.35 and 0.42 for Rambouillet and Targhee, respectively. Estimates of heritability for TW were 0.14 and 0.13, respectively. The direct genetic correlation between BW and TW was estimated to be 0.32 and 0.64, respectively. Estimates of heritability for WW were 0.02 and 0.46, respectively. For unknown reasons, there are distinct differences in estimates of genetic parameters for these two breeds in the Montana State University flock.

Key Words: Weaning Weight, Birth Weight, Sheep

M19 Genetic polymorphism of β -Lactoglobulin gene in Iranian Karakul sheep by DNA test. A. Javadmanesh*, M. R. Nassiry, H. Ghiasi, A. Samei, and A. Norouzy, *University of Mashhad, Mashhad, Khorasan, Iran.*

β -Lactoglobulin is the major milk whey protein in ruminants. Studies have shown that this protein is polymorphic in many breeds and the allele B is associated with higher milk yield than allele A. This is the result of single base pair substitution in the β -Lactoglobulin gene which also rises to an RsaI restriction fragment length polymorphism (RFLP). The genotype BB of β -Lactoglobulin seems to be associated with higher milk yield; on the other hand genotypes AA and AB seem to be superior in protein and casein content of milk. The aim of the present study was to identify two genetic variants (A and B) and three genotypes (AA, AB and BB) of β -Lactoglobulin gene in Iranian Karakul sheep by PCR-RFLP. 83 blood samples were supplied from Karakul sheep station located in Sarakhs, Khorasan. Total DNA was extracted from 100 μ L blood according to Boom R. et al. (1989). 25 ng DNA was used to amplification in a total volume of 25 μ L. Samples were amplified for 34 cycles at the following steps: denaturation at 94°C for 50 sec, annealing at 59°C for 30 sec and extension at 72°C for 40 sec. Primers amplified a 301 bp fragment from the exon II of the ovine β -Lactoglobulin gene. PCR products were recognized by electrophoresis on 1% agarose gel stained with ethidium bromide. 5 μ L of each PCR products were incubated for 5 h at 37°C with 4 units of RsaI enzyme. Digestion products were separated by electrophoresis on 8% polyacrylamid gel and visualized with silver staining. The frequency of genotypes in co-dominant locus was analyzed by PopGen32 software ver 1.31. The allelic frequencies were 88% and 12% for A and B respectively. The genotype distributions were 76%, 24% and 0% for AA, AB and BB. G test did not confirm the H-W equilibrium. According to Vltaka et al. (2002) BB genotype of ovine β -Lactoglobulin not found in Russian Karakul sheep so this experiment confirmed the previous study. Since the allele B is more important in milk production and allele A is more responsible for protein content of milk and cheese quality, we can result that these Karakul sheep are suitable for cheese production.

Key Words: β -Lactoglobulin, Polymorphism, Karakul

M20 Comparison of maturity rate for bull daughters in the United States and Canada. H. D. Norman¹, J. R. Wright^{*1}, R. L. Powell¹, P. M. VanRaden¹, and F. Miglior^{2,3}, ¹*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD,* ²*Agriculture and Agri-Food Canada - Dairy and Swine Research and Development Centre, Lennoxville, QC, Canada,* ³*Canadian Dairy Network, Guelph, ON, Canada.*

Maturity rate of bull daughters in the United States and Canada were compared based on parity-specific predicted transmitting abilities (PTA) of sires. For US daughters, 305-d milk records for Holsteins with first-parity calving dates between 1960 and 1998 were used to calculate sire PTA based on first-parity daughter records (PTA₁), first- and second-parity daughter records (PTA_{1,2}), and first- through third-parity daughter records (PTA_{1,3}). Sire evaluations with contributions only from second- (PTA₂) or third-parity (PTA₃) daughter records were approximated by weighting based on numbers of daughters with first, second, and third parities. For Canadian daughters, parity-specific estimated breeding values (EBV₁, EBV₂, and EBV₃) of sires were those derived for November 2004 national evaluations. Correlations among parity-specific sire evaluations were calculated within birth year of bulls. Correlations for 101 bulls with ≥ 500 daughters in both countries were 0.87 between PTA₁ and PTA₂, 0.86 be-

tween PTA_1 and PTA_3 , and 0.97 between PTA_2 and PTA_3 for US daughters; corresponding correlations were 0.90, 0.88, and 0.98 for Canadian daughters. Correlations between PTA_2 - PTA_1 and EBV_2 - EBV_1 were 0.63 for 599 bulls with ≥ 20 daughters, 0.82 for 311 bulls with ≥ 100 daughters, and 0.89 for bulls with ≥ 500 daughters in both countries; corresponding correlations were 0.54, 0.76, and 0.85 for differences between third- and first-parity sire evaluations. Corresponding correlations for differences between third- and second-parity sire evaluations were considerably lower at 0.14, 0.27, and 0.52, probably because differences between second- and third-parity evaluations were small. Differences in maturity rate of bull daughters were reasonably consistent across countries. Modeling genetic evaluations to account for those differences would increase accuracy for bulls with daughters that deviate substantially from population mean.

Key Words: Maturity Rate, Milk Yield, Parity

M21 Factors affecting heifer fertility in US Holsteins. M. Kuhn* and J. Hutchison, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Heifer breedings from January 2003 to October 2004 were used to investigate factors affecting heifer fertility. There were 331,469 breedings on 220,624 Holstein heifers. Only artificial inseminations were analyzed. Age at breeding was required to be between 8 months and 3 years. Only 0.33% of breedings occurred at ages > 2.5 years; 98.2% of all breedings were at ages < 2 years. The dependent variable for analysis was 0 (no conception) or 1 (conception). A heifer's last recorded service was considered a success. Breedings were included only if there was at least 2 months for a repeated service to be reported. The linear model for analysis included the fixed effects of herd, year, month, and age-at-breeding, and the covariates of parent average predicted breeding value for milk, SCS, and daughter pregnancy rate (DPR). The overall arithmetic mean conception rate was 0.64 with a 0.48 standard deviation. The only factors that did not have a significant effect on heifer conception were parent average breeding values for milk and SCS. Year accounted for the most variation in heifer conception rate. Year 2004 had a 6% higher conception rate than 2003. This may be a realistic difference between years or it may indicate that additional editing needs to be investigated. Perhaps 2 months is not an adequate amount of time to wait for a reported service in the case of heifers. Month of breeding accounted for the second largest amount of variation with January and February having the poorest conception rates and September and October having the best. Parent average breeding value for DPR accounted for the third most variation with conception rate increasing as DPR increased. Selection on DPR will improve fertility in heifers as well. Age at breeding accounted for more variation than herd; conception rates increased with age. Further research will investigate appropriate edits for heifer breedings and also compare linear model results to results from logistic and probit models.

Key Words: Heifer Bbreedings, Daughter Pregnancy Rate, Fertility

M22 Effectiveness of estimating individual herd heritabilities using regression techniques. C. D. Dechow*¹ and H. D. Norman², ¹*Penn State University, University Park*, ²*Animal Improvement Programs Laboratory, Beltsville, MD.*

The objectives of this study were to estimate heritabilities for individual herds using regression techniques and determine if incorporating individual herd heritability would increase accuracy of genetic evaluations. First lactation mature equivalent milk (MEM) was obtained from 64,350 first lactation cows in 45 herds with 500 or more cows. Individual herd heritability was estimated using REML (h^2_{RML}), daughter-dam regression (h^2_{DD}), and daughter-sire estimated breeding value regression (h^2_{DS}). Regression coefficients were estimated for each herd with the MIXED procedure of SAS. The model included fixed year-season and age at calving effects, either dam MEM (DM) or sire estimated breeding value (SEBV) as a random covariable, and random error. Animal models were also used to estimate heritability for each herd with ASREML. Heritability from

daughter-dam regression was twice the regression of MEM on DM. Twice the regression of MEM on SEBV was multiplied by genetic variance of the US Holstein population and divided by herd phenotypic variance to estimate h^2_{DS} . Sex averaged heritability (h^2_{SA}) was the mean of h^2_{DD} and h^2_{DS} . Heritability estimates were constrained to range from 0.25 to 0.35 and were used to standardize records to a constant genetic variance across herds. Estimated breeding values (EBV) were generated with the adjusted records, which were weighted by the ratio of base error variance to herd error variance. Average individual herd heritability estimates ranged from 0.28 for h^2_{RML} to 0.31 for h^2_{DD} . Correlations of h^2_{RML} with h^2_{DD} , h^2_{DS} , and h^2_{SA} were 0.53, 0.42 and 0.61, respectively. Correlations among sire EBV generated with the adjusted records and official sire PTAM from November 2004 national genetic evaluations ranged from 0.007 to 0.012 higher than the correlation when using non-adjusted records. Correlations between yield deviations and parent averages were lower (range -0.026 to -0.002) after adjustment for heritability, except adjustments for h^2_{DD} (0.006 higher). Individual herd heritability estimates may improve accuracy of national genetic evaluations, or help identify progeny test herds with poor parent identification.

Key Words: Heritability, Yield, Accuracy

M23 Accounting for heterogeneous variances in multi-trait evaluation of Jersey type traits. N. Gengler¹, G. Wiggins², L. Thornton*², J. Wright², and T. Druet¹, ¹*National Fund for Scientific Research, B-1000, Brussels, Belgium*, ²*Animal Improvement Programs Laboratory, Beltsville, MD.*

The multi-trait genetic evaluation system for type traits was modified to estimate adjustments for heterogeneous variance (HV) simultaneously with estimated breeding values (EBV) for final score and 14 linear traits. Heterogeneity, estimated for transformed traits, was regressed within parity toward the population variance means by fitting a model with fixed effects of mean final score for herd, size of contemporary group, appraisal month, and appraisal year-season and a random effect for interaction between herd and appraisal date. Method R was used to estimate variances for the heterogeneity model in each EBV iteration. Data was from the 766,725 appraisals included in the official November 2004 evaluation. Parent averages were calculated from evaluations with recent appraisals removed. Annual trends for cow EBV were lower with HV adjustment than for unadjusted EBV for all traits. The SD of Mendelian sampling (evaluation minus mean of parent evaluations) declined less over time for HV adjusted than for unadjusted evaluations. The slope at year 2000 of Mendelian-sampling SD from HV adjusted evaluations was only 22% for udder depth to 48% for teat length of the slope of that for unadjusted evaluations. This adjustment for HV was implemented in May 2001 and should make selection decisions more accurate by using these proposed integrated HV adjustments.

Key Words: Heterogeneous Variance Adjustment, Type Evaluation

M24 Comparison of lifetime relative net income with and without adjustment for opportunity cost. E. Yook, R. Pearson*, and B. Cassell, *Virginia Polytechnic Institute and State University, Blacksburg.*

The purpose of this study was to compare relationship of lifetime relative net income (RNI) and RNI adjusted for opportunity cost (RNIOC) for 6 herd life opportunity lengths based on 305d or complete milk records. RNI and RNIOC were calculated on 70,167 cows born in 1988, 1990, and 1992 from IN, FL, NC, TX, VA, and VT using the milk pricing assumed in Net Merit calculations and based on either 305d or complete lactation records for periods of herd life from 5 to 10 years. Opportunity cost was estimated for each cow by multiplying her total days of productive life in herd times the mean herd RNI divided by mean herd days of productive life. RNIOC for 10yr herd life opportunity estimated from complete lactations was regressed on 5, 6, 7, 8, and 9yr herd life opportunity ($\beta = 1.2, 1.13, 1.07, 1.04, 1.01$; $R^2 = .74, .87, .94, .98, \text{ and } .99$). Similarly regressions predicting RNI for 10 yr herd life opportunity were run ($\beta = 1.45, 1.26, 1.14, 1.06, 1.02$; $R^2 = .72, .86, .94, .98, \text{ and } .99$). RNIOC for 10yr herd life opportunity estimated from complete lactations was regressed on 5 to 10 yr herd life opportunity based on 305d lactations ($\beta = 1.12, 1.05, 1.01, .97,$

.95, and .94; $R^2 = .62, .73, .79, .82, .84, \text{ and } .84$). Similar regressions for RNI 10yr opportunity based on 305d lactations were calculated ($\beta = 1.57, 1.38, 1.26, 1.19, 1.15, \text{ and } 1.13$; $R^2 = .66, .79, .87, .91, .93, \text{ and } .93$). Shorter herd life opportunities underestimate 10yr opportunities much less for RNIOC than for RNI. However, R^2 for RNI and RNIOC using complete lactations are nearly identical. Use of 305d records to predict RNIOC 10yr opportunity have substantially lower R^2 than for the same comparison with RNI. The simple regression of RNIOC 10yr opportunity on the PTA in the merit index was less for all of the PTA than for the similar simple regressions RNI on the PTA. The largest reduction (75%) was for PTA DPR and the smallest was for PTA FAT. Use of RNIOC based on complete lactations is recommended.

Key Words: Lifetime Net Income, Relative Net Income, Herd Life Opportunity

M25 A stochastic simulation study on validation of an approximate multitrait model for prediction of breeding values. J. Lassen^{*1,2}, M. K. Sorensen¹, and P. Madsen¹, ¹Danish Institute of Agricultural Sciences, Foulum, Denmark, ²The Royal Veterinary and Agricultural University, Frederiksberg, Denmark.

The aim of this study was to develop and validate an approximate multitrait model for prediction of breeding values. A population resembling Danish Holstein with 300,000 cows and a herd size of 100 was simulated. The simulation included the following eight traits: milk yield, mastitis, SCS, days open, non return rate, udder depth and dairy character. A 15 year breeding scheme with selection on an index of milk, mastitis and udder depth was simulated. The simulation was repeated 35 times.

For each replicate, univariate BLUP was performed to estimate fixed and predict random effects. Records were adjusted for all effects except the animal effect using the BLUP solutions. Variance components were estimated on preadjusted data using a simplified model with a mean, an animal effect and a residual. Two multivariate BLUP were conducted: 1) on preadjusted data using the estimated variance components and the simplified model. 2) on raw data using the true variance components and the complete model. Correlations between true and predicted breeding values were computed for both sets of BLUP breeding values.

The variance components estimated on preadjusted data were in close agreement with the true parameters and never with more than 10 % difference in absolute value. The correlations between true and predicted breeding values were from 1 to 8 % lower for BLUP based on preadjusted data compared to the BLUP from raw data. The largest differences were for traits with low heritability.

A full multitrait BLUP would be the optimal method, but computer power is a limiting factor when handling the large number of traits in the total merit index of today. Therefore, using multivariate BLUP on subsets of the traits and then combine the resulting breeding values using approximate methods to the total merit index is of interest.

Key Words: Multitrait Model, Variance Components, Simulation Study

M26 Genetic correlations between reproductive traits in swine. S.-H. Oh^{*} and M. T. See, *North Carolina State University, Raleigh.*

The objective of this study was to estimate genetic parameters among reproductive traits in swine. Traits analyzed included weaning to first service interval (WTE), litter birth weight (LBW), number of pigs born alive (NBA), number of pigs weaned (NW), and adjusted 21 day litter weight (LWT). The National Swine Registry provided reproductive records of Duroc sows. Numbers of records were 3,850 for WTE, LBW and NBA and 3,836 for NW and LWT. Genetic parameters were estimated using a five-trait model and the MTDFREML software program. The statistical model included fixed effects of contemporary group, farm and parity and random effects of animal and permanent environment. For

LBW and LWT, NBA and number of pigs at transfer (NAT), respectively, were added as a fixed effect in the model. Heritability estimates for WTE, LBW, NBA, NW and LWT were 0.09, 0.14, 0.10, 0.15, 0.17, respectively. Weaning to first service interval was genetically correlated with LBW (.13) but not NBA (-0.02), NW (0.01) or LWT (0.01). Genetic correlations between LBW and NBA, NW, and LWT were -0.06, 0.07 and 0.39, respectively, and are lower than previously reported estimates. Genetic correlations between NBA and NW and LWT were 0.86 and 0.65, respectively. The genetic correlation between NW and LWT was 0.81. These results indicate that in the Duroc breed response to genetic selection for these traits is possible and that when including WTE and LBW in genetic evaluations a multiple trait model with other reproductive traits should be considered.

Key Words: Pigs, Reproduction, Genetic Parameters

M27 Heritability of daily feed intake in swine. S.-H. Oh^{*1}, W. O. Herring², M. Culbertson², and M. T. See¹, ¹North Carolina State University, Raleigh, ²Smithfield Premium Genetics, Roanoke Rapids, NC.

Estimates of genetic parameters for daily feed intake in swine were obtained using a random regression model. Daily feed intake for 581 boars was recorded at two farms using feed intake recording equipment (FIRE[®]) resulting in 31,689 non-zero feed intake observations. Feed intake records were collected between 70 and 204 days of age. Before analysis, each individual's complete feed intake record was evaluated for outliers by plotting feed intake by day and testing each feed intake observation with the Cook's D test statistic and studentized residuals. After removal of outliers 30,358 feed intake observations were utilized in the subsequent analysis. The statistical model included herd-year-season as a fixed effect, and litter, animal and permanent environmental effects were included as random effects with levels of each effect of 249, 26, 2,236 and 529, respectively. The REMLF90 program was used to analyze the data with third degree Legendre polynomial and assumed homogeneous error variances. The mean additive genetic, litter and permanent environmental variances across all ages were 107.32, 0.23, and 0.11, respectively. Residual variance was 0.848. As a result, heritabilities of daily feed intake were estimated that ranged from 0.10 to 0.99 between 1 and 210 days of age. Between 90 and 150 days of age where most observations were collected, additive genetic, litter and permanent environment variances ranged from 0.120 to 0.708, 0.047 to 0.234, and 0.065 to 0.085, respectively. Heritability of daily feed intake ranged from 0.11 to 0.42 between 90 and 150 days of age where most intake observations were collected. To better understand the observed residual variance further study is needed to evaluate the effect of heterogeneous error variance in these data.

Key Words: Pigs, Feed Intake, Heritability

M28 Genetic parameter estimates for insulin-like growth factor I concentration and growth traits in Angus beef cattle divergently selected for serum insulin-like growth factor I concentration. M. Davis^{*}, *The Ohio State University, Columbus.*

Divergent selection for serum insulin-like growth factor I (IGF-I) concentration was initiated in 1989 using 100 spring-calving cows (50 high line and 50 low line) and in 1990 using 100 fall-calving cows (50 high line and 50 low line) at the Eastern Agricultural Research Station. The objective of the present study was to update genetic parameter estimates published in 1997 (J. Anim. Sci. 75:317-324) using data from the IGF-I selection experiment. The updated analysis included 1,761 calves produced from 1989 through 2000. Data were analyzed by multiple-trait, derivative-free, restricted maximum likelihood (MTDFREML) methods. Estimates of direct heritability for serum IGF-I concentration measured at d 28, 42, and 56 of the 140-d postweaning test and for mean IGF-I concentration (average of three IGF-I measurements taken on each calf) were 0.44, 0.51, 0.42, and 0.52, respectively. Heritabilities of maternal genetic effects were 0.18, 0.20, 0.10, and 0.20, respectively. The proportion of phenotypic variance accounted for by permanent environmental effects of dams was zero for all measures of IGF-I. Additive direct correlations with birth weight,

weaning weight, on-test weight, and off-test weight were -0.27, 0.12, 0.09, and 0.29, respectively, when averaged across all four measures of IGF-I. Phenotypic correlations were -0.08, 0.07, 0.10, and 0.16, respectively. The average direct genetic correlation of IGF-I with gain during the 140-d postweaning period was 0.29, whereas the average phenotypic correlation was 0.15. Updated results indicate that serum IGF-I concentration is moderately to highly heritable in beef cattle and that it has small positive genetic and phenotypic correlations with postnatal weight and gain traits. These findings contrast with those published from the same selection experiment in 1997, which indicated negative genetic correlations of IGF-I with weaning and postweaning weights and with postweaning weight gain (correlations ranged from -0.21 to -0.54 and averaged -0.38).

Key Words: Beef Cattle, Genetic Parameters, Insulin-Like Growth Factor

M29 Association of single nucleotide polymorphisms in bovine somatostatin and somatostatin Receptor 2 genes with growth traits in divergent IGF-I selection lines of cattle. W. Huang*, H. Hines, and M. Davis, *The Ohio State University, Columbus.*

Somatostatin (SST) plays an important role in inhibiting the secretion of growth hormone. Somatostatin action is mediated through its five G-protein-coupled receptors (SSTR1-5). Polymorphisms in SST and SSTR2 may have an effect on growth traits. The aim of this study was to investigate the associations of three SNPs, SST111 (*Dra* III) in SST, and SSTR339 (*Bcc* I) and SSTR393 (*Hpy*188 I) in SSTR2, with growth traits and IGF-I concentration in Angus cattle from two divergent IGF-I selection lines. Genomic DNA was extracted from 410 Angus cattle born in spring and fall of 2000 to 2002 at the Eastern Agricultural Research Station. The entire region of SST and SSTR2 was amplified by four overlapping primer pairs. The pool and sequence method was used to detect polymorphisms before genotyping. Five cattle, randomly chosen from eight combinations of sex, season, and line, formed the Angus panel. Three restriction enzymes (*Dra* III, *Bcc* I, and *Hpy*188 I) were used to perform the PCR-RFLP. We observed significant differences among SSTR339 polymorphisms for weight gain from d 84 to 112 (GG 24.1 kg, GC 25.2 kg, CC 28.8 kg) of the 140-d postweaning period in the across selection line analysis ($P < 0.05$). The transversion (C339G) results in an amino acid substitution (Ile113Met) in SSTR2. Results also showed significant associations of SSTR393 polymorphisms with weight gain from d 28 to 42 (CC 12.7 kg, CT 14.9 kg, TT 16.2 kg) and weight gain from d 56 to 84 (CC 33.9 kg, CT 34.0 kg, TT 38.1 kg) of the 140-d postweaning period in the across selection line analysis ($P < 0.05$). The SSTR393 polymorphism was determined to involve a T to C transition in codon 131, which does not change the amino acid cysteine. The SST111 polymorphism, identified in the promoter region of SST, involves an A to C transversion at nucleotide position 111, but significant differences were not found among the genotypes for any of the traits analyzed. Overall, these data indicate that two SNPs in the bovine somatostatin receptor 2 gene can be applied as markers in beef cattle breeding programs.

Key Words: Somatostatin, Single Nucleotide Polymorphism, Beef Cattle

M30 Test duration for growth, feed intake and feed efficiency in beef cattle using the Growsafe® System. Z. Wang*¹, D. Nkrumah¹, C. Li¹, J. Basarab², L. Goonewardene³, E. Okine¹, D. Crews⁴, and S. Moore¹, ¹University of Alberta, Edmonton, Alberta, Canada, ²Lacombe Research Center, Alberta Agriculture, Food and Rural Development, Lacombe, Alberta, Canada, ³Alberta Agriculture, Food and Rural Development, Edmonton, Alberta, Canada, ⁴Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.

Shortening the duration of tests to reduce the cost of measurement without compromising the data accuracy and reliability would be highly beneficial to beef cattle production. This study was conducted to determine the optimum test duration for the measurement of average daily gain (ADG), dry matter intake (DMI), feed conversion ratio (FCR) and residual feed intake (RFI) using data

on 303 beef steers with 3,318 repeated feed intake and growth measurements. Data was collected using the Growsafe® System at the University of Alberta's Kinsella Research Ranch. Daily feed intake and weekly growth data on individual animals were obtained for a total of 84 days. Residual variances and serial correlations (Pearson and Spearman) between data from shortened tests (7, 14, 21, 28, 35, 42, 49, 56, 63, 70, and 77 days) against an 84-d test were used as criteria to determine the optimum test duration. The four traits were analyzed using the MIXED procedure of SAS®, Version 9.1.3 as a repeated measures analysis. Results showed that tests for ADG, DMI, FCR and RFI could be shortened to 56-63 d without significantly reducing the accuracy of the test under the Growsafe® System when growth is measured weekly. These results have valuable practical implications for performance and feed efficiency testing in beef cattle.

Key Words: Feed Intake and Feed Efficiency, Test Duration, Beef Cattle

M31 Full genome scan of quantitative trait loci (QTL) for net feed efficiency in beef cattle. D. Nkrumah¹, C. Li*¹, Z. Wang¹, R. Bartusiak¹, B. Murdoch¹, J. Basarab², D. Crews³, and S. Moore¹, ¹University of Alberta, Edmonton, Alberta, Canada, ²Lacombe Research Center, Alberta Agriculture, Food and Rural Development, Lacombe, Alberta, Canada, ³Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.

Profitability of the beef industry relies on minimizing inputs while maintaining high levels of production of quality products. The cost of feeding has been shown to be the single largest variable cost in most beef production systems. Studies on feed efficiency have demonstrated considerable genetic and phenotypic variation among individual animals. Thus, the identification and characterization of genes controlling feed efficiency has tremendous implication potentials to the beef industry. In the current study, we attempted to identify and map quantitative trait loci (QTL) for net feed efficiency through a genome scan using animals of the University of Alberta's experimental beef cattle population. Phenotypic data was collected using the Growsafe® System and animals were typed using genetic markers, SSRs and SNPs, spanning the whole genome. Preliminary QTL interval mapping analysis detected seven chromosomal regions for net feed efficiency above suggested significance ($p < 0.05$) in the cattle populations examined. The chromosomal regions identified in the present study provides a valuable reference for further fine mapping of the QTL and identification of positional candidate genes for net feed efficiency in beef cattle.

Key Words: Quantitative Trait Loci (QTL), Net Feed Efficiency, Beef Cattle

M32 Using simulation models to predict feed intake: Phenotypic and genetic relationships between observed and predicted values. C. B. Williams*, G. L. Bennett, T. G. Jenkins, L. V. Cundiff, and C. L. Ferrell, *USDA-ARS; U.S. Meat Animal Research Center, Clay Center, NE.*

The objectives of this study were to evaluate the accuracy of the Decision Evaluator for the Cattle Industry (DECI) and the Cornell Value Discovery System (CVDS) in predicting individual feed intake, and the feasibility of using predicted feed intake data in genetic evaluations. Observed individual animal data on the average daily feed DMI (OFI) were obtained from postweaning records of feed consumption of 504 steers from 52 sires. The experimental data also contained individual growth performance and carcass measurements. The experimental data, and daily temperature and wind speed data were used as inputs to predict average daily kg feed DMI required for maintenance, cold stress, and ADG with the CVDS model (CFI_{mcg}) and the DECI model (DFI_{mcg}). Average daily feed DMI required for maintenance and ADG (CFI_{mg} , DFI_{mg}) were also predicted with both models. Genetic parameters were estimated by REML, using an animal model with age on test as a covariate, and genotype, age of dam, and year as fixed effects. Regression equations for observed on predicted DMI were: $OFI = 1.27 \pm 0.27 + 0.83 \pm 0.04 * CFI_{mcg}$ ($R^2 = 0.44$) and $OFI = 1.32 \pm 0.22 + 0.8 \pm 0.03 * DFI_{mcg}$ ($R^2 = 0.53$). Phenotypic correlations between OFI and CFI_{mcg} , CFI_{mg} , DFI_{mcg} , and DFI_{mg} were 0.67, 0.69, 0.73, and 0.77, respec-

tively. Heritabilities for OFI, CFI_{mcg} , CFI_{mg} , DFI_{mcg} , and DFI_{mg} were 0.27, 0.34, 0.34, 0.34, 0.33, respectively with all $SE = 0.012$. Genetic correlations between OFI and CFI_{mcg} , CFI_{mg} , DFI_{mcg} , and DFI_{mg} were 0.95 ± 0.07 , 0.95 ± 0.07 , 0.96 ± 0.07 , 0.96 ± 0.06 , respectively. Genetic correlations between CFI_{mcg} and DFI_{mcg} and between CFI_{mg} and DFI_{mg} were both 0.99 ± 0.005 . The strong genetic relationships between OFI and the predicted DMI data suggest that predicted DMI may be used in genetic evaluations. Genetically, there appears to be little difference between DECI and CVDS predicted feed intakes.

Key Words: Mathematical Models, Feed Intake, Genetic Correlations

M33 Genetic parameters and environmental factors for growth traits in Bali cattle. L. Praharani^{*1}, D. G. Riley², and T. A. Olson², ¹Research Institute of Animal Production, Bogor, Indonesia, ²University of Florida, Gainesville.

A genetic evaluation of Bali cattle (*Bos javanicus*) using data collected from the Bali Cattle Improvement Project on the island of Bali was conducted to determine the non-genetic and genetic parameters influencing growth traits and to evaluate their phenotypic and genetic trends. There were 7,980 calves born from 1985 through 2000. Traits evaluated were weight at 190 days (W-190d) and 350 days (W-350d). A connectedness program was used to evaluate genetic linkages between contemporary groups defined as a location-year-season combination. Variance components were computed by the AsREML using two-trait animal models that included contemporary group (CG), sex of calf, cow age, and the sex of calf by cow age interaction as fixed effects and calf age as a covariate. Genetic trends were plotted as average of estimated breeding values on year of birth. All non-genetic effects including CG, calf age (in W-190d), calf sex (in W-350d), calf age x calf sex (in W-190d), and cow age x calf sex (in W-350d) were found significant ($P < 0.05$). Estimates of direct additive heritability were 0.3 and 0.5 for W-190d and W-350d, respectively. The estimated maternal heritabilities were not different from 0. The estimated correlations between W-190d and W-350d were 0.74 (genetic), 0.19 (environmental) and 0.33 (phenotypic). These findings suggest that the genetic progress for W-350d might be expected to be faster than at for W-190d and increasing W-190d can be achieved by selection for W-350d since their genetic correlation was strong and positive. Failure to detect significant maternal effects may have been due to the unique management system (small shareholders with one or a few cattle) or there may have been inadequate pedigree/data structure for estimation. The decline in W-350d ($P < 0.01$) might be caused by factors other than genetic due to the observed genetic trend of W-190d and W-350d.

Key Words: Genetic Parameters, Growth Traits, Bali Cattle

M34 Sire x maternal grandsire interaction for pre-weaning growth traits in Brazilian Nellore cattle. A. de los Reyes¹, M. Elzo^{*1}, R. Lobo², and L. Bezerra², ¹University of Florida, Gainesville, ²University of Sao Paulo, Ribeirao Preto, SP, Brazil.

Non-additive genetic effects are currently ignored in the genetic evaluation of beef cattle in Brazil. However, non-additive genetic effects have been found to be important for beef cattle in several studies. The objective was to assess the importance of the sire x maternal grandsire (SMGS) interaction on standardized weights at 120 d (W120) and at 240 d (W240) in a Brazilian Nellore cattle population. Weight records came from 10,302 calves born and raised on pasture in 60 herds, and collected from 1976 to 1998. The single-trait mixed model included: 1) the fixed effects of contemporary group (CG = herd-year-season-sex-management group) and calving age subclass (2, 3, 4, 5 to 9, 10 yr and older), 2) the random effects of animal additive genetic (direct and maternal), maternal permanent environmental, SMGS subclass and residual. Each CG had a minimum of 10 records, two different sires, and two different SMGS subclasses per sire. The REMLF90 program was used to estimate (co)variance components. Direct and maternal heritabilities were 0.31 and 0.12 for W120, and 0.18 and 0.10 for W240. Direct-maternal genetic correlations were -0.23 for W120 and -0.05 for W240. Maternal permanent environmental variance ratios (relative to phenotypic variances) were 0.21 for W120 and 0.20 for W240. The

SMGS variance ratios, as a fraction of the phenotypic variance, were 0.09 for W120 and 0.08 for W240. The SMGS variance ratios were comparable to maternal heritabilities. These results indicate that, in this subpopulation of Nellore cattle, SMGS interaction effects may need to be included in genetic evaluation models for W120 and W240. However, this may not be the case in other Nellore subpopulations in Brazil. Thus, this research needs to be repeated within each subpopulation, and, if the objective were the development of a national genetic evaluation, then data from all Nellore subpopulations would be required.

Key Words: Beef Cattle, Growth, Interaction

M35 Gene expression profiling in bovine adipose tissues by serial analysis of gene expression. J. Bong¹, K. Cho², and M. Baik^{*1}, ¹Chonnam National University, Gwangju, South Korea, ²Jinju National University, Jinju, South Korea.

Serial analysis of gene expression (SAGE) was done in subcutaneous and intramuscular adipose tissues of Korean cattle to identify and quantify expressed genes. Sequencing of clones revealed about 11,000 tags in SAGE libraries from subcutaneous and intramuscular adipose tissues. We report here abundantly expressed genes identified in adipose tissues. Included in 50 most abundant tags in the subcutaneous adipose tissues were osteonectin, cyclin-dependent kinase regulatory subunit 1, annexin A2, tumor protein translationally-controlled, ferritin heavy polypeptide, cofilin, diacylglycerol O-acyltransferase, thymosin beta 4, and inositol 1,4,5-triphosphate receptor type 1 genes. Included in 50 most abundant tags in the intramuscular adipose tissues were cyclin-dependent kinase 5 regulatory subunit 1, tumor protein translationally-controlled gene, myosin light polypeptide 1, a transcribed sequence with strong similarity to human troponin C slow, osteonectin, eukaryotic translation elongation factor 1 alpha, and annexin A2 genes. For about 50 genes, the number of tags was over 2 fold higher in subcutaneous adipose tissue compared to intramuscular adipose tissue. In contrast, about 30 genes showed over 2 fold higher tag number in intramuscular adipose tissue. RT-PCR or northern analyses confirmed that expression of osteonectin, annexin A2, ferritin heavy polypeptide 1, and thymosin beta 4 genes was higher in subcutaneous tissues compared to intramuscular adipose tissues. Expression of heat shock 70 kDa protein 1 and N-myristoyltransferase 2 genes were higher in intramuscular tissues compared to subcutaneous adipose tissues. The current SAGE analysis provides overall differential gene expression profile in subcutaneous and intramuscular adipose tissues of Korean cattle. The deposition of intramuscular adipose tissue (marbling) is an important factor for high quality beef, especially in Korean cattle. Understanding the differential gene expression mechanism that regulates the deposition of fat between intramuscular tissues and subcutaneous adipose tissues will lead to develop methods to produce high-marble beef.

Key Words: Expression Profile, SAGE, Bovine Adipose Tissues

M36 Somatic cell banking-an alternative technology for conservation of endangered livestock breeds. N. Gupta^{*}, S. P. S. Ahlawat, and S. C. Gupta, National Bureau of Animal Genetic Resources, Karnal, Haryana, India.

Each cell of an animal body contains full genetic code for the whole animal and nuclear transfer provides a way of converting a cell to whole animal. Cells from endangered breeds collected by biopsy or from scrapings of soft skin or ear tissue or from hair follicle can be grown and multiplied in laboratory and this would then be stored frozen indefinitely at -196°C in liquid nitrogen. With this principle in consideration, a somatic cell bank has been created at the Bureau for the cryopreservation of skin fibroblast cell lines from different breeds of buffalo, camel, sheep and goat species as competent nuclear donor for the revival of the endangered germplasm through nuclear transfer and animal cloning at later stage. Skin samples of 0.25 cm² from ear pinna of 10 male and 10 female animals keeping effective population size in mind were collected from the main breeding tract of the breeds. The samples were transferred into complete media (DMEM+ HamsF12 with 10% FBS and antibiotic-antimycotic solutions) within 2 hrs and were transported in thermos flask at 4°C to the labora-

tory within 72 hours of collection. The skin fibroblast cells were purified from epithelial contaminations by repeated multiple passaging. All the quality assays like cell viability, mycoplasma, fungal and bacterial contamination detection, cell counts, cell proliferation rates, growth curve, cell senescence, genetic stability (karyological, DNA finger printing and frame shift mutations), replicative aging (telomeric dynamics) were studied in different passages. The cell freezing rates, thawing and different cryoprotectants were also studied. In this paper, details of the indigenously standardized somatic cell banking technology have been described. The present status of cryofrozen germplasm in somatic cell bank at -150°C is given in the table.

Cryopreserved germplasm of different livestock species in somatic cell bank

Species	Breeds	Male cell line	Female cell lines	No of samples
Buffalo	2	19	10	1200
Sheep	4	43	46	3500
Goats	2	24	28	2200
Camel	1	12	–	650

Each sample had 1 million cells per ml

Acknowledgements: Authors thank the World Bank for funding the project under National Agricultural Technology Project, Indian Council of Agricultural Research

Key Words: Somatic Cell Banking, Skin Fibroblast Cell Line, Nuclear Transfer

Dairy Foods: Cheese

M37 Chemical, textural and sensory properties of fresh Turkish Kashar cheese. N. Koca^{*1,2}, M. Metin¹, and V. B. Alvarez², ¹Ege University, Izmir, Turkey, ²The Ohio State University, Columbus.

Kashar cheese is a semi-hard Turkish cheese made by heating and stretching its curd. Kashar is one of the most consumed cheeses in Turkey and is classified as fresh or mature depending on its ripening level. The aims of this study were to characterize the chemical composition, texture and sensory properties of commercial cheeses and to determine how those properties relate to each other. Sixteen full fat cheese samples produced by different manufacturers were obtained from retail stores in Izmir, Turkey. Cheese samples were analyzed for pH, moisture, protein, fat and salt. Textural properties were measured by using an Instron Universal Testing Machine. Sensory properties (appearance, texture, flavor and overall acceptability) were determined by nine trained panelists using a scale of 1 to 5 (1:the worst, 5:the best). All cheese properties varied widely. The moisture, fat, protein and salt value ranges were 38.7-50.9%, 17.0-35.0%, 24.09-29.35% and 1.40-2.58% respectively. Hardness, springiness, cohesiveness, adhesiveness, gumminess and chewiness values were between 16.79-59.12 kg, 0.130-0.323, 0.107-0.249, 0.000-0.072 kgcm, 2.770-8.395 kg and 0.360-2.338 kg respectively. Mean appearance scores ranged from 1.78 to 4.67, texture from 2.78 to 4.22, flavor from 2.44 to 3.78 and overall acceptability from 2.44 to 4.11. As expected, the hardness values had significant correlation with moisture contents (P<0.01), because high moisture content weakens the cheese matrix by dissolution of proteins. The cheeses having moisture contents between 54.00-58.5% and hardness values between 23.00-33.45 kg had higher overall acceptability and texture scores. The same trend was observed for cohesiveness and springiness. Texture, flavour as well as appearance significantly affected overall acceptability (P<0.01). Properties characterization of fresh Kashar cheese and good understanding of their relationship are very important for manufacturers to make good quality and wholesome cheese products

Key Words: Fresh Kashar, Composition, Texture

M38 Yield enhancement of cottage cheese curd manufacture through milk protein fortification. Methods for quality evaluation. C. Kohen^{*1,2}, R. Hallab¹, A. Grandison¹, M. Lewis¹, and D. Marriott², ¹The University of Reading, Reading, Berkshire, UK, ²Creative Food Systems Limited, Marlow, Buckinghamshire, UK.

Cottage cheese curd was prepared using milk fortified with a milk protein powder preparation (92.6 % protein - produced from skimmed milk by co-precipitation and spray drying), and compared to non-fortified controls. Fortification led to significant increases in yield; for example, yield increased by over 10 %

when the addition level was 0.4 %.

Methods were developed to assess the quality of curd, based on analysis of firmness, microstructure, total solids content, curd size distribution, and sensory evaluation.

Firmness was assessed on dressed and undressed curd with a TA-XT2i Texture Analyser (Stable Micro Systems Ltd, Godalming, UK). Curd microstructure was observed using scanning electron microscopy. Size distribution of curd particles was estimated using a sieving technique. Sensory evaluation was used to assess differences between the curd samples (with added dressing), with significant differences evaluated through triangle tests.

The curd obtained with fortified milk (0.4% protein addition) retained more water than the control (Total solids values 20.9 ± 0.25 % for control and 19.2 ± 1.3 % for fortified) and was softer than the control (Firmness as maximum force 20.6 ± 3.5 g for control and 14.2 ± 3.5 g for fortified). In addition, electron micrographs of fortified curd displayed many more pores than control curd.

The difference in firmness was not detectable after the addition of dressing (Firmness: control 10.7 ± 2.8 g, fortified 11.2 ± 2.6 g). Also, there were no significant differences detected by sensory evaluation between the samples with added dressing. The dressing had a masking effect on minor differences in the curd quality. Hence, fortification with protein during curd manufacture produced a product with equivalent quality with reduced manufacturing costs/kg of finished product through the increased yield.

Key Words: Cottage Cheese, Fortification, Texture

M39 A one-dimensional dynamic model of curd syneresis based on viscoelastic properties of curd. M. Castillo^{*}, S. Torrealba, and F. Payne, University of Kentucky, Lexington.

Syneresis is a major process in cheese making. The extent of syneresis during cheese making controls the moisture, mineral and lactose content of curd which affects cheese ripening and subsequently the final cheese sensory attributes. Better curd moisture control would decrease the production of under-grade cheese. Estimated annual losses to the U.S. cheese industry in 2001 due to downgrades for cheese defects were \$29 million for cheddar cheese. Alternatively, the appearance of whey on the surface of a gel, or wheying-off, is a common defect during storage of fresh cheeses and fermented dairy products. Very little is known about syneresis. Limited knowledge is available about the mechanisms by which the microstructure and rheological properties of gels influence gel porosity, permeability, endogenous syneresis pressure and whey drain-