936 Characterization of residual feed intake and relationships with serum insulin-like growth factor-I in growing Brangus heifers. P. A. Lancaster*[1], G. E. Carstesn[1], J. G. Lyons[1], T. H. Welsh, Jr.[1], R. D. Randel[2], and T. D. A. Forbes[3], [1]*Texas Agricultural Experiment Station*, *College Station*, [2]*Texas Agricultural Experiment Station*, *Overton*, [3]*Texas Agricultural Experiment Station*, *Uvalde*.

The objective of this study was to characterize residual feed intake (RFI) and examine phenotypic correlations with serum insulin-like growth factor-I (IGF-I) in growing heifers. Average (± SD) initial age and BW of Brangus heifers (Camp Cooley Ranch) were 225.8 ± 9.1, 236.0 ± 10.7 and 235.6 ± 14.6 d, and 285.1 ± 28.0, 268.5 ± 23.8 and 267.8 ± 25.8 kg for year 1 (N=114), 2 (N = 115) and 3 (N = 119), respectively. Heifers were individually fed a roughage based diet (ME = 2.1 Mcal/kg DM) using Calan gate feeders for 70 d. Weekly BW were measured and ultrasound measures of 12th rib fat thickness (BF) and longissimus muscle area (LMA) obtained at d 0 and 70. Whole blood was collected at weaning, and at d 0 and 70 of the intake measurement period, and serum assayed in duplicate aliquots for IGF-I by EIA procedures (IDS, Inc., Fountain Hills, AZ). RFI was computed as actual minus predicted DMI, with predicted DMI determined by linear regression of DMI on mid-test BW$^{.75}$ and ADG with year as a random effect using a variance component covariance structure (R2 = 0.57). Overall ADG, DMI and RFI were 0.90 ± 0.15, 1.06 ± 0.16 and 1.00 ± 0.13 kg/d, 9.10 ± 1.11, 9.47 ± 1.04 and 9.92 ± 1.06 kg/d, and 0.00 ± 0.75, 0.00 ± 0.68 and 0.00 ± 0.70 kg/d for year 1, 2 and 3, respectively. ADG was strongly correlated with FCR (-0.67), but not with RFI, whereas, DMI was correlated with both RFI (0.67) and FCR (0.17). In addition, RFI was strongly correlated with FCR (0.60). Heifers with low RFI (< 0.5 SD; n = 112) consumed 16% less (P < 0.01) DMI and had 15% lower (P < 0.01) FCR than heifers with high RFI (> 0.5 SD; n = 98), even though ADG and final BW were similar. Overall IGF-I concentrations were 113.3 ± 27.4, 121.0 ± 29.6 and 116.6 ± 28.7 ng/ml for weaning, d 0 and d 70 sampling times. RFI was not correlated with IGF-I concentration at any of the sampling times. However, weaning IGF-I concentration was weakly correlated (P < 0.05) with ADG (-0.11) and final BF (0.11) and LMA (0.17), but not with DMI or FCR. These data suggest serum IGF-I concentration may be indicative of growth, but not feed intake or efficiency in Brangus heifers.

Key Words: Residual Feed Intake, IGF-I

937 Feed efficiency and residual feed intake of Nelore young bulls selected for yearling weight. R. Almeida*[1], R. F. Nardon[2], A. G. Razook[2], L. A. Figueiredo[2], and D. P. D. Lanna[3], [1]*Universidade Federal do Paraná*, *Paraná, Brazil*, [2]*Instituto de Zootecnia*, *São Paulo, Brazil*, [3]*ESALQ/USP*, *São Paulo, Brazil*.

A Nelore herd at the Sertãozinho Experimental Station, São Paulo, Brazil has been selected for yearling weight for more than 25 years. The feedlot test used 72 young bulls from the 12-13-14th progenies of the Selection Program for Zebu Breeds. Thirty-six intact males from the Selected Nelore (NeS) line and 36 from the Control Nelore (NeC) line, with the same initial age of 13 months, were transferred to the feedlot and fed a high roughage diet and slaughtered at a similar age (19 months). Predicted DM intake and residual feed intake (RFI) were calculated from average intakes regressed on metabolic mid-test body weight, average daily gain and 9-11th rib fat content. RFI mean was 0.00 ± 0.41 kg/d, with minimum and maximum of -0.73 and +0.95 kg/d. Results confirm there is considerable variability for this trait in *Bos indicus*. NeS young bulls were heavier (P<0.01) at the beginning and at the end of the trial and grew faster (P<0.01) than NeC. NeS bulls had greater (P<0.01) DM intakes than NeC bulls: 8.18 vs 7.03 kg/d and 92.5 vs 87.5 g/kg BW$^{0.75}$. DMI expressed as a % of BW was not different (P>0.10) between NeS and NeC lines (2.08 vs 2.03% BW). When efficiency was analyzed as feed conversion, there were no (P>0.10) differences between the two lines. However, for RFI the NeS young bulls were less eficient and ate 0.263 kg/d more (P<0.05) than NeC. There were no (P>0.10) differences for EBW fat content between the two lines, compared at the same age, but NeC were much lighter than NeS (428 and 481 kg, respectively). Consequently, the estimated energy retained was similar (P>0.05): 5.23 and 5.27 Mcal/kg EBWG, respectively for NeC and NeS. While NeS young bulls retained 11.7% more energy per day, their heat production was 17.9% larger than NeC. Thus, NeS bulls had greater (P<0.10) maintenance requirements than the control line: 78.6 and 68.0 kcal/kg BW$^{0.75}$, respectively. In conclusion, results suggest that selection for yearling weight may increase heat production and maintenance requirement. Is is also shown that selection changes RFI, but it does not change feed conversion efficiency, when animals are fed to the same fat endpoint.

Key Words: Feed Conversion, Zebu Breed

Breeding and Genetics - Livestock and Poultry: Analyses and Methods II

938 Genetic parameters estimation for Test Day Model evaluation in Italy. F. Canavesi* and S. Biffani, *ANAFI*, *Cremona, Italy*.

In November 2004 the first Italian genetic evaluation based on Test day random regression model (TDRRM) was published. The model is a Multiple-Trait-Multiple-Lactation model including four traits and three lactations for each trait. The four traits evaluated are milk, fat and protein kg and somatic cell counts. Genetic parameters used in the current model were estimated in 2003 (Muir et al, 2007). The estimated parameters were close to the parameters estimated for the same model in Canada. Heritability was close to the one used for the Lactation Repeatability model used in the past for official evaluations. Genetic correlations within trait and across traits were very similar to the parameters estimated for the same model in Canada. Research is ongoing in order to improve the stability of proofs over time and the predictive ability of the model. Pre adjustment of test day for number of days of pregnancy and the inclusion of the effect of single years in the fixed effect structure showed better results in residual analysis and a slight reduction in proof variability. The new model with pre-adjusted data was used to estimate genetic parameters with a four and three traits analysis. The three trait analysis did not consider somatic cell count. Estimations of genetic parameters of variances and covariances for the two models were achieved by Bayesian methods using the Gibbs sampler as described by Jamrozik and Schaeffer (2003). The four traits analysis resulted in very similar correlation within and across traits and a lower heritability (0.25) than the current used (0.30). The three traits analysis resulted in a higher correlations within traits across lactations very similar to correlations from single trait analysis (Muir, 2004) which may lead to a decrease in variability of proofs from run to run. Correlations between first and second lactation increased by about 0.06 and correlations between first and third lactation increased by 0.10. The new parameters are under test to verify their impact on stability of proofs.

Key Words: Genetic Parameters, Test Day Model, Multiple Trait

939 Use of a mathematical computer model to predict feed intake in Angus cattle: Genetic parameters between observed and predicted values, and relationships with other traits. D. P. Kirschten*, E. J. Pollak, and D. G. Fox, *Cornell University*, *Ithaca, NY*.

The objectives of this study were to investigate the suitability of using dry matter required (DMR) as predicted by the Cornell Value Discovery System (CVDS) in genetic evaluations and to determine relationships between model predicted and individual DMI and other traits. Group 1 (659 finishing steers) and group 2 (309 yearling bulls) had observed feed intake (FI) records. Group 3 (1586 yearling bulls and heifers) had pedigree ties to the other datasets, but did not have FI data. The data also contained records of ADG and body weight (BW). Two predictions of DMR were made with the CVDS model iterating on BW (DMR-W) and ADG (DMR-G). For purposes of parameter estimation, CVDS DMR predictions were considered surrogates for FI. Genetic parameters were estimated with MTDFREML, using an animal model with fixed effects of weaning weight contemporary group and pen. Phenotypic correlations between FI and DMR-W and DMR-G were 0.69 and 0.71. The phenotypic correlation between DMR-W and DMR-G was 0.98. Genotypic correlations between FI and DMR-W and DMR-G were 0.79 and 0.85. The genetic correlation between DMR-W and DMR-G was 0.97. Heritabilities for FI, DMR-W and DMR-G were 0.42, 0.31 and 0.33, respectively. Genetic correlations between ADG and FI, DMR-W and DMR-G were 0.45, 0.80, and 0.83, respectively. Genetic correlations between mean body weight (MW) and FI, DMR-W, and DMR-G were 0.50, 0.64 and 0.58, respectively. Residual feed intake (RFI) was calculated using FI, metabolic MW ($MW^{0.75}$) and ADG. The heritability of RFI was 0.36. The phenotypic correlation between RFI and FI was 0.57. Phenotypic correlations between RFI and MW and ADG were not estimated. Genetic correlations between RFI and FI, MW, and ADG were 0.77, 0.09, and 0.01, respectively. Heritabilities of ADG and MW were 0.27 and 0.48. Standard errors for all genetic correlations were less than 0.06. The genetic relationships between FI, DMR-W and DMR-G suggest that CVDS predictions of FI may be used as surrogates for actual FI in genetic evaluations.

Key Words: Feed Intake, Mathematical Models, Beef Cattle

940 Computing options for genetic evaluation with a large number of genetic markers. S. Tsuruta, I. Misztal*, and J. K. Bertrand, *University of Georgia*, *Athens*.

Test data set included records on about 110,000 animals for 11 growth, reproduction and other traits. Also available were marker genotypes or marker probabilities on 78 markers. The model included the effects usually fitted for these traits plus two covariables per marker; only selected markers were fit for each trait. Computing was by program blup90iod, which uses iteration on data using a preconditioned conjugate gradient algorithm with a diagonal preconditioner. Without the markers in the model, the evaluation finished in 421 rounds and 2.5 h. With the markers included, the evaluation took one week of computing and 797 rounds of iteration. Modifications included the algorithm by Strandén and M. Lidauer (SL) to reduce the number of operations for each record, a block preconditioner for traits (BT), and a block preconditioner for all markers (BM). With the markers included in the model, the number of rounds (computing time) were 797 (7.8 h.) for SL, 544 (6.2 h) for SL+BM, 459 (4.3 h) for SL+BT, and 431 (5.2 h) for SL+BT+BM. The memory requirements for all methods except BT were around 60 Mbytes; with BT, the memory requirements increased 10 times. The most important modification to decrease the computing time was the SL algorithm. Setting up BM was computationally demanding, and would be very expensive if the number of markers is increased. BT would show greater advantage with higher genetic correlations among traits. With careful programming, adding markers fitted as covariables to a genetic evaluation increases the computing time only a few times.

Key Words: Genetic Evaluation, Genetic Markers, Molecular Information

941 Sampling genotype configurations in large complex pedigree. M. Szydlowski*[1] and N. Gengler[1,2], [1]*Gembloux Agricultural University*, *Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *Brussels, Belgium*.

Efficient genotype samplers are needed for Bayesian and maximum-likelihood analysis of complex genetic problems implemented via Markov Chain Monte Carlo (MCMC) algorithms. The examples of such analysis include polygene mapping in complex pedigrees and prediction of total genetic value using genome-wise dense marker maps. For large complex pedigree sampling from desired probability is impossible. We present a simple method to sample genotype configurations for large pedigree from approximate probability. The sampler uses combination of exact (simple peeling) and iterative methods (iterative peeling) to approximate target probability. Two techniques were applied to reduce computational burden: genotype elimination and set-recoding of alleles. The new sampler was evaluated on a large complex pedigree using simulated data sets for various experimental designs and degree of marker polymorphism. The pedigree used in simulation was real bovine pedigree of 907 903 animals born between 1960 and 2005 derived from Belgian dairy and dual-purpose cattle database. Four types of experimental designs were considered: (i) genotyping sires only, (ii) genotyping dams only, (iii) genotyping half of the dams but no sires, and (iv) genotyping half of the sires and half of the dams. For hypothetical single nucleotide polymorphism the new sampler reached 100%, 100%, 44% and 89% of maximum efficiency for the four experimental designs respectively. For microsatellite polymorphism the efficiency of the sampler reached 100%, 100%, 32% and 76%, respectively. To exemplify the use of the new sampler it was applied to estimate genes shared identical by descent (IBD). The calculation of genes shared IBD among relatives is an important component of gene mapping in complex diseases and quantitative traits. The convergence diagnostic methods gave indirect evidence of irreducibility of the new sampler and showed its good mixing performance.

Key Words: MCMC Sampler, Genotype Estimation, IBD

942 Comparisons of single and multiple trait random regression models for analyses of multi-parity test-days. S. Tsuruta* and I. Misztal, *University of Georgia*, *Athens*.

The objective of this study was to compare a single-trait (ST) test day model with combined covariance functions for DIM within lactation

and for across parities with a multiple-trait (MT) test day model with random regressions on DIM treating each parity as a separate trait. Analyses involved records on 50,494 Holstein cows calved from 1993 to 2003 in Georgia. The data contained 495,455 test day records from first to third parities. The number of animals in the pedigree file was 118,281. The MT model for each trait (parity) included herd-test-date, age × month of calving group, milking frequency and cubic regressions on DIM using Legendre polynomials as fixed effects, and random effects of additive genetic, permanent environmental with cubic random regressions on DIM and residual. The ST model included the same fixed and random effects as the MT model except for additive genetic and permanent environmental effects with cubic random regressions on DIM within lactation and quadratic random regressions on parities. The MT model required 288 parameters and the ST model required 72 parameters. Variance components were estimated using an MCMC approach. Breeding values were obtained using the preconditioned conjugate gradient algorithm with iteration on data. With the MT model, heritability estimates were 0.22, 0.19 and 0.23 on average for first, second and third parities, respectively. With the ST model, those estimates were 0.21, 0.17 and 0.21, respectively. Correlations of EBV between MT and ST models at 65 (245) DIM were 0.99 (0.98) for first parity, 0.98 (0.97) for second parity and 0.94 (0.96) for third parity. Correlations of EBV between MT and ST models averaged over 5-305 d were 0.99, 0.99 and 0.98 for first, second and third parities, respectively. The MT model required 2 times of computing time and memory for the ST model. Results of tests with larger data sets will be presented. The ST test day model as presented may be a cost-effective alternative to the MT test day model.

Key Words: Test Day Model, Random Regressions

943 Investigation of genetic differences in feed efficiency through comparison of observed versus model predicted feed intake in *Bos indicus – Bos taurus* F_2 full sib steers. T. S. Amen*, J. E. Sawyer, A. D. Herring, J. O. Sanders, D. K. Lunt, and C. A. Gill, *Texas A&M University*, *College Station*.

Individual feed intake (DMI) and body weight were measured on 149 F_2 Nellore-Angus steers born and raised at the Texas A&M University Experiment Station at McGregor. Steers belonged to 12 full sib embryo transfer families sired by 4 bulls and from 11 dams born in the spring and fall of 2003 to 2005. At approximately 12 months of age, steers were placed on feed for an average of 140 d with individual intake measured using Calan gates. Using the NRC (2000) model, daily feed intake was predicted based on observed weight gain for each animal and standardized input for animal type, age, sex, condition, and breed. This model predicted intake (MDMI) was then subtracted from observed DMI and the difference defined as model predicted residual consumption (MPRC) such that those animals that consumed less than predicted (and thus, were more efficient) had negative MPRC. This method was utilized instead of traditional residual feed intake in order to make simultaneous use of data from multiple contemporary groups. Mixed procedures of SAS were then used to analyze MPRC with fixed factors of sire and family nested within sire. Initial analysis also included contemporary group; however, substantial imbalance existed with sire and family, so it was subsequently omitted. Sire ($P = 0.016$) and family(sire) ($P < 0.001$) both accounted for variation in MPRC. Least squares means for MPRC by sire ranged from a low of -0.51 ± 0.22 kg day $^{-1}$ to a high of 0.65 ± 0.36 kg day $^{-1}$. Least squares means for MPRC by family(sire) ranged from -2.13 ± 0.48 kg day $^{-1}$ to 1.45 ± 0.60 kg day $^{-1}$ across families. Variation between sires and families for MPRC indicates that genes affecting this trait are segregating in this population and presents future opportunities for QTL analysis, and subsequent gene discovery; further, MPRC holds promise as a model derived method of evaluating efficiency across contemporary groups.

Key Words: Predicted Intake, NRC Model, *Bos indicus*

944 First screening of QTL using a segment mapping approach. M. Sargolzaei*[1], F. Schenkel[1], and H. D. Daetwyler[2], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*Roslin Institute*, *Roslin, Midlothian, Scotland, UK*.

Panels of SNP markers are rapidly increasing in size and are being used for fine mapping. The first step in fine mapping is to identify potential regions which are more likely to harbor QTL. The objective of this study was to evaluate a modified version of the segment mapping method (SM) for a first screening of QTL using simulated SNP data. The SM included the polygenic effect, the putative QTL effect and the whole chromosome effect excluding the putative QTL. The SM was compared to the point identity by descent (IBD) method (PM), in which only the polygenic effect and the putative QTL effect were fitted, using 4 simulated generations of randomly mated sires (15) and dams (300; 1 progeny per dam). A trait with heritability of 0.3 was considered. A 1-Morgan chromosome with 100 evenly spaced SNPs was simulated. Two bi-allelic QTL with additive effects were symmetrically located at 20, 15, 10 and 5 cM from the centre of chromosome. Each QTL explained 16.6% of total additive genetic variance. In every generation, 50% of the oldest sires and dams were randomly replaced. The software Loki was used to compute IBD at every cM. For SM, the average of 99 point IBDs was used as an approximation of IBD for the rest of chromosome. The full models, with putative QTL included, were tested against the corresponding models with no putative QTL, using the software ASReml. The likelihood ratio peaks for the QTL positions given by SM were always narrower and clearer than PM. However, when the two QTL were located less than 20 cM apart, both SM and PM revealed a single peak. The SM seemed to separate loosely linked QTL better than PM. Thus, SM might be useful for first screening of QTL, but the number of QTL, their precise positions and effects should be estimated by fine mapping methods in a second step.

Key Words: First Screening, QTL, Segment Mapping

945 Evaluating the feasibility of fitting haplotype effects as random: Variance component estimation. L. A. Kuehn*, R. M. Thallman, and K. A. Leymaster, *USDA-ARS U.S. Meat Animal Research Center*, *Clay Center, NE*.

Fitting haplotypes as random effects in association studies may prevent overestimation of haplotypic effects with low frequencies. The objective was to determine whether haplotypic variance could be accurately estimated. Using simulation, haplotypic effects were deterministically assigned to either 2 or 16 haplotypes with variances of haplotypic effects set at 2, 4, or 16.67 units^2. Haplotypes were

assigned stochastically to base animals in frequencies such that the 3 haplotypic variance scenarios accounted for 3, 6, and 25 units^2 of genetic variance, respectively. Polygenic additive effects were assigned from a normal distribution so that a total of 25 units^2 of the phenotypic variance was genetic. Residual effects were sampled from a normal distribution with a variance of 75 units^2. Either 250 or 1,000 progeny (5 or 15 per sire) with performance records were simulated. With varying levels of haplotype number, haplotypic variance, numbers of progeny, and numbers of progeny per sire, there were a total of 24 different simulation scenarios. Each simulation scenario was replicated 100 times and analyzed using MTDFREML with a model that included a random independent regression for the number of copies of each haplotype (0, 1, or 2), a random polygenic effect, and error. Estimates of polygenic and residual variance were accurate for all scenarios. Standard errors of the mean estimates for both variance components were greater with 250 than 1,000 progeny and with 5 than 15 progeny per sire. When 16 haplotypes were simulated, the variances of haplotypic effects were accurately estimated when the pedigree contained 1,000 progeny and underestimated with 250 progeny. Haplotypic variance was consistently overestimated when only 2 haplotypes were simulated, possibly due to the small number of classes for the haplotypic regression. Large, phenotyped pedigrees are important when estimating haplotypic variance for association studies.

Key Words: Haplotype, Simulation, Variance Components

946 Interval mapping of deleterious recessive loci in half-sib families. L. Gomez-Raya* and W. M. Rauw, *University of Nevada*, *Reno*.

Deleterious recessive genes in farm species with a half-sib structure are difficult to eliminate by breeding. However, their frequency can be increased by the widespread use of semen of carriers with high genetic value. In this study, we developed maximum likelihood interval mapping methods to detect deleterious recessive genes. The methods were developed for recessive genes that are lethal in homozygotes before birth, and also in homozygotes that are born with a disease. The available DNA marker data in the first situation is that one fragment in one of the two chromosomes is inherited in a lower number of offspring than the other chromosomal fragment. For this situation, we carried out a Monte Carlo computer simulation modeling a heterozygous sire with one copy of the recessive allele and a varying number of progeny and frequency of the recessive allele among the progeny. The simulated chromosomal fragment was bracketed by DNA markers separated 20cM, with the recessive locus equally distant from each of the two markers. The percentage among 10,000 replicates with a lod score greater than 2 for 100 tested offspring were 2.69, 8.56, 23.65, and 51.05% for a frequency of the recessive allele of 0.20, 0.30, 0.40 and 0.50, respectively. The percentage of replicates with a lod score greater than 2 for a progeny size of 2000 was 21.44, 60.83, and 92.65% for allele frequencies of 0.10, 0.15, and 0.20, respectively. The average estimate of the position of the recessive locus was 0.5cM or less in all simulations. Estimates of the allele frequency of the deleterious locus were unbiased except when the frequency or the progeny group was small. The percentage of replicates that located the locus within 1cM of the simulated position was 16.9% for a progeny size of 2,000 and allele frequency of the recessive allele of 0.20. The results illustrate that large progeny groups are required to detect recessive alleles at low frequency. Mapping strategies, including selective genotyping of offspring of dams genetically related to the sire, are discussed.

Key Words: Linkage Analysis, Half-Sibs, Gene Mapping

947 Investigating the role of genetics on bovine respiratory disease incidence. M. J. Schneider*, J. R. Tait, M. V. Ruble, and J. M. Reecy, *Iowa State University*, *Ames*.

Bovine Respiratory Disease (BRD) is one of the most costly diseases facing the cattle industry. Therefore, the objective of this study was to examine the role genetics has on susceptibility and resistance to bovine respiratory disease. Calving, pedigree, and health treatment records were collected on 1400 cattle born from 1997 through 2006 at the Iowa State University beef teaching farm with majority of cattle sired by Angus or Simmental bulls. Calves were born in both the Spring and Fall seasons for each year with the exception of 2006 where only Spring calves were used. The number of treatments for BRD varied with 80% of cattle never being treated for respiratory symptoms, 16% treated once, 3% treated twice, and 1% treated three to five times. The highest incidence of BRD treatment occurred in calves born in the Spring of 2001 when 74.8% of calves were treated at least once, whereas the lowest incidence of treatment occurred in calves born in the Fall of 2003 (1.5%). Statistical analysis was performed using general linear models to estimate significance level and effects. Traits showing significant effects ($P<0.05$) on the number of times an animal was treated for BRD included sire nested within breed, calving season group, and birth weight these accounted for 28.4% of the variation in number of BRD treatments. Calving ease score and sex did not have a significant effect on the number of treatments for BRD ($P>0.10$). LSMeans estimates of sire effect for number of respiratory treatments within Angus ranged from -0.22 to 1.96 and in Simmental ranged from -0.06 to 1.77. The results from this study show a significant effect on number of treatments for BRD among sires within breeds. Thus, further investigation into the genetic control of BRD is warranted.

Key Words: Bovine Respiratory Disease, Genetics, Beef Cattle

948 Simulation study controlling inbreeding in litter size. S.-H. Oh*[1], G.-M. Kim[1], and Y.-C. Jung[2], [1]*North Carolina A&T State University*, *Greensboro*, [2]*Jung P&C Institute*, *Seongnam, Gyeonggi, South Korea*.

Inbreeding is the mating of relatives that produces progeny having more homogenous alleles than non-inbred animals. Inbreeding causes an increase of recessive alleles, which is often associated with a decrease in performance, known as inbreeding depression. The magnitude of inbreeding depression depends on the level of inbreeding expressed by coefficients. Litter size is a quantitative trait compound of effects from two generations. The number of pigs born in a litter depends partly on the dam and partly on the offspring of the dam. Therefore both the dam's fertility and the litter's viability influence litter size at the same time. The fact that the inbreeding rate of young in the litter is always one step ahead of that of the dam seems to be more of an influence of the litter on reduction of litter size. One of breeding goal in livestock is uniform productivity which means uniform progeny from homogenous

parents, maintaining optimal inbreeding level, especially keeping inbreeding lower than 20%. The concept of the theory of optimum genetic contribution (OGC) uses the relationships between individuals as weights. The objective of this study was to compare simulated results of the OGC algorithm in different conditions for 30 generations. Results showed this algorithm could effectively control inbreeding maintaining a consistent increase in selection responses. The difference of breeding values between selection based on the OGC algorithm compared with with EBV was only 13%, but the rate of inbreeding could be controlled as much as ~67% after 30 generations, indicating that the OGC algorithm can be effectively used for long-term selection programs.

Key Words: Inbreeding, Simulation, Litter Size

Contemporary & Emerging Issues - Livestock and Poultry: Contemporary and Emerging Issues

949 Avian H5N1: Still an animal virus? F. C. Leung*, *The University of Hong Kong*, *Hong Kong, HK-SAR, China*.

As of Feb 6, 2007, the cumulative number of confirmed human cases of avian influenza A/(H5N1) reported to World Health Organization (WHO) is 272 with 166 deaths. Avian influenza including H5N1 refers to a large group of different influenza viruses of which the primary host is birds. Only on rare occasions do these viruses cross over and infect other species including pigs and humans. Pandemic influenza happens when a new subtype emerges that has not previously circulated in humans. Since H5N1 is a strain of such potential, WHO and other health experts, for this reason, have been priming the world to prepare for this threat along with OIE and FAO calling for culling million of poultry world-wide. During my presentation, I will present a model based on the most recent event of an animal virus 'crossing over' to become a human virus, SARS, and argue that the scale of the warnings appears to outstrip the magnitude of the real threat. Culling millions of chicken may not have actually lowered the actual risk and efforts and resources should be directed to research in understanding the molecular and genetic mechanisms underlying the virus-crossing species event. Only then can effective barriers be set up to limit the direct contact of susceptible species; to lower the transmission rate; and avoid establishing/adaptation to a new host. In addition, I shall review recent scientific findings that avian H5N1 remains as an animal virus and the probability and possibility for H5N1 successfully adapting to humans as a new host remains low at this particular moment!

i**Key Words:** Avian Influenza, H5N1, Virus

950 Bovine spongiform encephalopathy in the United States. J. A. Richt*, *National Animal Disease Center-ARS-USDA*, *Ames, IA*.

Transmissible spongiform encephalopathy (TSE) agents or prions induce fatal neurodegenerative diseases in humans and in other mammalian species. They are transmissible among their species of origin, but they can also cross the species barrier and induce infection with or without disease in other species. In animals, four distinct TSE diseases are recognized: scrapie in sheep and goats, transmissible mink encephalopathy (TME) in mink, chronic wasting disease (CWD) in cervids, and bovine spongiform encephalopathy (BSE) in cattle. BSE was first identified as a TSE of cattle in the mid 1980s in the U.K. and more than 180,000 positive cases have been diagnosed in the U.K. to date. Using epidemiological surveillance programs, many European and non-European countries have discovered BSE-positive animals within the last decade. In the U.S., the first BSE case (case 1) was identified in December 2003; this animal was determined to be imported from Canada. After this animal was identified, the USDA began its enhanced BSE surveillance program in June 2004. Since then, two additional animals (cases 2 and 3) have been identified as being positive for BSE. Both animals were born and raised in the U.S. Case 1 showed molecular features similar to typical BSE isolates, whereas cases 2 and 3 revealed unusual features referred to as atypical BSE isolates. Unusual cases of BSE are an unexpected finding since it was previously believed that BSE disease in cattle is caused by a single strain of infectious agent, which has been shown to be very consistent and uniform in appearance, even after transmission to other species. The appearance of unusual phenotypes of BSE in cattle suggests that different BSE strains exist in cattle.

Key Words: Prion Diseases, U.S BSE Cases, BSE Strains

951 Scenario and economic analysis of a hypothetical link between MAP and Crohn's disease. H. Groenendaal* and F. Z. Zagmutt, *Vose Consulting*, *Boulder, CO*.

Johne's disease (JD) is an infectious disease of cattle caused by the agent Mycobacterium avium subspecies paratuberculosis (MAP). Crohn's disease is a disease of unknown etiology that causes chronic bowel inflammation in humans. No causal link between MAP and Crohn's disease in humans has been scientifically established but given the potential for such discovery, it is important to understand its possible impacts on society. In this presentation, we will show the implications and the possible economic impacts on the dairy industry and to provide a framework for further discussion among stakeholders. Three scenarios were developed based on the effectiveness of possibly risk mitigation strategies. In the first scenario, it was assumed that an effective strategy would exist, resulting in negligible demand effects. In the second scenario it was assumed that new risk mitigation would need to be implemented, in which case a small milk demand was expected, with the potential of being large. The third scenario assumes that no fully effective risk mitigation would be available, which more likely results in a considerable demand decrease and a reduction in milk supply as a result of government regulations. With milk demand of 1% or 5%, a reduction in consumer surplus of $600 million and $2.9 billion and a reduction in dairy farm income of $270 million and $1.3 billion respectively was found. The true shift in demand is however impossible to predict. An decrease in milk supply would slightly increase total losses, but would cause great losses to MAP positive dairy farms. Given the current scientific knowledge about the link between MAP and Crohn's and the effectiveness of risk mitigation methods, it is concluded that in case a link would be established, it is most likely that the first scenario or potentially the second scenario could occur. Consumer response and economic consequences to discovery of such link are therefore expected to be limited, but could