**W34 Weaning performance of Charolais calves.** F. Szabó*[1], A. Fördös[1], Z. Domokos[2], and S. Bene[1], [1]*University of Pannonia, Keszthely, Hungary*, [2]*National Association of Hungarian Charolais Breeders, Miskolc, Hungary*.

Weaning weight (WW), preweaning daily gain (PWDG) and 205-day weight (205DW) of 23010 Charolais calves (10696 male and 12314 female) born between 1990 and 2005 from 10098 cows mated with 149 sires were analyzed. Breeding region, year and season of birth, age of dam, and sex of calves were fixed effects, and sire was random effect. Data were analyzed with Harvey (1990) Least Square Maximum Likelihood Computer Program, and two animal models were used for breeding value estimation. Variance, covariance components, heritability, correlation coefficients and the effect of the maternal environment on genetic parameters and breeding values were examined. The overall mean value and standard error of WW, PWD and 205DW were 219±7.60 kg, 939±40.63 g/day and 227±8.58 kg, respectively. Significant (P<0.005) region, year, season, sire and dam age effects, and sire × herd interaction were found. Weaning performance increased with increasing dam age up to six years of age. The direct heritability (h2d) of the evaluated traits was between 0.54 and 0.59. The maternal heritability (h2m) of these traits was 0.32 and 0.38. The direct-maternal correlations (rdm) were strong and negative (-0.84). Contribution of maternal heritability and maternal environment to phenotype was smaller than that of direct heritability (h2m + c2 < h2d). The proportion of the variance of maternal permanent environment in the phenotypic variance (c2) changed from 0.02 to 0.03. The rank of animals based on breeding value for weaning traits was not changed whether the maternal environmental effect was modeled. The genetic value for weaning results of Charolais population has increased since 1993.

**Key Words:** weaning weight, environmental effects, heritability

**W35 Improving the profitability of beef from pastures: A case study of Tasmania's Circular Head Beef Business Group.** A. E. O. Malau-Aduli*[1], I. D. Bruce[1], B. Doonan[2], and P. A. Lane[1], [1]*School of Agricultural Science, University of Tasmania, Hobart, Tasmania 7001, Australia*, [2]*Davey & Maynard Consultants, Davenport, Tasmania 7310, Australia*.

This case study on improving grazing management skills was conducted over a 12-month period in 2007 utilizing 1200 beef cattle on two properties of 60 hectares each, subdivided into 24 paddocks. The objectives were to evaluate pasture utilisation, liveweight gains and profitability using a multi-faceted economic model. Leaf emergence rate, average pasture cover, pasture growth rate, pre-grazing pasture mass, post-grazing residual and cattle liveweight gain data were collected monthly. Data were analysed using mixed (PROC MIXED) and general linear (PROG GLM) models in SAS to test for the fixed effects of property, date of sampling, cattle type and their second order interactions, while age of cattle and paddocks were fitted as random effects. Relationships between livestock and pasture variables were tested in correlation analyses using PROC CORR and significance established using Bonferroni probabilities. Results demonstrated that significant improvement in grazing management led to an increase in total pasture utilisation per hectare of over 40%, significantly greater than the set target of 7000kgDM/Ha on both properties. Pasture utilised directly for liveweight gain was positively correlated with total pasture utilised (r = 0.8686, p<0.0001). Energy partitioning for animal maintenance was found to be negatively correlated with total pasture utilised (r = -0.5927, p<0.05), and pasture utilised for liveweight gain (r = -0.8112, p<0.0001) and related to the nutritive value and species composition of the pastures. Average daily liveweight gain was found to be positively correlated with total pasture utilisation (r = 0.7302, p<0.0001) and pasture utilised for liveweight gain (r = 0.9181, p<0.0001) and negatively correlated with energy partitioned for animal maintenance (r = -0.9263, p<0.0001). It was concluded that increased pasture utilisation per hectare allowed for stocking rate increases across each property resulting in significant increases of approximately 73% in beef produced per hectare, thus increasing profitability by an overwhelming average of 250% across both properties.

**Key Words:** beef, pasture grazing, profitability

## Breeding and Genetics: Genomic Evaluation, Molecular Genetics, Statistical Methods, Sheep Breeding, and Swine Breeding

**W36 Value of genome-wide selection in Japanese dairy population.** H. Ohmiya* and M. Suzuki, *Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Hokkaido, Japan*.

Little research has been done on the genomic breeding program for the Japanese dairy cattle population. Therefore, we examined the rate of genetic gain, the rate of inbreeding increase, and the reduction of economic costs associated with the implementation of genome-wide selection in the Japanese dairy cattle population. The simulation data, which mimics the Japanese dairy population, were used to evaluate progeny testing by BLUP with an animal model and genome-wide selection scheme by improved BayesB (Meuwissen et al. 2001). These simulations were replicated 20 times with 30 chromosomes and having 100 QTLs and 101 biallelic SNP markers per chromosome. The candidate bulls in the progeny testing scheme were raised for 5 years until their semen could be used, however in the genome selection scheme candidate bulls were selected at birth and put into service in one year. All records and pedigree information were used for calculating breeding values by BLUP, whereas only records and genotyping information of each generation were used in the BayesB scheme because of recombinant locus. The results showed that the accuracy of estimated breeding value for bulls by BayesB was a little lower than BLUP (0.82 vs 0.89), however, the reduction of generation interval and larger selection differential per generation in the genome-wide selection led to more genetic gain than BLUP. The rate of inbreeding increased 0.44 during the 10-year period in the progeny testing scheme, but the genome-wide selection scheme was 0.28. Furthermore, the economic costs in genome-wide selection scheme were reduced by 63% compared with the traditional progeny testing strategy. This suggests that genome-wide selection is effective genetically and economically.

**Key Words:** genome-wide selection, BayesB

**W37 Genomic heritability of beef cattle growth.** W. M. Snelling*, L. A. Kuehn, R. M. Thallman, J. W. Keele, and G. L. Bennett, *USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE*.

Calf weights were examined to determine association between high-density SNP genotypes and growth, in order to estimate additive genetic variation explained by SNP. Data taken from Cycle VII of the US Meat Animal Research Center Germplasm Evaluation Project included birth weight (BWT), 205-d preweaning gain (WG), and 160-d postweaning gain (PWG) records of over 2,500 animals genotyped with the BovineSNP50 BeadChip. Polygenic and genomic direct and maternal variances were estimated in single-trait analyses. Fixed effects included sex, age of dam, year-season-location contemporary group, and covariates for calf and dam breed composition and heterosis. Direct and maternal additive polygenic and genomic effects, and maternal permanent environment effects were considered random. Polygenic effects were correlated according to a pedigree-based relationship matrix (**A**). Genomic effects were correlated with genotype-based relationship matrices ($\mathbf{A_g}$) constructed from sets of SNP meeting single-SNP association criteria. The 4,242 animals represented in both **A** and $\mathbf{A_g}$ included 2,918 genotyped individuals. Genotypes of the remainder (mostly dams) were predicted by a single-locus BLUP procedure. SNP with minor allele frequencies < 0.05 were excluded. Tests to choose SNP sets were Bonferroni-corrected $P$ ($P_b$) < 0.05 (~35 SNP), false discovery rate (FDR) < 0.05 (~280 SNP), nominal $P$ ($P_n$) < 0.01 (~1,760 SNP) and < 0.05 (~5,030 SNP), FDR > 0.90 (~15,760 SNP unlikely to affect phenotype), and all SNP (44,163). Unweighted $\mathbf{A_g}$, with each SNP making equal contribution to relationships, and weighted $\mathbf{A_g}$, with contributions weighted according to estimated effects, were evaluated. Additive variance was split between polygenic and genomic components with $P_b$ < 0.05 and FDR < 0.05, and shifted almost wholly to genomic components using $P_n$ < 0.01, $P_n$ < 0.05, and all SNP. Estimates of genomic variance were negligible for FDR > 0.90. Analyses with weighted $\mathbf{A_g}$ were more likely than with the corresponding unweighted $\mathbf{A_g}$. The most likely model for each trait was with weighted $\mathbf{A_g}$ using $P_n$ < 0.05, which yielded genomic direct heritability estimates of 0.46, 0.27 and 0.44 for BWT, WG and PWG, and genomic maternal heritability estimates of 0.29, 0.41 and 0.21.

**W38 Genomic evaluation of Holstein cattle in Canada utilizing MACE proofs.** F. S. Schenkel*[1], M. Sargolzaei[1], G. Kistemaker[2], G. B. Jansen[3], P. Sullivan[2], B. J. Van Doormaal[2], P. M. VanRaden[4], and G. R. Wiggans[4], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*Canadian Dairy Network*, *Guelph, ON, Canada*, [3]*Dekoppel Consulting*, *Chiaverano, TO, Italy*, [4]*Agricultural Research Service-USDA*, *Beltsville, MD*.

Researchers in Canada and the United States are collaborating to develop and integrate genomic evaluations into their national genetic evaluations for dairy cattle in 2009. There are substantially more genotyped Holstein bulls with MACE proofs than with domestic Canadian proofs in Canada. The use of MACE proofs in addition to domestic proofs for estimating marker effects might, therefore, increase the reliability of genomic prediction in Canada. A validation study was carried out to assess the usefulness of MACE proofs for genomic prediction of 34 traits, including production, SCS and type traits. De-regressed proofs (DD) of genotyped bulls born between 1952 and 2000 (predictor bulls) with February 2005 domestic proofs (*n=1,097*) or alternatively with February 2005 domestic proofs or November 2004 MACE proofs (*n=4,127*) were used to estimated the effect of 38,416 SNP that were selected from the Illumina BovineSNP50™ chip used for genotyping. Then 2005 genomic enhanced parent average (GPA) of younger proven bulls born between 2000 and 2004 (*n=524*) with domestic proofs in November 2008, but only a parent average available in 2005, were predicted using the estimated SNP effects. The squared correlation ($r^2$) between GPA and the 2008 domestic DD was calculated. The average reliability of the DD of predictor bulls was 0.93, 0.88 and 0.89 for production, SCS, and type traits using domestic proofs only, and 0.82, 0.68 and 0.67 when MACE proofs were included. Despite the lower average accuracy of DD, the use of MACE proofs on average increased the $r^2$ by 0.12, 0.10 and 0.06 points compared to the use domestic proofs only for production, SCS and type traits, respectively. Thus, the use of MACE proofs increased the prediction ability of GPA and, therefore, should be considered in the genomic evaluation of Holstein cattle in Canada.

**Key Words:** genomic evaluation, MACE proofs, Holstein cattle

**W39 Integrated software tools for genome-wide association analysis and genomic prediction in livestock.** J. R. O'Connell*, *University of Maryland School of Medicine*, *Baltimore*.

With the availability of dense SNP chips in many livestock species such as bovine, porcine and ovine, software tools designed to efficiently analyze large numbers of single nucleotide polymorphisms (SNPs) for association to quantitative traits and calculate genomic breeding values are needed. The program MMAP (mixed model analysis in pedigrees) integrates both established and novel algorithms to efficiently analyze SNP data in pedigrees. MMAP allows genome-wide association analysis using single or multi-SNP and/or haplotype fixed effect models accounting for residual variation through a relationship matrix derived from pedigree or genomic data. Genomic selection is implemented using both fixed and random effect models. Genotype error detection is implemented using a penetrance model to compute posterior probability distributions for each animal with genotype calls. The 2008 QTL-MAS workshop data set was used validate the algorithms and performance. The data comprises 6000 SNP genotypes simulated in a seven-generation swine pedigree and a quantitative trait with 30% heritability controlled by major and random QTLs. Genomic regions harboring simulated QTLs were accurately identified in the single SNP analysis. Regression model building identified multi-SNP models that contained location specific signals with effect size estimates similar to simulated values. Genomic breeding values derived from multi-SNP effect estimates had correlation of 0.8 with the true breeding values, similar to values reported using Bayesian methods on this data set. In summary, MMAP has user-friendly command line options to choose analysis option. The program is written in C and will be distributed under the GNU Open Source license.

**Key Words:** genomic selection, genomewide association, quantitative trait

**W40 Effect of CSN2 gene polymorphism on somatic cell count in Czech Fleckvieh.** J. Riha*, I. Manga, J. Bezdicek, and J. Subrt, *Agroresearch, Ltd.*, *Rapotin, Czech Republic*.

The goal of this study was to assess the genetic variability of *CSN2* gene polymorphism and its effect on somatic cell count (SCC) in the milk of Czech Fleckvieh. SCC is a key milk quality parameter and status indicator of mammary gland health with high economic impact. Currently, the *CSN2* gene is being used as a major tool in a number of marker assisted selection breeding schemes in dairy cows. The reason for its use is the known positive influence of allele *A2* on human health. The DNA

samples required for molecular analysis were isolated from cattle blood using a columned method (Jet quick DNA spin kit, Genomed$^{SM}$, USA). Amplification of the PCR product and PCR-RFLP test was performed according to standard method. The dataset consisted of the genotypes of 230 unrelated Czech Fleckvieh cows. The effect of the genotypes was calculated using the GLM procedure with the effects of lactation number and genotype of the *CSN2* gene. The milk SCC was represented as a decadic logarithm. The estimated genotype frequencies consisted of *A1A1* (7.44%), *A1A2* (41.36%) and *A2A2* (51.2%). The basic statistical parameters of the whole model were: r = 0.502, p = 0.000. Likewise, the effect of the lactation stage on SCC reached statistical significance as well as the effect of the *CSN2* genotype ($P \leq 0.05$). Using the Post-hoc Tukey HSD test, significant differences between *CSN2* polymorphisms and SCC were revealed. Individuals with *A1A1* genotype had higher SCC than the *A2A2* ($P \leq 0.001$) and *A1A2* genotypes ($P \leq 0.05$). The SCC decreased according to genotypes in the order: *A1A1* > *A1A2* > *A2A2*. The existence of possible positive phenotypic effects between milk yield and SCC failed to explain this observation as the cows with the *A2A2* genotype had the highest milk production in our dataset. The positive finding is that the valuable *A2A2* genotype is associated with the lowest number of somatic cells and this may indicate new possibilities for applying the *CSN2* marker in the process of Czech Fleckvieh selection. However, the general biological mechanism of this association remains unknown.

**Key Words:** CSN2 gene, somatic cell count, Czech Fleckvieh

**W41 Molecular genetic characterization of Nigerian goats.** M. Okpeku*[1], M. Ozoje[2], M. J. O'Neill[3], and I. Imumorin[4], [1]*Niger Delta University, Amassoma, Bayelsa State, Nigeria*, [2]*University of Agriculture, Abeokuta, Ogun State Nigeria*, [3]*University of Connecticut, Storrs, CT*, [4]*Cornell University, Ithaca, NY*.

The domestic goat is one of the important livestock species in Nigeria. They are adapted to the varied climatic conditions and representative of an uninvestigated source of genetic diversity. In this study, we assess genetic diversity in Nigerian goats using 10 microsatellite markers in 295 goats. Breeds were sampled from farms, market places and rural homesteads in the South-western region of the country. The mean number of alleles per locus (NA) ranged from 6.8 in Sahel goats to 10.8 in West African Dwarf (WAD) goats. The mean expected heterozygosity (He) ranged from 0.732 in Sahel to 0.834 in WAD goats. Deviations from Hardy-Weinberg Equilibrium (HWE) were statistically significant ($P < 0.05$). The DA measure of genetic distance between pairs of breeds indicated that the lowest distance was between WAD and Sahel (0.293) and the highest distance was between Red Sokoto and Sahel (0.585). An analysis of molecular variance (Fst) of 0.078 indicated that 89.6% of variance exists among Nigerian goat breeds. Our dendogram clustered Nigerian goats into two major breeds. Our study concludes that Nigerian goat populations can be classified into distinct two genetic groups or breeds and not three current breeds based on these microsatellites. Further studies using more molecular makers in a much larger population would be worth exploring.

**Key Words:** microsatellite DNA, genetic diversity, Nigerian goats

**W42 Analysis of distributions of estimated QTL effects for dairy cattle.** G. Gaspa, M. A. Pintus, R. Steri, S. Sorbolini, and N. P. P. Macciotta*, *Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari, Italia*.

The infinitesimal model used to explain the inheritance of quantitative traits has been the paradigm of selection so far. However, results of QTL studies seems to support a model with a small number of loci with large effect and several ones with small effect. In this study three theoretical distributions (Lognormal, Weibull and Gamma distribution) were used to model QTL effect distributions for milk yield (MY), protein yield (PY), protein percent (PP), fat yield (FY), fat percent (FP), type traits (TT) and all milk production traits scaled by genetic standard deviation (AT). All data were retrieved from published QTL mapping experiment in the period 1995-2008. Inclusion of records in the analysis was based on the significance level of the test (p-value<0.05). The goodness of fit of the three distributions was assessed using Kolmogorov-Smirnov, Cramer-von Mises and Anderson-Darling test. Table 1 reports gamma function parameters. The gamma function fitted all QTL effects data but MY and PP. The lognormal distribution fitted FY, FP, PY and AT data. Weibull distribution showed a goodness of fit only for FY, FP and PP (data not shown). These figures partially agree with previous results, that indicated the gamma distribution as the most suitable one for modelling QTL effects. Even if the effect of the genes are affected by bias due to the specific conditions if each study, these results seems to confirm the general hypothesis of the existence of a large number of QTLs with small effects and of a few ones with large effects.

**Table 1. Parameters of Gamma distribution used to fit QTL effects**

| Trait | n | Mean±sd | Scale (α) | Shape (β) |
|---|---|---|---|---|
| AT (σA) | 148 | 0.764 ± 0.410 | 0.243 | 2.879 |
| MY (Kg) | 115 | 189.9 ± 134.2 | 94.574 | 2.004 |
| FY (Kg) | 79 | 9.335 ± 4.575 | 2.244 | 4.159 |
| PY (Kg) | 80 | 7.018 ± 3.489 | 1.735 | 4.045 |
| FP (%) | 87 | 0.0013 ± 0.0008 | 0.00059 | 2.205 |
| PP (%) | 48 | 0.0005 ± 0.0003 | 0.00015 | 3.226 |
| TT (σA) | 91 | 0.811 ± 0.328 | 0.13285 | 6.111 |

**Key Words:** QTL, gamma distribution

**W43 Investigation for increase reproduction rate with used of identification QTL associated with twining in Shall sheep.** N. Hedayat-Evrigh*, S. R. Miraei-Ashtiani, and A Nejati-Javaremi, *University of Tehran, Karaj, Tehran, Iran*.

reproduction is one of the most important economical traits in sheep breeding and recent discoveries shows that it is influenced by a number of major genes. The high prolificacy in Inverdal sheep is the result of a mutation in the BMP15 oocyte-derived growth factor gene. this study was carried out to detect the possible polymorphisms in FecXI gene. the Inverdale prolificacy gene could markedly improve reproductive efficiency in commercial flocks, but as homozygous carrier Inverdale ewes are infertile, it is imperative that these animals are identified at an early age and excluded from breeding stock. Also because native sheep of Iran have low fertility and that substituted with foreign sheep, Therefore for conserved biodiversity in native sheep This study carried out to detect the possible polymorphism in FecxI gene until used of results for increas fertility in this sheep. PCR-RFLP method used to be developed fecXI mutant allele. This study was performed using a

Blood samples were collected from 239 ewes of Shall sheep. Genomic DNA was extracted using modified salting-out method. The polymerase chain reaction (PCR) was carried out for amplification of a fragment with 204 bp at the mentioned locus. For genotyping the individuals at Inverdal locus, the resulted amplified fragments were digested using XbaI restriction enzyme. Shall breed sheep was tested for the presence of the FecXI mutation of BMP15. There was no evidence of FecXI in shall breed sheep sampled. All individuals in the sample showed wild genotype (++). Considering the phonotypic records, the obtained result indicates that in this breed, the relationship of genetic factor responsible for twining or multiple lambing rates with reported mutated alleles at Inverdal major gene is very unlikely. For suppression of elimination native breed we must increase fertility and multiple lambing rates in this sheep and others native sheep. Therefore can with identify and detected major genes affective on this trait increase twinning in native breed. We offer investigate for other major genes effect that identified.

**Key Words:** Shall sheep, FecXI, PCR-RFLP

**W44 Diversity of *ureC* genes from rumen microflora metagenomic library.** S. G. Zhao, J. Q. Wang*, K. L. Liu, D. Li, P. Yu, and D. P. Bu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Due the fact that the majority of rumen bacteria were still uncultured, information about ruminal urease gene sequence and phylogenetic diversity were scare. To resolve this problem, a functional screen for urease-active clones was conducted for a rumen bacterial artificial chromosome library from dairy cow rumen microflora. Polymerase chain reaction degenerate primers based on the *ureC* gene which was conserved in ureolytic bacteria were designed and used to amplify the *ureC* genes from positive clones. The universal 16s bacterial primers were used to amplify the 16s rRNA gene of positive clones. Sequences were blasted against GenBank database, and phylogenetic tree were built by Mega 4.0 software. Sixteen clones (U1-U16) were identified as ureolytic positive using urease segregation agar. Four clones (U1, U5, U13 and U15) containing *ureC* genes were identified. The phylogenetic tree based on *ureC* revealed that U1, U5, U13 and U15 clustered to Firmicutes, ε-Proteobacteria, β-Proteobacteria and Actinobacteria, respectively. U1 clone contained a partial 16s rRNA sequence had the most identity to Staphylococcus, which was in agreement with *ureC* phylogenetic analysis. Taking together, this study provided first evidence for the phylogenetic diversity of ureolytic bacteria from cow rumen.

**Key Words:** metagenome, *ureC* diversity, rumen microflora

**W45 Analysis in silico and in vitro of caseinophosphopetides from different genetic variants.** A. M. Caroli*[1], O. Bulgari[1], S. Chessa[2], D. Rignanese[1], D. Cocchi[1], and G. Tulipano[1], [1]*Dept. SBB*, *Brescia, Italy*, [2]*Dept. VSA*, *Milano, Italy*.

Milk proteins are the main source of bioactive peptides with different functions. These milk activities are hidden in the native proteins and require the proteolitic cleavage to become extrinsic. Among biopeptides, caseinophosphopeptides (CPPs) possess the ability to bind and solubilise minerals, such as Ca++. The studies on the biological effect of different CPPs were carried out mainly in the bovine species, without taking genetic polymorphism into account. The biological activity of peptides released from milk protein digestion may be affected by amino acid exchanges or deletions resulting from gene mutations, as well as by prost-translational changes. The aim of this work was, first, to carry out an in silico analysis of the CPPs in order to detect differences in the amino acid sequence linked to species (bovine, caprine, and ovine) and genetic variants within each species. We analysed 3, 2, and 3 CPPs respectively carried by αs1-casein, β-casein, and αs2-casein. A total of 29 differences were detected among and within the considered species. Breeding could exploit such differences for improving dairy food biological value. Secondly, an in vitro test was developed to compare the effect on bone mineralization of four selected casein peptides which differ in the number of phosphorylated serines. The chosen peptides, related to different casein genetic variants, were obtained by chemical synthesis and tested on murine osteoblast cell line (MC3T3-E1). The main difference between peptide 1 and 2 was the occurrence of one phosphorylated serine at position 35 of the mature β-casein in the latter peptide. Moreover, Glu at position 37 of peptide 3 was substituted with Lys in peptide 4, carried by bovine αs2-casein C variant. Our results suggest that the distinct peptides in protein hydrolysates may differentially affect calcium deposition in the extracellular matrix. The higher content of phosphorylated serines might compete with calcium deposition, probably subtracting Ca++ from the culture medium. In addition, the genetic variation within peptides may influence their differential effect on osteoblast in vitro mineralization.

**Key Words:** caseinophosphopeptide, milk protein, genetic variant

**W46 Differential gene expression in the testis of adult male mice after treatment with Aflatoxin B1.** K. J. Austin*, R. R. Cockrum, A. M. Kaiser, and K. M. Cammack, *University of Wyoming*, *Laramie*.

The dietary mycotoxin, aflatoxin B1 (AFB1), adversely affects the reproductive health of humans and domesticated livestock through variable effects on oocytes in females and spermatogenesis and steroidogenesis in males. The genetic mechanisms by which fertility is disrupted by AFB1 are not known. The objective of this study was to determine changes in gene expression due to exposure to AFB1 in male mice. Male mice 4 wk of age were administered a placebo (control) or 50 μg/ kg BW AFB1 (AFB1 treated) daily for 45 d. Following the treatment period, males were mated to females for 10 d and then euthanized for testis tissue collection. Pregnant females were euthanized on gestational d 17. Fetuses were counted and examined for gross abnormalities. Among treated males, AFB1 tolerant and intolerant males were identified based on average number of fetuses produced per female and number TUNEL positive epididymal cells. Tolerant males produced a similar average number of fetuses (12.5 fetuses) as control males (13.4 fetuses), but a higher ($P$ = 0.01) number than intolerant males (7.6 fetuses). The number of TUNEL positive cells in intolerant males was numerically greater (136.5 cells) than in tolerant (55.0) and control (54.3) males. Microarray analyses were performed on selected control (n = 3), AFB1 tolerant (n = 3) and AFB1 intolerant (n = 3) males. Functional analyses revealed differential expression ($P < 0.05$) of 193 extra cellular space regulation genes, 45 immune response genes, 230 cell differentiation genes, and 49 signal transduction genes. Real-time RT-PCR confirmed numerical upregulation of IBSP and CCK genes and numerical downregulation of PGA, Crisp, and AR genes in AFB1 treated males compared to control males. Similar changes in expression of these genes were observed between AFB1 tolerant and intolerant males, with IBSP and CCK genes upregulated and Crisp and AR genes downregulated in intolerant males. Results from this study demonstrate that testicular gene expression is altered by administration of AFB1, and these genomic changes may contribute to variation in fertility observed among AFB1 exposed males.

**Key Words:** gene expression, aflatoxin, testis

**W47 Development of a two-species cDNA microarray for transcriptional profiling of sow and dairy cow reproductive traits.** M. F. Palin*[1], D. Beaudry[1], M. Vallée[2], N. Bissonnette[1], B. D. Murphy[3], and H. V. Petit[1], [1]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [2]*Université Laval, Québec, QC, Canada*, [3]*Université de Montréal, St-Hyacinthe, QC, Canada*.

Limited genetic progress has been reported for livestock reproductive traits in recent years. This is mainly due to the low heritability of these traits and because they are sex-limited and not measurable until sexual maturity is reached. Moreover, most economically important reproductive traits are polygenic. The development of transcript profiling techniques, such as microarray technology, offers the possibility to study polygenic traits more easily and provides the capacity to uncover molecular mechanisms and pathways that regulate reproductive functions. A two-species cDNA microarray was developed for profiling sow and dairy cow transcripts believed to associate with embryo survival during the peri-implantation period. This microarray comprises 1128 unique genes. Among them, are genes expressed in endometrial and embryonic tissues (day 15) and displaying differential expression between prolific Meishan X Landrace and Landrace breeds. This microarray also includes differently expressed genes from embryonic and endometrial tissues that were previously identified in day 17 pregnant dairy cows fed a diet containing flaxseed. Additional cDNAs have been included based on available literature on candidate genes or transcriptional profiling studies related to bovine and pig reproductive traits. This microarray was first used to identify transcripts differently expressed during the peri-implantation period (day 17) in dairy cows fed a control diet or a diet with 10% flaxseed. A list of up- and down- regulated genes was obtained for both embryonic and endometrial tissues. Among those, several prostaglandins-, immune- and development-related genes were identified. These genes illustrate the broad range of biological processes influenced by a diet rich in n-3 fatty acids. It also helps further the comprehension of different molecular pathways which modulate reproductive traits.

**Key Words:** microarray, reproduction, flaxseed

**W48 Genome-wide analysis of QTL effects in Canadian Holstein cattle using empirical Bayes method.** H. Li*[1], Z. Wang[1], P. Stothard[1], M. Sargolzaei[2], F. S. Schenkel[2], and S. Xu[3], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*University of Guelph, Guelph, ON, Canada*, [3]*University of California, Riverside*.

A whole-genome analysis to identify QTL affecting milk production traits was conducted on Canadian Holstein bulls using an empirical Bayes method. This method estimates prior variance components using marginal maximum-likelihood and then estimates QTL effects using the Bayesian shrinkage method given the estimated prior variance components as if they were the true prior variances. This method allows simultaneous estimation of all marker effects in a single model. An evenly spaced 316 SNP marker set covering the autosomal bovine genome with an average inter-maker distance of 8.80 Mb was selected from the Illumina BovineSNP50 BeadChip using the deferential evolutionary algorithm. De-regressed EBV of the traits from 646 proven bulls born in North America between 1985 and 2002 were used in this study. Genome-wise critical values for significant QTL effects at 5% level ($\alpha$=0.05) were determined by permutation tests. The numbers of significant QTL detected were 35, 27, 9, and 19 for fat yield, protein yield, fat percentage and protein percentage, respectively. On average, the sum of all the significant QTL effects contributed 18.6% of the total variance among the de-regressed trait EBVs, with fat percentage having the highest (28.0%) and protein yield the lowest (11.8%). The highest single marker effect explained 10.8% of the de-regressed EBV variance (fat percentage). The significant putative QTLs identified in this study will be further investigated to potentially identify the causal mutations within the nearby candidate genes.

**Key Words:** QTL effect, bovine genome, Canadian Holstein cattle

**W49 Associations of single nucleotide polymorphisms in bovine fatty acid synthase gene with fat deposition and carcass merit traits in Hybrid, Angus and Charolais beef cattle.** K. Islam*[1], M. Vinsky[2], R. Crews[3], E. Okine[1], S. S. Moore[1], D. H. Crews Jr.[1,4], and C. Li[1,2], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [2]*Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, Alberta, Canada*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403-1st Avenue South, Lethbridge, Alberta, Canada*, [4]*Colorado State University, Fort Collins*.

The gene-specific polymorphisms of fatty acid synthase (FASN) were studied for their associations with fat deposition and carcass merit traits in beef cattle. FASN has functional importance in lipogenesis and its location is under the quantitative trait loci (QTL) region for subcutaneous fat on bovine chromosome 19, making it an attractive positional candidate gene. Genotyping of 3 non-synonymous, 1 synonymous and 1 intronic single nucleotide polymorphisms (SNP) between exon 20 and exon 36 of FASN were conducted in populations of 206 Angus, 187 Charolais and 464 Hybrid beef steers. Association analyses were carried out using an animal model as implemented in ASREML with a pedigree depth of 9, 6 and 1 generations for Angus, Charolais and Hybrid cattle populations, respectively. Fat deposition and carcass merit traits analysed in this study included ultrasound backfat thickness, ultrasound rib-eye area, average daily gain of ultrasound backfat thickness during feedlot test, average daily gain of ultrasound rib-eye area, carcass average backfat thickness, lean meat yield, carcass marbling score, carcass rib-eye area, slaughter weight, and hot carcass weight. A non-synonymous SNP was found to be significantly associated with carcass marbling ($P<0.05$), carcass average backfat thickness and lean meat yield in the Angus steers ($P<0.10$). An intronic SNP was also significantly associated with carcass marbling in the Angus steers ($P<0.05$). In the Charolais population, an intronic SNP had associations with slaughter weight ($P<0.05$) and ultrasound rib-eye area ($P=0.055$). In the Hybrid cattle population, a non-synonymous SNP was found to be significantly associated with carcass rib-eye area ($P<0.05$). These findings may provide insight into the role of FASN in regulating fat deposition in beef cattle.

**Key Words:** fatty acid synthase (FASN), single nucleotide polymorphisms (SNP), fat deposition and carcass merit in beef cattle

**W50 Association analyses of single nucleotide polymorphisms in bovine stearoyl-CoA desaturase and fatty acid synthase genes with fatty acid composition in commercial crossbred beef steers.** C. Li*[1,2], M. Vinsky[1], M. E. R Dugan[1], N. Aldai[1], and T.A. McAllister[3], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, Alberta, Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403-1st Avenue South, Lethbridge, Alberta, Canada*.

Single nucleotide polymorphisms (SNP) of bovine stearoyl-CoA desaturase (SCD) and fatty acid synthase (FASN) genes have been reported to have significant associations with fatty acid composition in Japanese

Black cattle and in purebred American Angus cattle, respectively. This study was conducted to evaluate associations of SNPs in SCD and FASN genes with fatty acid composition in commercial crossbred beef steers that originated from Desert Ranches near Lethbridge, Alberta. Fatty acid contents of 84 individual and groups of fatty acids in brisket adipose tissues from 235 steers were analyzed using a combination of GLC and silver-ion HPLC methods. The steers were genotyped on two previously reported SNPs of the SCD and FASN genes, the [C/T] SNP in the exon 5 of SCD that causes an amino acid change from alanine (type A) to valine (type V) and the g:17924A>G SNP in FASN that causes an amino change from threonine to alanine. Association analyses found that the ′C′ allele or type A of the SCD SNP was significantly associated with lower saturated fatty acids including 10:0, 14:0 and 20:0, higher monounsaturated fatty acids including 9c-14:1, 12c-16:1, 13c-18:1, 9c-20:1, higher polyunsaturated fatty acids including 10c12c-18:2, 11c13t-18:2, 12c14t-18:2, 9c15c-18:2, but lower polyunsaturated fatty acids of 9c13t-18:2 and 20:2n-6 ($P<0.05$). The `A' allele of the FASN SNP was significantly associated with higher saturated fatty acids of 13:0, 14:0. 15:0 and 17:0, lower unsaturated fatty acids of 9c11t-18:2, 9c-18:1, 9c-20:1, 20:3n-6, 22:4n-6, and higher unsaturated fatty acids of 9t11c-18:2, 10t12c-18:2, 9c-14:1, 12c-16:1, 10t-18:1, 6-8t-18:1 ($P<0.05$). These results provide further evidence that SCD and FASN are strong candidate genes influencing fatty acid composition in beef cattle.

**Key Words:** stearoyl-CoA desaturase (SCD), fatty acid synthase (FASN), fatty acid composition in beef cattle

**W51 Validation and characterization of 1536 fat-related gene-specific SNPs in beef cattle.** M. Vinsky*[1], K. Islam[2], P. Stothard[2], and C. Li[1,2], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, Alberta, Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*.

Gene-specific single nucleotide polymorphisms (SNP) are of particular importance in dissecting the genetic basis of quantitative traits as they can the direct genetic causes of phenotypic variation. In order to facilitate a whole genome candidate gene association study for fat deposition and carcass merit in beef cattle, a fat related gene-specific SNP panel consisting of 1536 SNPs was developed through searching public databases, mining the bovine SNP databases and through in-house SNP discovery. The 1536 SNPs were located in 418 candidate genes spanning 25 bovine autosomes. The fat related candidate genes were chosen based on their chromosomal location within or in close proximity to reported quantitative traits loci (QTL) for fat deposition in cattle and(or) their possible function and involvement in fat metabolism. Genotyping of the 1536 gene-specific SNPs was performed using the Illumina® Golden Gate Assay across Angus (N=313), Charolais (N=258) and Hybrid (N=456) cattle populations. In total, 1309 SNPs were successfully amplified in all 1027 animals with a successful call rate of 99.3% across all three populations. Of the 1309 SNPs amplified, 357 SNPs were found monomorphic across all the three beef cattle populations. In the Angus population, 827 SNPs were polymorphic and 69 SNPs of those had a minor allele frequency (MAF) less than 0.05. In the Charolais population, 918 SNPs were polymorphic and 82 of those had a MAF smaller than 0.05. In the Hybrid population, 64 of the 918 polymorphic SNPs had MAF smaller then 0.05. This gene-specific SNP panel will provide a useful tool for whole genome candidate gene association studies for fat deposition and carcass merit traits in different breeds of beef cattle.

**Key Words:** single nucleotide polymorphisms (SNP) validation, candidate genes, beef cattle

**W52 Use of low density SNP chip for parental verification in US Holsteins.** S. Tsuruta*[1], I. Misztal[1], and T. J. Lawlor[2], [1]*University of Georgia, Athens*, [2]*Holstein Association USA Inc., Brattleboro, VT*.

A subset of SNPs from the Illumina BovineSNP50 genotyping Beadchip, consisting of 73 loci on 28 chromosomes, was evaluated for their effectiveness to verify parentage in Holsteins. These 73 SNPs are part of the parentage panel, being recommended by Heaton et al. (2002), which could be included in a low density SNP chip. Genotypes on 10,442 Holsteins were available, including 9128 animals with only their sire genotyped, 1331 animals with both sire and dam genotyped and 61 animals with only the dam genotyped. The average minor allele frequency (MAF) was 40%, with a minimum and maximum of 19%, and 49%, respectively. Number of exclusions (incompatible alleles: AA/BB or BB/AA) was used to test parentage. The probability of zero exclusions among random pairs of animals can be calculated as $[1-2q^2(1-q)^2]n$ and the average number of exclusions as $2nq^2(1-q)^2$ , for n loci and MAF of q, assuming no genotyping errors, no mutation, and unlinked loci. For n=73 and q=0.4, the probability is 0.00013 and the average number of exclusions is 8.4. In our putatively known animal-sire combinations, 9120 pairs had zero exclusion, 5 pairs had a single exclusion, and 3 pairs each with 2, 4 or 6 exclusions. In our putatively known animal-dam combinations, 1390 pairs had zero exclusion and 2 pairs had a single exclusion. Using a threshold of less than 2 exclusions, the rate of false negatives was 0.00099. For 9069 random animal-bull and 1373 animal-cow combinations, excluding our putatively known animal-parent pairs, the average numbers of exclusions were 12±7 and 11±6 with a minimum of 1 and a maximum of 51 and 46, respectively. The modes were 8 and 9, respectively, reflecting a skewed distribution. A single exclusion occurred in 23 animal-bull and 1 animal-dam combinations. Using a threshold of less than 2 exclusions, the rate of false positives was 0.0025. A low density chip may be quite useful for parentage testing.

**Key Words:** SNP, parental verification, Holsteins

**W53 Characteristics of the bovine PL10 gene and its evolution in mammals.** T.-C. Chang and W.-S. Liu*, *The Pennsylvania State University, University Park*.

PL10 exists in a wide range of eukaryotes, from yeast, plants to animals. This gene has been evidenced to play an important role in male fertility in mouse. In order to investigate the biological roles and evolution of PL10, we first characterized PL10 in bovine (bPL10) and conducted a phylogenetic analysis for PL10 related genes. PL10 contains a DEAD motif and belongs to the DEAD box polypeptide 3 (DDX3) subfamily. DDX3 is a highly conserved helicase family with essential function in RNA metabolism. The other two major members of DDX3 are DDX3X and DDX3Y, located on the sex chromosome, while mammalian PL10 is autosomal. The human PL10 is a pseudogene, whereas the mouse PL10 (mPL10) is a major gene involved in spermatogenesis and believed to replace the role of mDDX3Y in male fertility. The bovine PL10, like mPL10, is intronless and expressed not only in testis but also in other tissues based on our RT-PCR expression analyses. The nucleotide similarity between bPL10 and mPL10 is 72.7%. Besides, the similarity between bPL10 and bDDX3X is 81.5%, while it's lower, ~74.6%, between bPL10 and bDDX3Y. The further sequence comparisons revealed that the PL10 homologous sequences are present in genomes of many other mammalian species, but most likely in a pseudogene format, which could be the relics of PL10 during evolution. The phylogenetic tree built from these homologous sequences among different species indicated that mammalian PL10 is closer to DDX3X. Therefore, we

proposed that mammalian PL10 could evolve from the DDX3X through the retroposition mechanism.

**Key Words:** PL10, DDX3 subfamily, bovine

**W54 Using a repeated measurements mixed model to analyse some environmental factors affecting weight at different ages of Arabi sheep breed of Iran.** H. Farhangfar*[1], B. Zinvand[2], M. B. Sayyadnezhad[3], and I. Mirzaee[4], [1]*Birjand University, Birjand*, [2]*Azad University of Shooshtar, Shooshtar, Iran*, [3]*Animal Breeding Centre, Karaj, Iran*, [4]*Agricultural Jihad Organisation, Khuzistan, Iran*.

A total of 2265 weight records at different ages belonging to 755 Arabi sheep breed of Iran were used to study some environmental factors applying a repeated measurements mixed model. Determining environmental factors affecting body weights is of great importance as genetic evaluation of candidate animals has to be practiced. The lambs in the data set were born between 1994 and 2004 in 16 herds of Khuzestan province. The traits studied were weight at ages 0 (birth), 3 (weaning) and 6 months. In the model, fixed environmental effects of herd, year of birth, sex, litter size, order of ewe lambing, lamb age at weighing, and two way interactions between sex and litter size, between lamb age and sex, between lamb age and litter size, between lamb age and year of birth, and between lamb age and herd were included. Lambs were also included in the model as subjects having repeated measurements over three categories of weighing. Unstructured variance-covariance option was assumed for fitting the model. Analysis was undertaken by using SAS software through mixed model procedure applying repeated measurements. The results obtained in the present research showed that except the order of ewe lambing, all other environmental factors significantly statistically ($P<0.05$) affected weight records of Arabi sheep. Least squares means of female lambs at ages 0, 3 and 6 were 3.54, 20.53 and 29.45 kg respectively and the corresponding figures for male lambs were found to be 4.42, 23 and 33.16 kg respectively. The results also indicated that the least squares means of weight at ages 0, 3 and 6 for single birth lambs were 3.97, 22.04 and 32.52 kg respectively and for twin birth lambs were 3.99, 21.48 and 30.09 kg respectively.

**Key Words:** Arabi sheep, weight, environmental effects

**W55 Improve reproduction with identification of polymorphism in FecXH gene in Shall sheep.** N. Hedayat-Evrigh*, S. R. Miraei-Eshtiani, and A. Nejati-Javaremi, *University of Tehran, Karaj, Tehran, Iran*.

Twinning is one of the most important traits in production of sheep breeding and also native breed sheep in Iran have low fertility and twining. Studies of the inheritance pattern of ovulation and litter size in prolific flocks have shown that major genes for prolificacy are segregated example Hanna gene (FecxH) in Hanna sheep. FecXH is a dominant located on the X chromosome. Knowledge of this mutation has prompted researchers to screen other prolific sheep breeds to determine whether this mutation is responsible for their high prolificacy. We considered an Iranian fat tail sheep known as Shall for this study. The ability to adapt to different environmental circumstance is a desirable characteristic of this breed. Therefore with increase twining this breed, used consistently for production by farmer. Shall ewes were sampled from commercial flock in Qazvin provinces. Blood sample were collected from 239 Shall ewes. PCR-RFLP method used to be developed FecXH mutant allele. This study was performed using a Blood samples were collected from 239 ewes of Shall sheep. Genomic DNA was extracted using modified salting-out method. For genotyping the individuals Hanna locus, the resulted amplified fragments were digested using SpeI restriction enzyme. SpeI restrictions enzyme were used to detect possible mutation. In this study we show that none of the sheep sampled carried the Hanna FecXH mutation in the BMP15 gene. And all samples showed wiled allele and fecX+/FecX+ genotype. Although Shall sheep breed has relatively high fecundity. But there are big differences in husbandry systems in which it evolved, and this could affect whether a spontaneous mutation leading to large litter size is retained or lost. Considering the phenotype records in this breed, the obtained result indicates that the genetic factor responsible for twining or multiple lambing rates is not related to reported mutant allele at Hanna major gene.

**Key Words:** native breed, FecXH, prolificacy

**W56 Comparison of genetic diversity between US and Kazak sheep breeds.** H. D. Blackburn*[1], Y. Toishibekov[2], C. Welsh[1], S. Spiller[1], and M. Brown[3], [1]*ARS-National Animal Germplasm Program, Ft. Collins, CO*, [2]*Institute of Experimental Biology, Almaty, Kazakhstan*, [3]*ARS-Grassinglands Research Laboratory, El Reno, OK*.

To secure US genetic diversity it is beneficial to compare US and non-US breeds. Such information may also be used to identify areas of sampling for diverse genetic resources. Kazakhstan (KZ) provides an interesting comparison due to its history of sheep production and proximity to the Silk Route, which likely facilitated genetic migration from the Fertile Crescent to China. With microsatellite markers it is possible to quantify genetic differences between US and KZ sheep breeds. Five KZ breeds were sampled: Arkharo-Merino (AM), Chyisskaya (CHY), Degresskaya (DEG), Edil-baevskaya (EDI), and Sary-Arkinsskaya (SA). The AM is a hybrid between wild Arkhar rams (Ovis ammon) and Merino, Precoce and Rambouillet ewes (Ovis aries), the other four breeds are coarse wooled and fat rumped. The 13 US breeds included: fine wool, meat types, long wool, hair, prolific, and fat rumped. Blood and semen samples were collected from both countries (n = 24.5/breed). DNA was extracted and genotyped using 29 FAO/ISAG panel microsatellites. Genotype data were analyzed using GENALEX and PHYLIP. The KZ breeds had greater allelic richness when compared to US breeds (7.8 vs 4.8, respectively). However, Rambouillet and Dorper were similar to KZ breeds with average allele numbers of 8.2 and 7.5, respectively. The KZ breeds had higher levels of heterozygosity when compared to US breeds. Among the four fat-rumped KZ breeds the genetic distances (GD) were relatively small (< 0.14), despite large geographic differences in sample derivation. Dorper and Karakul were the US breeds most closely associated with the CHY, DEG, EDI, and SA with GD ranging from 0.22 to 0.35. The GD between AM and Rambouillet (0.13) was unexpected given the Ovis ammon component of the AM, and suggests that during the formation of the AM that many of the genes associated with the Arkhar were selected against resulting in a population that is primary comprised of Merino/Rambouillet. Concluding, these results indicate substantial GD and variability between the US and KZ breeds evaluated, except for the AM and Rambouillet. The results also illustrate that genetic diversity is greater near the center of domestication.

**Key Words:** sheep, genetic diversity, conservation

**W57 Effect of vitamin E on chromatin integrity of ram epididymal sperm.** B. L. Sartini*, K. H. Petersson, and M. Procopio, *University of Rhode Island*, *Kingston*.

Oxidative stress can impair sperm function by peroxidation of the lipid bilayer and fragmentation of sperm chromatin impacting fertilization and subsequent embryonic development. If sperm are not adequately protected against oxidative damage, cyropreservation can enhance the effects of oxidative stress reducing post-thaw fertility. In livestock, addition of antioxidant vitamin E (VE) during sperm cyropreservation improves post-thaw ejaculated sperm quality although the impact of VE supplementation on epididymal sperm has not been investigated. In this study, the effect of VE (d-alpha tocopherol in emulsified base) supplementation on ram epididymal sperm chromatin integrity was examined. Starting at birth, rams (n= 12) were assigned to one of three treatment groups: 1.) 30 IU VE /kg body weight (BW) + 0.1 mg selenium (Se)/kg BW (VE 30, n = 3), 2.) 15 IU VE/kg BW + 0.1 mg Se/kg BW (VE 15, n= 3), or 3.) Emulsified base + 0.1 mg Se/kg BW (placebo, n=3). VE was administered parenterally every two weeks from birth to seven months of age. Selenium was given once within two days of birth. At seven months of age, epididymal sperm was collected at slaughter, cryopreserved, then analyzed for DNA fragmentation using the sperm chromatin structure assay (SCSA Diagnostics, Brookings, ID). Sperm motility was subjectively assessed microscopically before freezing. The DNA fragmentation index (% DFI) of the epididymal sperm from VE treated rams was not significantly different from placebo (VE 30 = 0.887% ± 0.3; VE 15 = 1.4% ± 0.7; placebo = 1.1% ± 0.2). In addition, sperm motility before cryopreservation was not significantly correlated with % DFI. In conclusion, VE treatment did not improve the integrity of ram epididymal sperm chromatin. Further study on the effects of vitamin E during the establishment of spermatogenesis in prepubertal animals will help elucidate the role of vitamin E in sperm production.

**Key Words:** sperm, ram, vitamin E

**W58 Association of beta-lactoglobulin and prolactin genes with milk production in East Friesian sheep.** E. A. Staiger*[1], M. L. Thonney[2], B. W. Buchanan[1], and R. G. Mateescu[1], [1]*Oklahoma State University*, *Stillwater*, [2]*Cornell University*, *Ithaca, NY*.

Milk production is an economically important trait for the sheep industry, however the trait is moderately heritable, expressed relatively late in life, and sex limited. The efficiency of selection for milk production in sheep would be improved by the identification of informative genetic markers. A single nucleotide polymorphism in β-lactoglobulin gene (BLG) and prolactin gene (PRL) were investigated with respect to the genetic merit (EBV) for milk production in East Friesian sheep. The EBV was estimated as the phenotypic deviation from the population mean of the animal's own performance combined with all its relatives' performance. Blood samples were collected from East Friesian ewes. Genotypes were determined by PCR amplification of a 120bp fragment of ovine BLG and 2.5kb fragment of ovine PRL followed by restriction enzyme digestion. The frequency of A and B allele for BLG was 0.69 and 0.31, respectively and the frequency of P and p allele for PRL was 0.13 and 0.87, respectively. Genotypic frequencies for AA, AB, and BB genotypes for BLG were 0.43, 0.52, and 0.05, respectively, and 0.01, 0.23, and 0.76, respectively for PP, Pp and pp genotypes for PRL. The Least Square Means (LSM) for EBV of AA, AB, and BB genotypes in BLG were 112.16, 112.25, and 72.53g of milk per day, respectively, indicating that ewes with at least one A allele would produce 40g of milk per day more than ewes with no A allele. However, this difference was not significant (P = 0.28), possibly due to the low occurrence of BB genotype given the selection for high milk yield within this population. The LSM for weighted EBV of PP, Pp, and pp genotypes in PRL were 153.21, 167.44, and 91.17g of milk per day, respectively, indicating that ewes with no P alleles would produce 73.6g of milk per day more than ewes with at least one p allele (P = 0.0001). These results show an association between PRL gene and milk production in sheep suggesting that this polymorphism could be used in a marker assisted selection program. However, additional genotyping in a different population may be necessary to prove an association between BLG gene and milk production in sheep.

**Key Words:** β-lactoglobulin, prolactin, milk production

**W59 An R package for fitting generalized linear mixed models in animal breeding.** A. Vazquez*, D. M. Bates, D. Gianola, K. A. Weigel, and G. J. M. Rosa, *University of Wisconsin*, *Madison*.

Linear mixed models have been extensively used in animal breeding for estimation of genetic parameters and prediction of breeding values associated with normally distributed traits. A more general class of mixed models is represented by the generalized linear mixed models (GLMM), which are appropriate for analysis of data from additional members of the exponential family, such as the Poisson or binomial. This class includes discrete variables such as disease records (e.g., absence or presence of clinical mastitis during lactation) or reproductive traits (e.g., number of inseminations). A standard quantitative genetic model poses that the effects of levels of some random factor (e.g., sire) are correlated. For this reason, routines for mixed models available in standard packages cannot be used for genetic analysis. The pedigreemm package for R was developed as an extension of the lme4 package and allows fitting mixed models with correlated random effects for Gaussian, binary and Poisson responses among others. A correlation between levels of the grouping factor is induced by post-multiplying the incidence matrix of the levels of this random factor by the Cholesky factor of the corresponding (co) variance matrix, e.g., the numerator relationship matrix between sires. Estimation methods available in pedigreemm include approximations to maximum likelihood and restricted maximum likelihood. The pedigreemm also allows the extraction of inbreeding coefficients and relationship matrix from a pedigree. Additionally, the general methods applicable to lme4, as ranef(), plot(), or anova() to name a few, can be also used with pedigreemm.

**Key Words:** R package, generalized linear mixed models, pedigree

**W60 Genetic analysis of lean tissue growth and carcass traits in Large White swine.** T. M. Gonçalves*[1], A. L. L. Costa[1], A. I. G. Oliveira[1], and M. C. A. M. Bink[2], [1]*University of Lavras*, *Lavras, Minas Gerais, Brazil*, [2]*University of Wageningen*, *Wageningen, the Netherlands*.

A Bayesian approach was undertaken to estimate genetic parameters and detect major genes (MG) to dressing percentage (DP), carcass length by the Brazilian method of carcass classification (CLMB), average backfat thickness (ABT), backfat thickness at 6.5cm from the dorsal line (P2), loin eye area (LEA), ham yield (HY), lean (LP) fat (FP) and lean cut percentages (LCP), fat weight:lean weight ratio (FLR), and lean tissue growth rate (LTGR). Data from 711 Large White swine were analysed by fitting different genetic models, i.e., the Finite Polygenic Model (FPM), where the number of genes in the FPM is included as an additional random variable, the Infinite Polygenic Model (IPM) and a combination

of these two models. The heritability estimates in the IPM model were 0.17, 0.30, 0.15, 0.16, 0.33, 0.20, 0.51, 0.38, 0.38, 0.42 and 0.42 for traits DP, CLMB, ABT, P2, LEA, HY, LP, FP, LCP, FLR, and LTGR, respectively. The FPM model yielded clearly lower estimates for traits CLMB, ABT, P2, HY, LP, FP, LCP and FLR, respectively. The FPM model revealed posterior evidence for at least one MG at decisive level for traits CD, LEA, LCP and LTGR; at strong level for traits CLMB, FP and FLC; and at positive level for traits P2 and HY. The combined model yielded decisive evidence for presence of one MG for traits CD, LEA and LTGR, while the heritability estimates for these traits were 0.11; 0.36 e 0.17, respectively. These findings suggest that the genetics of growth and carcass traits may be better studied by using models that combine polygenic and major gene effects.

**Key Words:** swine, finite polygenic model, major genes

**W61 Factors affecting weaning-to-first service interval in a Landrace-Large White swine population in Northern Thailand.** C. Chansomboon[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand*, [2]*University of Florida, Gainesville.*

Non-productive sow days measured as weaning-to-first service interval (WSI) is an economically important trait in commercial swine production. Thus, a reduction in WSI would help increase efficiency and lower production costs. The aim of this study was to characterize factors affecting WSI in a Landrace-Large White commercial swine population in the province of Chiang Mai, Northern Thailand. The dataset contained 12,974 litter records from 2,596 sows collected from 1989 to 2008. Sows were raised in an open-house system and received the same feeding and management. Sows were from 4 breed groups: Landrace (L), Large White (Y), L × Y (LY), and Y × L (YL). Parity of sow was classified as 1, 2, 3, 4, 5, 6, and ≥ 7. Seasons were winter (November to February), summer (March to June), and rainy (July to October). Preliminary analyses showed no effect of age at farrowing of the sow and number piglets weaned on WSI. Thus, the model for WSI contained the fixed effects of farrowing year-season of the sow, parity of the sow, lactation length, and breed group of sow, and a random residual effect. Year-season of farrowing was an important source of variation ($P < 0.01$). Year-season effects for WSI ranged from 4.60 ± 0.51 days (1991-summer) to 9.22 ± 0.87 days (1989-rainy). The WSI was longer ($P < 0.01$) for first-parity sows (7.91 ± 0.12 days) than for sows of other parities (5.72 ± 0.15 days to 6.10 ± 0.12 days). Landrace sows had similar WSI (5.89 ± 0.09 days) to Y sows (6.00 ± 0.09 days). Crossbreds LY sows (6.23 ± 0.16 days) and YL sows (6.67 ± 0.16 days) had longer WSI than purebreds sows ($P < 0.01$). Heterosis estimates were 0.29 days (4.8%) for LY sows, and 0.73 days (12.2%) for YL sows. Reciprocal differences for WSI indicated that LY sows had lower production costs than YL sows. Crossbred sows had longer WSI than purebred sows, perhaps due to lower adaptability to tropical conditions and unmet higher nutritional requirements.

**Key Words:** swine, weaning-to-first-service interval, tropical

**W62 Use of random regression models for the genetic analysis of weight gain from electronic swine feeders.** C. Y. Chen*[1], I. Misztal[1], S. Tsuruta[1], B. Zumbach[1,2], M. Łukaszewicz[1,3], W. O. Herring[4], J. Holl[4], and M. Culbertson[4], [1]*University of Georgia, Athens*, [2]*Norsvin, Hamar, Norway*, [3]*Institute of Genetics and Animal Breeding, Polish Academy of Sciences, Wólka Kosowska, Poland*, [4]*Smithfield Premium Genetics Group, Rose Hill, NC.*

Body weights (BW) of 1,921 Durocs from electronic feeders were used for genetic analysis of weight with random regression models (RRM). Daily, weekly, and bi-weekly average daily gain (DG, DGW, and DGB) were calculated from the average daily BWs with 69,068 records of DG. Estimates from various RRM for DG were erratic. Subsequent tests using a repeatability model for DG, DGW and DGB indicated that heritability of daily gain averaged over d days is approximately 1/(3.3+100/d) and is very low for DG (< 1%) but higher for DGW (6%) and DGB (9%). Subsequent analyses with RRM used DGB. Two RRM were used: with quadratic Legendre polynomials (RRM-L) and with three knot (100, 125, and 150 d) linear splines (RRM-S). Effects in the model included fixed year-biweek-pen and random litter, animal, permanent environment. For both models, the residual variances at 100 d and 150 d were much bigger than at 125d while the genetic variance was the highest at 125d. For RRM-L, heritabilities were 8%, 33%, and 9% at 100 d, 125 d, and 150 d of age. Same estimates were 2%, 26%, and 7% with RRM-S models. Repeatabilities estimated at the three ages were similar (13% to 40% with RRM-L and 9% to 40% with RRM-S). Correlations of 100-125 d, 100-150 d, and 125-150 d of ages were 0.23, -0.07, and 0.66 with RRM-L and 0.39, -0.42, and 0.67 with RRM-S. Adaptation to the feeder in the beginning of test and crowded environment at the end of the test period could cause large residual variances observed in the study. Data from feeder stations can be used for longitudinal analysis of daily gain averaged biweekly. The genetics of daily gain at the beginning and at the end of trail can be different.

**Key Words:** daily gain, pig, random regression

## Dairy Foods: Dairy Products/Chemistry/Enzyme

**W63 Calcium reduces DMH-induced large intestinal tumors in male Wistar rats.** K. Sivieri*[1] and E. Rossi[2], [1]*Universidade Norte do Paraná-UNOPAR, Londrina, Paraná, Brasil*, [2]*Universidade Estadual Pulista-UNESP, Araraquara, São Paulo, Brasil.*

Different dietary factors can affect colorectal cancer incidence. However, the effect of increased levels of dietary calcium on neoplasms is unclear. The present study was designed to examine the influence of the yogurt fermented with *Enterococccus faecium* CRL and added calcium (600mg/l) on experimental colon carcinogenesis induced by parenteral administration of dimethylhydrazine (DMH). 8-week old rat were given subcutaneous DMH injections at 20 mg/kg once a week during three months. Four groups were used: 1) non-treatment control; 2)DMH control; 3) yogurt fermented with *Enterococcus faecium* CRL 183-DMH plus calcium and induced with DMH (Calcium yogurt) and 4) yogurt fermented *Enterococcus faecium* CRL 183 and induced with DMH (yogurt). Animals were then sacrificed and the incidence of tumors and the number of tumors per tumor-bearing rat were determined. The all groups were compared histologically and TNF-α, IFN-γ and IL-4 cytokines. The non-treatment control not develop tumor. Calcium yogurt group showed a 50% inhibition in incidence in average number of tumors and significantly decreased the number of rats with multiple tumors and TNF-α, IFN-γ and IL-4 cytokines increasing in this group. We conclude that a low dietary calcium supplement in rats inhibits colon cancer carcinogenesis induced by DMH and enhanced the immune response.

**Key Words:** calcium, yogurt, colon cancer