607 cows) and Holstein (n = 702 cows). Significance of differences is marked as *($P \leq 0.05$), **($P \leq 0.01$). A found higher protein content in Czech Fleckvieh was associated with particular genotypes: BB (3.56%) > AB (3.55%) > *AA (3.48%) > AE (3.43%) > EE (3.41%) > * BE (3.37%). Protein in Holstein: AB (3.32%) > AA (3.31%) > AE (3.30%) > BE (3.28%) > * EE (3.26%). Fat in Czech Fleckvieh: AB (4.2%) > AA (4.14%) > BB (4.11%) > BE (4.09%) > EE (4.05%) > **AE (3.93%). Fat in Holstein: AB (3.86%) > AA (3.85%) > EE (3.83%) > AE (3.82%) > ** BE (3.72%). From the above it is clear that differences between CSN3 genotypes were not considerable and only in some cases significant.

Key words: kappa-casein, milk composition

T43 Effect of DGAT1, TG and leptin gene polymorphisms on milk production traits in Holstein-Friesian cows in Hungary. I. Anton*[1], K. Kovács[1], G. Holló[2], V. Farkas[3], F. Szabó[3], and A. Zsolnai[1], *[1]Research Institute for Animal Breeding and Nutrition, Herceghalom, Hungary, [2]University of Kaposvár, Faculty of Animal Science, Kaposvár, Hungary, [3]University of Pannonia, Georgikon Faculty of Agriculture, Keszthely, Hungary.*

The objective of this study was to estimate the effect of the acylCoA-diacylglycerol-acyltransferase 1 (DGAT1), thyroglobulin (TG) and leptin locus on milk fat, milk protein and milk yield in Hungarian Holstein-Friesian cows. A lysine/alanine (K232A) polymorphism in DGAT1 -a microsomal enzyme that catalyzes the final step of triglyceride synthesis- has been proved to affect milk yield, as well as milk fat and protein content in different dairy cattle breeds. The effect of a 5′-polymorphism of TG gene- which product is the precursor of hormones that influence lipid metabolism- has been shown to affect milk fat content in cattle. Polymorphisms in the leptin gene have been associated with milk protein yield and milk yield. A total of 417 blood samples have been collected from different Holstein-Friesian herds and genotypes were determined by PCR-RFLP (polymerase chain reaction-restriction fragment length polymorphism) assay. Milk production data were recorded throughout 3 consecutive lactations and statistical analyses have been carried out to find association between individual genotypes and milk production traits. The data set was analyzed with SPSS 15.0 for Windows software. Multivariate ANOVA (general linear model, GLM) was applied to determine differences in milk production traits, where DGAT1, TG and leptin genotypes, birth year, number of lactations and calving season were included as fixed effects and 305-d-milk yield, 305-d-milk fat percentage and yield and 305-d-milk protein percentage and yield were considered as dependent variables. In case of DGAT1 locus, AA homozygous animals produced the highest values of fat yield and protein yield ($P < 0.05$). Milk yield decreased consistently ($P < 0.05$) from genotype AA/AA through to GC/GC. Among TG genotypes, TT animals had the highest ($P < 0.05$) 305-d-milk fat percentage and yield values. Referring to leptin polymorphism, CC cows produced higher ($P < 0.05$) 305-d-milk protein values than TC animals. The project was supported by the Hungarian Scientific Research Fund (project 78174).

Key words: DGAT1, TG, leptin

T44 Correlation analysis of hepatic transcript abundance and lactational performance in postpubertal Holstein dairy heifers. J. Doelman, J. M. Kim*, H. Cao, N. G. Purdie, and J. P. Cant, *University of Guelph, Ontario, Canada.*

Dairy genomic research has recently grown in popularity, though investigation into the use of transcript abundance as a marker of future performance remains limited. The objectives of this study were to employ a statistical method to reduce variability within a microarray data set and subsequently identify correlations between gene expression signal intensity and performance measures during first lactation of 81 Holstein dairy heifers. Pearson correlation can be used to determine the underlying structure of a large data set through identification of a data subset that is well correlated to a particular variable. Partial Least Squares regression seeks to model dependent variables by means of a set of predictor variables but has yet to be applied in the field of dairy genomics. These 2 types of analysis were performed on microarray data from previous research that quantified gene expression signal from yearling Holstein heifers. To reduce the total number of genes used in the data set for regression analysis, the linear dependence of all genes in the entire normalized data set was measured against 18 DHI variables using Pearson correlation analysis. Results were pooled to generate 4 lists based on coefficient values and significance of $P < 0.05$. List 4 featured 1541 genes ($r^2 > 0.04$), list 3 contained 453 genes ($r^2 > 0.09$), list 2 was comprised of 140 genes ($r^2 > 0.12$) and list 1 consisted of 31 genes ($r^2 > 0.16$). Test set validation was used to fit the partial least squares model by creating a test and training set using the normalized expression data sets. The strongest correlation coefficients, $r^2 = 0.62$ (protein percentage) and $r^2 = 0.54$ (fat percentage) were obtained using list 1. Strong correlations were also found for 305 d protein yield ($r^2 = 0.40$, list 3) and protein percentage ($r^2 = 0.33$, list 4). Moderate correlation coefficients were also identified for breed class average milk ($r^2 = 0.21$, list 1) and protein ($r^2 = 0.24$, list 1). Identification of gene expression patterns in a predictive nature such as this offers a potential selection tool to be employed by producers.

Key words: heifer, correlation, gene expression

T45 Identification of a SNP in the gene *IL2* and its association with resistance against gastrointestinal infection by nematodes in goat. F. A. Bressani[1,5], P. C. Tizioto*[2], S. L. Meirelles[2], W Malagó Junior[1,2], R. Giglioti[3], A. M. G. Ibelli[2], J. G. G. Gromboni[4], E. Carrilho[5], L. G. Zaros[6], L. da Silva Vieira[7], and L. Correia de Almeida Regitano[1], *[1]Embrapa Southeast Embrapa Southeast Cattle Research Center, São Carlos, São Paulo, Brazil, [2]Federal University of São Carlos - UFSCar, São Carlos, São Paulo, Brazil, [3]State University of São Paulo - UNESP, Jaboticabal, São Paulo, Brazil, [4]UNICEP, São Carlos, São Paulo, Brazil, [5]University of Sao Paulo, São Carlos, São Paulo, Brazil, [6]Federal University of Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil, [7]Embrapa Goats and Sheep, Sobral, Ceará, Brazil.*

The gene IL2 encodes an interleukin which plays a role in inducing the maturation of T and B cells, important factors in the immune response to parasites in several species. Two hundred twenty-nine individuals of a F2 goat population were studied aiming at finding genetic markers for resistance to gastrointestinal infection. To accomplish this, a SNP in the IL2 gene was identified and its association with resistance to gastrointestinal infection was tested. The population investigated was an F2 generated from F1 Saanen (susceptible to gastrointestinal endoparasites), Anglo-nubian (resistant) crosses. Phenotypes consisted of eggs per gram (EPG) and were obtained by parasitological examination of feces samples. The data were transformed as log 10(EPG+1) and analyzed using the mixed procedure of SAS. Fixed effects included in the model were sex, sampling order, and age at sampling; while animal was fitted as random effect. Based on this analysis, 44 individuals with extremes EPG were selected. The gDNA of these animals

was obtained from isolated leukocytes by the salting-out method. Specific oligonucleotides were designed to obtain PCR products from IL2 gDNA which were sequenced in the ABI Prism 3100 Avant Sequencer (Applied Biosystems). The sequences were further analyzed using the Phred, Phrap, and Consed programs. A SNP (G/A) identified within the intron 2 of IL2 gene was analyzed by Fisher test and showed association with resistance against gastrointestinal infection by nematodes ($P = 0.0489$). Further studies with the whole F2 population are in progress to confirm this association.

Key words: IL2, SNP, goat

T46 Effect of the DGAT1 gene polymorphism on the backfat thickness and fat-tailed weight in Iranian Lori-Bakhtiari sheep. H. Mohammadi*, M. Moradi Shahrebabak, and M. Sadeghi, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

Backfat thickness refers to the amount of fat over the animals back and strongly associated with percentage of retail product, represents a valuable sheep quality trait, and fat-tail demands sheep industry attention for many reasons. To name a few, lean to fat-tail ratio improvement means better feed conversion efficiency. The DGAT1 catalyzes the final step of triglyceride synthesis and the gene is located on the centromic end of bovine chromosome 14. The DGAT1 gene has been mapped to ovine chromosome 9. Polymorphism in the DGAT1 gene has been associated with milk fat percentage and body fatness. The objective of this study was to evaluate the effect of the DGAT1 gene locus on ovine quality traits in the Lori-Bakhtiari sheep breed in Iran. A total of 152 blood samples were obtained from different sex Lori-Bakhtiari sheep. PCR primers were assumed from previously reported studies (Xu et al., 2008). A 309 bp fragment from exon 17 was amplified and digested by AluI with PCR-RFLP method. The association between genotypes and fat-tailed weight and backfat thickness was analyzed. DGAT1 CC animals showed the highest fat percentage values for fat-tail and backfat thickness, the difference between CC and TT genotypes was significant ($P < 0.05$). The results of this study identified novel associations; The C allele had a positive effect on fat-tail weight and backfat thickness in fat-tailed sheep. The results of this study suggest that the TT genotype of DGAT1 could be regarded as a molecular marker for breeding programs to improve carcass traits in fat-tailed sheep breed.

Key words: DGAT1, single nucleotide polymorphisms (SNP), fat deposition and carcass traits

T47 Identification and evaluation of an IGF-I gene polymorphism in a Zel sheep population using RFLP/HaeII. S. M. Kazemi*[1], C. Amirinia[2], S. Gharaveysi[1], H. Emrani[2], and A. Yilmaz[3], *[1]Department of animal Science, Islamic Azad University, Qaemshahr Branch, Qaemshahr, Mazandaran, Iran, [2]Department of Animal Biotechnology, Animal Science Research Institute of Iran, Karaj, Alborz, Iran, [3]Department of Animal Sciences, The Ohio State University, Columbus.*

The IGFs play an important role in regulating somatic growth, and they are affected by nutritional and other conditions during growth. Polymorphisms of IGF genes are reported to be significantly associated with many traits including growth and reproductive traits. In this study, 142 DNA samples from Zel sheep were used to detect a promoter region polymorphism in the insulin-like growth factor-1 (IGF-1) gene. To extract DNA from blood we used a Salting-out procedure. Primers were obtained for amplification of the specific segment. Polymerase Chain Reaction (PCR) was accomplished after finding the best reaction conditions and the specific segment amplified well. RFLP fragments were used to detect the polymorphism in the segment. RFLP analysis was performed by incubating the PCR products with HaeII restriction enzyme at 37°C for 4 h. Gels (3.5% agarose) were visualized by using ethidium bromide. The polymorphism was observed and the evaluation of the results relieved 2 alleles and 3 genotypes. The alleles were A and B with frequencies of 0.71 and 0.29, respectively. The genotypes AA, BB and AB had frequencies of 0.47, 0.06 and 0.47, respectively. The data were analyzed for genetic variation statistics using PopGene software (version32) and no deviation from Hardy-Weinberg equilibrium was observed in this study.

Key words: Zel sheep, IGF-1, polymorphisms

T48 Haplotype structure of telomerase reverse transcriptase (*turTERT*) gene in the turkey, *Meleagris gallopavo*. A. M. J. B. Adikari*, J. Xu, X. Guan, and E. Smith, *Virginia Polytechnic Institute and State University, Blacksburg.*

The recently released turkey genome sequence offers an opportunity to characterize and define the role of some genes that affect turkey performance and productivity. Our objective for this study was to screen the telomerase reverse transcriptase (*turTERT*) gene for structural variation based on single nucleotide polymorphisms (SNPs) and haplotypes using a diversity panel consisting of birds from heritage, commercial, and wild varieties. The rationale is that TERT influences some metabolic diseases including heart diseases, metabolic syndrome, and hypertension. Further, the levels of functional telomerase are critical for telomere maintenance whose shortening is associated with organismal aging and concomitant metabolic diseases. Primers used for long-range polymerase chain reaction (LR-PCR) were designed using the Primer 3 software. Each amplicon was gel purified, sequenced, and the SNPs detected using standard methods. Linkage disequilibrium (D') among SNPs was estimated using Visual Haplotype software. From 34 kb of *turTERT* gene screened, a total of 4 SNPs were detected in the introns. Allelic diversity ranged from 0.14 to 0.68. A total of 3 haplotypes were derived from the SNPs with frequencies that ranged from 0.09 to 0.59. While the diversity panel maximized detection of variation, both the SNPs and haplotypes appear to show that the Royal Palm's *TERT* alleles appear to be distinct. Visual haplotype analysis revealed that the first 3 SNPs, which were about 300 bp apart, were strongly associated ($r^2 = 0.87–1.00$) while the fourth, about 9 kb from the nearest SNP, was not strongly linked ($r^2 < 0.1$) to the others. The distribution of the SNPs and haplotypes, as well as the D', provide a foundation that will facilitate future association and linkage studies between *turTERT* and metabolic diseases in the turkey.

Key words: Turkey, single nucleotide polymorphisms, linkage disequilibrium

T49 Changes in the proteome and metabolic profiles of broiler chickens during adipose tissue accretion. G. Kelley*, X. Wang, F. Chen, and S. Nahashon, *Tennessee State University, Nashville.*

Fat accretion in poultry directly influences the efficiency of feed utilization and consumer acceptability of poultry and poultry products. Losses estimated at about US$250–300 million are incurred by consumers and processors annually in pollution control, extraction and disposal of excess carcass fat. Understanding underlying mechanisms of excessive fat deposition in poultry will aid in improving carcass