TH178 Association of neonatal Fc receptor α-chain gene (FCGRT) promoter haplotypes with FcRn expression of dairy cows. X. L. Hu, J. Q. Wang*, S. G. Zhao, J. W. Zhao, and D. P. Bu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Bovine colostrum contains a large amount of immunoglobulin G (IgG). Fc receptor (FcRn) plays an important role in either the secretion of IgG or the intake of IgG in the mammary gland. This study was conducted to analyze the association of neonatal Fc receptor α-chain gene (FCGRT) haplotypes with the activity of FCGRT promoter and the expression of mRNA and protein. Two SNPs were identified by sequencing the promoter region of FCGRT genomic DNA from mammary gland samples which were collected from 40 healthy Chinese Holstein dairy cows. The 2 SNPs (which were named C-1116T and C-756A) defined 3 different haplotypes which belonged to CC/CC, CA/CA and TA/TA genotypes respectively. The luciferase reporter gene vectors were constructed to identify the transcriptional activity of FCGRT gene promoter in 293 cells. Correlations of FcRn mRNA and protein expression with haplotypes of FCGRT in mammary gland were assessed by Real-time PCR and Western blotting. The results showed as follows: The expression vectors containing 3 different haplotypes of DNA (CC/CC, CA/CA, TA/TA) were successfully constructed. The activities of CC-PGL3-Basic was significant higher than those in CA-PGL3-Basic and TA-PGL3-Basic ($P < 0.05$), CA-PGL3-Basic was significant higher than that of TA-PGL3-Basic ($P < 0.05$). The expression of FcRn mRNA in haplotype C-C was associated with highest level in the mammary gland of Holstein cows ($P < 0.05$). And haplotype T-A was significantly higher than C-A ($P < 0.05$). The protein expression of FcRn in haplotype C-C was significantly higher than C-A and T-A ($P < 0.05$), but there were not significant differences between C-A and T-A. We concluded that the SNPs in the FCGRT promoter did produce an effect on transcriptional activity, mRNA level and protein expression of Fc receptor in mammary gland. The polymorphism of FCGRT promoter gene can modulate the FcRn expression in mammary gland, and make further effects on expression of FcRn and transportation of IgG.

Key Words: Fc receptor, FCGRT, Chinese Holstein cow

TH179 X marks the spot: Region of bovine chromosome X associated with heifer fertility traits in Brangus cattle. K. L. DeAtley[1], M. G. Thomas*[2], M. R. S. Fortes[3], J. F. Medrano[4], G. Rincon4,8, A. Islas-Trejo[4], M. L. Colgrave[5], R. L. Ashley[1], G. A. Silver[1], S. O. Peters1,7, A. Reverter[5], A. Canovas[4], and W. M. Snelling[6], *[1]New Mexico State University, Las Cruces, [2]Colorado State University, Fort Collins, [3]University of Queensland, Brisbane, QLD, Australia, [4]University of California, Davis, [5]CSIRO, Brisbane, QLD, Australia, [6]USDA-ARS-MARC, Clay Center, NE, [7]Berry College, Mount Berry, GA, [8]Zoetis, Kalamazoo, MI.*

Discovery of favorable reproductive genotypes could facilitate early-life selection in replacement female programs using *Bos indicus*-influenced heifers. In Brangus heifers, we identified a gene associated with heifer fertility traits on the X chromosome using complementary -omics technology (i.e., genomics, transcriptomics and peptidomics). Specifically, 802 Brangus heifers were genotyped with 53,692 SNP and evaluated for reproductive phenotypes (i.e., first service conception (FSC) and heifer pregnancy (HPG)). Yearling heifers were estrous synchronized, bred by AI, and exposed to natural service breeding for 70 d. Reproductive ultrasound and DNA-based parentage testing were used to determine if the heifer conceived by AI or natural service and to code for the traits of FSC and HPG. Success rates for FSC and HPG were 53.3 and 78.0 ± 0.01%, respectively. Genome-wide association studies revealed 2 QTL on the X chromosome spanning positions 90 to 110 Mb (UMD 3.1 assembly). The hypothalamus and anterior pituitary were harvested from pre- and post-pubertal heifers (n = 8) from this population and analyzed using quantitative transcriptome (RNA-sequencing) and peptidome (neuropeptides ≤10 kDa) techniques. In these tissues, the PCSK1N transcript was detected in the transcriptome. The locus (92.02 Mb) for this gene resides within the QTL observed on the X chromosome. Two peptide derivatives of this gene, PCSK1N[61–89 and 221–240] were detected in the peptidome of the tissues. Peptide quantification was performed using multiple-reaction monitoring mass spectrometry of peptide extracts. Post-pubertal heifers had ($P < 0.05$) higher pituitary peptide levels relative to pre-pubertal heifers (i.e., peak area estimates were 1,118,058 ± 91,847 > 65,504 ± 8,761 for PCSK1N [221–240] and 2,308,678 ± 71,117 > 490,032 ± 11,969 for PCSK1N[61–89], respectively). The gene ontology of PCSK1N and its peptide derivatives include peptide hormone processing and modulation of pro-hormone convertase activity. The PCSK1N gene should be considered a positional and functional candidate for study of the reproductive endocrine axis and heifer fertility.

Key Words: cattle, gene, neuropeptide

TH180 Association between IgE single nucleotide polymorphisms and parasite resistance in Senepol × Charolais crossbred heifers. M. Pagán, L. Emmanuelli, I. Rivera, E. Jiménez, D. Vélez, and G. Ortiz-Colón*, *University of Puerto Rico, Mayagüe, Puerto Rico.*

Bovine immunoglobulin E (IgE) was selected as a candidate gene to evaluate the association between single nucleotide polymorphisms (SNPs) and resistance to parasite infestation. Senepol × Charolais crossbred heifers (n = 46) weighing 250.85 ± 9.24 kg were used in the study. Upon weaning, all heifers were put on a rotational pasture system in a single group, and fecal samples were taken every 2 wk for a period of 16 wk. Parasite infestation levels were determined by McMaster's Fecal Egg Count Method (FEC). Animals whose FEC were ≥100 eggs/gram of feces were treated with commercial anthelmintics. During the study 14 heifers were never treated with anthelmintics. Single nucleotide polymorphisms were identified at intron #1 and exon #3 [both adenine (A)/guanine (G) transition] by means of a pool and sequencing strategy using primers designed to amplify coding and noncoding fragments of the heavy chain constant region of IgE (GenBank Accession # U63640). In non-treated animals nucleotide substitutions in intron #2 had the following genotypic frequencies: AA 0.31, AG 0.38, and GG 0.31 (A 0.5/G 0.5). Animals treated on one or more occasions during the study had the following frequencies: AA 0.83, AG 0.17, and GG 0.00 (A 0.92/G 0.08), which were different from the non-treated animals ($P = 0.0199$). In non-treated animals nucleotide substitutions in exon #3 showed the following frequencies: AA/0.14; GA/0.50; and GG/0.36 (A 0.39/G 0.61). Animals treated on one or more occasions during the study showed the following frequencies: AA/0.53; GA/0.00; and GG/0.47 (A 0.53/G 0.47), which were different from the non-treated animals ($P = 0.0015$). Because IgE polymorphisms has been implicated in resistance to gastrointestinal nematodes infection in ovines, the segregation pattern of IgE SNPs reported suggests a similar scenario in bovines.

Key Words: IgE, polymorphism, bovine

TH181 Characterization of milk composition in Charolais cows and its association to SNP's in candidate genes. V. I. Pacheco Contreras*, A. M. Sifuentes Rincón, G. M. Parra Bracamonte, and V. R. Moreno Medina, *Centro de Biotecnología Genómica, Instituto Politécnico Nacional, Reynosa, Tamaulipas, México.*

We evaluated the gene-trait association of 62 SNPs panel located in 26 candidate genes involved on milk yield and composition. The main milk components (MMC), i.e., lactose (L), protein (P) and fat (F); were evaluated in a population of Mexican Charolais cows (n = 67), in periods of 30 ± 10 d during 4 to 5 mo. P, F and L percentage were determined according to the infrared technique and the cows were genotyped using the Sequenom MassARRAY technique. Genotype effect on MMC was analyzed using a MIXED model which included lactation period, calving season, age of the dam at calving and the herd as fixed effects. Ten markers were significantly ($P \leq 0.05$) associated with P, F and L percentage. GHR F279Y, FASN 17924A>G, LEP *Mbo*IA>B and LEP1180 were significant for protein percentage. For fat percentage 2 SNPs (CCR2 414C>T and PPARGC1A c.1847C>T) were significant and 3 (LTF 28A>C, CCL2 1364A>C and PRL RsaIA>G) showed a trend. Six SNPs (PRL RsaI A>G, DGAT K232Aa, DGAT K232Ab, PPARG1A c.1847C>T, LEP 1180C>T and LEP 3100C>T) were significant for lactose percentage. In beef cattle, several studies had shown the effect of environmental factors on milk yield and composition; however, the association of these traits with genotypes is scarce. Here we show novel associations of SNP markers to MMC in a Charolais population, further studies in a higher population are required to confirm our results.

Key Words: milk component, candidate gene, Charolais cattle

TH182 A SNP in the DRD2 gene influences adjusted birth and 205-day weights of calves grazing endophyte-infected tall fescue. K. M. Ely*[1], C. J. Kojima[1], A. M. Saxton[1], and R. L. Kallenbach[2], *[1]University of Tennessee, Knoxville, [2]University of Missouri, Columbia.*

Tall fescue (*L. arundinaceum* Schreb.) is the most prevalent forage in the Southeastern United States due to the presence of the endophytic fungus *N. coenophialum*. The fungus enhances the persistence of tall fescue, but decreases the productivity of cow-calf herds grazing it. A SNP at the dopamine receptor D2 (DRD2) gene yields genotypes of AA, AG or GG. We evaluated the relationship between DRD2 genotype and adjusted birth weight (ABW) and adjusted 205-d weight (A205) in fall- and spring- calving beef herds (FC and SC respectively) grazing endophyte-infected tall fescue in Missouri. The herds were AI-bred and managed similarly. The ANOVA model included genotype, calving season, and their interaction (SAS 9.3, Cary, NC). Comparisons of least squares means are shown in Table 1. Both A205 and ABW were lower in FC compared with SC ($P < 0.0001$). Genotype influenced ABW such that calves of GG dams were lighter ($P = 0.0008$). An interaction was noted between calving season and genotype ($P = 0.0346$) due to FC calves of AA and GG cows having lower ABW. Genotype influenced A205 ($P = 0.002$) with calves of AG dams being heavier than their AA or GG counterparts within calving season. Genotype and allele frequencies in FC were AA = 0.23, AG = 0.43, GG = 0.34, A = 0.45 and G = 0.55; frequencies in SC were AA = 0.22, AG = 0.51, GG = 0.27, A = 0.475 and G = 0.525. These results suggest that the AG genotype is advantageous for calf growth in both fall- and spring- calving herds grazing endophyte-infected tall fescue. Selection for the advantageous genotype may already be occurring in managed spring-calving herds.

Table 1. Least squares means of phenotypes by genotype (AA, AG, and GG) and calving season (fall and spring)

	AA		AG		GG	
	Fall	Spring	Fall	Spring	Fall	Spring
ABW (kg)	34.95^{B}	36.96^{A}	36.96^{A}	37.22^{A}	35.21^{B}	36.73^{A}
A205 (kg)	231.08^{CD}	243.12^{B}	236.56^{C}	250.52^{A}	224.68^{D}	245.14^{AB}

Key Words: fescue toxicosis, DRD2, beef cattle

TH183 Effect of stearoyl-CoA desaturase gene polymorphism on milk production traits of Hungarian Holstein Friesian cows. T. G. Jaleta*[1] and L. Czeglédi[2], *[1]Max Planck Institute for Developmental Biology, Tuebingen, Baden Wurteenberg, Germany, [2]University of Debrecen, Center of Agricultural Sciences and Engineering, Institute of Animal Science, Debrecen, Hajdu Bihar, Hungary.*

The objectives of this study were to estimate the genotype and allele frequencies of SCD gene and to investigate the effect of SCD 878 C/T gene polymorphism on milk production traits in Hungarian Holstein Friesian cows. Hair root samples were collected from 277 Hungarian Holstein Friesian lactating dairy cows. Genotyping and amplification of SCD gene was done using TaqMan probe method. The alanine valine amino acid substitution of 878 C/T SNPs at A293V were considered according to Tanguichi et al. (2004). Descriptive statistics, Hardy-Weinberg equilibrium and ANOVA were used for the analysis TaqMan probe results and recorded 305-d milk yield, fat and protein yield, SCC, fat and protein content. The estimated genotype frequency of the SCD gene polymorphism of Hungarian Holstein Friesian population were CC (34%), CT (53%) and TT (13%) and the allele frequency was C (61%) and T (39%). Hardy-Weinberg equilibrium ($P = 0.046945$, $\chi^2 = 3.947$) was not maintained in the studied population. Analysis of variance result showed that no significant difference ($P > 0.05$) between the SCD genotypes and milk production traits under study. Even though the difference was not statistically significant, 305-d milk yield, fat and protein yield, fat and protein content were higher for cows with TT genotype and SCC was lower when compared with cows with CC genotype. Detailed studies have to be conducted on the effect of SCD gene on dairy production traits especially fat composition which has significant role in human health.

Key Words: SCD gene, genotype, polymorphism

TH184 Developmental gene expression patterns in the skeletal muscle transcriptomes of Yorkshire and Tongcheng pigs. Y. Zhao*[1,2], M. Lei[1], J. Li[1], J. P. Steibel[2], H. Liu[1], G. Liu[1], S. Xu[3], Y. Xiong[1], D. Xu[1], and C. W. Ernst[2], *[1]Huazhong Agricultural University, Wuhan, China, [2]Michigan State University, East Lansing, [3]Animal Husbandry Bureau of Tongcheng County, China.*

Pig skeletal muscle growth is a complex process initiated early in fetal development and involving coordinated gene expression, which ultimately affects the quantity and quality of meat produced. The aim of this study was to examine gene expression patterns at 11 developmental stages (30, 40, 55, 63, 70, 90 and 105 d postcoitum (dpc), birth, 1, 3 and 5 wks postnatal) in pigs from the Yorkshire (YK; lean-type Western breed) and Tongcheng (TC; meat-type native breed, Hubei Province, China) breeds. RNA from longissimus dorsi muscle of 5 pigs (different litters) per stage for each breed was evaluated by sequencing (Illumina Genome Analyzer IIx). Short read sequence tags

were assembled and aligned to the pig reference genome (v. 10.2). Within-breed differential expression was examined by comparison of consecutive stages (FDR <0.001). Differentially expressed (DE) genes were observed between all stages in both breeds with more DE genes in fetal stages. The largest numbers of DE genes were between 30 and 40 dpc (1536 and 436 increased expression, 2379 and 681 decreased expression in TC and YK, respectively). In late gestation, more TC genes were DE between 90 and 105 dpc with fewer DE genes between 105 dpc and birth, whereas for YK fewer genes were DE between 90 and 105 dpc with more genes DE between 105 dpc and birth. DE genes were classified by gene ontology (GO) and pathway analyses. As expected many DE genes fell under the biological process GO classification of muscle system. Evaluation of muscle genes revealed that while many genes exhibited similar expression patterns in the YK and TC breeds, some genes exhibited breed-specific expression patterns. GDF11 was more highly expressed in TC than YK pigs at 30 dpc ($P < 0.001$). MYOG and TNNC2 were more highly expressed in TC than YK at 90 dpc ($P < 0.001$). MYLPF and TNNC2 were more highly expressed in YK than TC at 5 wk of age ($P < 0.001$). This study provides a comprehensive transcriptome evaluation of 11 developmental stages from 30 dpc to 5 wk of age in 2 pig breeds. Results reveal both developmental and breed-specific gene expression patterns.

Key Words: pig, skeletal muscle, transcriptome sequencing

TH185 Abundance of total genomic 5-methylcytosine and 5-hydroxymethylcytosine in different pig tissues. B. A. Freking* and D. J. Nonneman, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Methylation of genomic DNA is essential in regulating gene expression in many biological processes including reproduction, development, and growth. Cytosine residues in mammalian genomes are enzymatically modified to 5-methylcytosine (5MC), which participates in transcriptional regulation of genes. The 5MC modified base can be further enzymatically altered to 5-hydroxymethylcytosine (5hMC) by the TET family of methylcytosine dioxygenases. The function of 5hMC in gene regulation is not clear. Because these 2 modifications are indistinguishable by traditional sequencing methods even when supplemented by bisulfite conversion, analysis of 5MC and 5hMC is confounded using that approach. Our objective was to quantify the abundance of both modified bases in several porcine tissues using a colorimetric immunoassay specific for each modification. The content of 5MC or 5hMC DNA was quantified using a commercially available kit according to the manufacturer's instructions. Eight mature pregnant females (4 multiparous Meishan, 4 primiparous white composite) were sampled for 11 different tissues at critical periods during gestation to contribute fetal tissues for a separate study. Tissues included brain, endometrium, heart, small intestine, kidney, muscle, liver, lung, ovary, pancreas, and uterus. Data were analyzed by mixed-model ANOVA procedures fitting breed and tissue as fixed effects and gilt as a random effect. Breed was not significant for any of the variables tested so data are presented by tissue across breeds as a percentage of total DNA. Values for 5MC ranged from 1.25 ± 0.26% for pancreas to 5.68 ± 0.26% for small intestine. Values for 5hMC ranged from 0.006 ± 0.014% for pancreas to 0.294 ± 0.014% for brain. These data indicated a higher abundance of 5hMC and a higher ratio of 5hMC to 5MC in brain tissue (1.7-fold) compared with all other tissues examined, perhaps indicating a greater role of this modified base in tissues of the central nervous system.

Key Words: methylation, pig

TH186 Genomic regions associated with resistance to necrotic enteritis in chicken lines. Y. H. Hong*[1], E. Kim[2], D. Hue[1], S. I. Jang[3], and H. S. Lillehoj[3], *[1]Chung-Ang University, Anseong, Gyeonggi-do, Republic of Korea, [2]Iowa State University, Ames, [3]USDA-ARS, Beltsville, MD.*

Necrotic enteritis (NE) is an infectious disease caused by toxins produced by *Clostridium perfringens*, affecting 40% of the commercial broilers. The chicken lines selected and inbred for resistance to Malek's disease were found to be subject to resistance to NE. Two highly inbred chicken lines of Fayoumi and Adol were applied to identify the regions responding to intensive artificial selection for resistance to NE in chickens. The genome of resistant line and susceptible line in each breed was scanned with the 60K SNP panels. A total of 155 regions completely fixed in resistant or susceptible lines were found across the genome of both breeds. The comparison of divergently fixed regions between breeds allowed reducing the number of candidate region affecting the resistance to NE. Consequently, common haplotype of 5 regions (>200 kb and 50 SNP) subject to the susceptibility to disease were detected in the resistant or susceptible lines of 2 different chicken breeds. Annotation of the regions spanning divergently fixed regions revealed a set of candidate genes such as IL12A and TLR4 participating in immune response. The comparative analysis of both breeds revealed the evidence of selection in the region of the 6.2–6.4 Mb on chromosome 18, which overlap a previously reported QTL on disease resistance in broiler. Besides, consensus haplotypes associated with resistance to NE were found in regions of possibly relevant genes including myostatin (MSTN) and myosin (MYH3) that play an important role in muscle development. The high-resolution genome scans of divergent selection within- and between-breed suggest the candidate genes influencing the resistance to necrosis enteritis for the future study. This project was supported by the NRF grant funded by the Korea government (MEST; No. 2010–0009360), Republic of Korea.

Key Words: chicken, SNP, necrotic enteritis

TH187 Associations of pituitary specific transcription factor-1 (*POU1F1*) gene polymorphisms with growth and carcass traits in sheep. A. Jalil-Sarghale[1], M. M. Shahrebabak[1], H. M. Shahrebabak*[1], M. Sadeghi[1], and M. C. Mura[2], *[1]University of Tehran, Karaj, Tehran, Iran, [2]University of Sassari, Sassari, Italy.*

POU1F1 (PIT-1 or GHF-1) as a member of the POU family of transcription factors, is mainly expressed in the pituitary and upregulate the growth hormone, prolactin, thyroid-stimulating hormone β, *POU1F1* itself and also growth hormone releasing hormone receptor genes. This gene is located on chromosome 1. The aim of this research was to study the polymorphism of the *POU1F1* gene and its relationships with growth and carcass traits in 3 Iranian sheep breeds: Zel (thin-tail), Lori-Bakhtiari (fat-tail) and Zel-Atabay (fat-tail) crossbred. Blood samples from 90 Lori-Bakhtiari (research station), 60 Lori-Bakhtiari (slaughterhouse) 90 Zel (research station) and 40 Zel-Atabay (slaughterhouse) crossbred sheep were collected to extract DNA and the desired fragment was amplified and digested with Aci1 endonuclease. Research station samples were analyzed with statistical model including: sex, age and genotype. Similar model were used for samples derived from slaughterhouse except animal weight before slaughtering was included in the model. The results showed that the genotypes frequency varied between breeds. In the Lori-Bakhtiari breed A allele and in the of Zel breed and Zel-Atabay crossbred G allele was most frequent. When *POU1F1* genotypes were tested, animals with AG genotype showed a smaller breast circumference than those with AA genotype in Lori-Bakhtiari breed and Zel-Atabay crossbred ($P < 0.05$). Also, animals with GG genotype have more blood

triglycerides compared with those with AG and GG genotypes in Zel breed ($P < 0.05$). In addition, genotypes had significant association with abdominal fat in Lori-Bakhtiari breed (slaughterhouse) and with body length, height, thigh environment in Zel and Zel-Atabay crossbred ($P < 0.05$). In conclusion, the results confirm the hints proposing that *POU1F1* is a preferential target for further investigation on mutations that influence growth and carcass traits variations.

Key Words: *POU1F1* gene, polymorphism, sheep

TH188 Molecular analysis of calpastatin gene in fat-tailed Lori-Bakhtiari sheep in Iran. A. H. F. Khaltabadi[1], H. M. Shahrbabak*[2], and M. A. Talebi[3], *[1]Department of Animal Science, faculty of agriculture, University of Arak, Arak, Iran, [2]Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Iran, [3]Department of Animal Science, Agriculture and Natural Resources Research Center, Shahrekord, Iran.*

Calpastatin inhibits both the rate and extent of postmortem proteolysis and plays a role in muscle growth and meat quality. Lori-Bakhtiari sheep is gene pool reservation and suitable for meat and wool production that until now has not been studied using molecular markers, especially with the view of calpastatin gene. Therefore, the present study was conducted to determine the genetic diversity of calpastatin gene in Lori-Bakhtiari sheep station. The 622-bp fragment of this gene was amplified by polymerase chain reaction (PCR) from DNA samples of 100 Lori-Bakhtiari sheep. Polymerase chain reaction products were characterized by the restriction fragment length polymorphism (RFLP) technique using 2 restriction enzymes, *Msp*I, and *Nco*I, yielding all 3 genotypes, MM, MN and NN. The results of this experiment indicated that this population is highly polymorphic, furthermore in the most studied Iranian sheep breeds, all 3 genotypes of this gene have not been detected whereas we detected all 3 genotypes, and hence researchers must increase attention to meat quality and quantity in breeding programs of this breed. Because polymorphism in this breed is high and there are all 3 genotypes in their population, we can simply achieve effect of any genotype in increasing of meat quantity and quality with information recording and genotyping in next studies and select the best genotypes in breeding programs. The PCR products were electrophoresed on 1% agarose gel and stained by etidium bromide. Then, they were digested with restriction enzyme *Msp*I and then electrophoresed on 2.5% agarose gel with ethidium bromide and revealed 2 alleles, allele A and allele B. Data were analyzed using PopGene32 package. In this population, MM, MN, NN genotype have been identified with the 53, 40, 7% frequencies. M and N allele frequencies were 0.73, 0.27, respectively. The population was found to follow Hardy-Weinberg equilibrium

Key Words: calpastatin, Lori-Bakhtiari, sheep

TH189 Association between transferrin polymorphism and some blood parameters in Makoei fat-tailed sheep. A. H. F. Khaltabadi[1], H. M. Shahrbabak*[2], and H. Mohammadi[3], *[1]Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran, [2]1Department of Animal Science, Faculty of Agricultural Sciences and Engineering, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Alborz, Iran, [3]Department of Animal Science, Faculty of Agriculture, Tabriz, Iran.*

Transferrin (TF) is a serum glycoprotein that binds free iron ions. The objective of the present research was to determine transferrin polymorphism and to find association between transferrin polymorphism and some blood parameters of blood in the population of Makoei sheep lambs. Blood samples were collected from a total 576 sheep of both sexes in Iranian fat-tailed breed Makoei sheep from the jugular vein in tubes containing EDTA and centrifuged at 4°C. Separate aliquots of plasma and erythrocytes were stored at −20°C until they were analyzed. Transferrin (TF) typing was performed using PAGE, as described by Tucker and Clarke (1980). The levels of triglyceride blood, total protein blood, glucose blood and cholesterol blood have been measured. Significant differences in Transferrin genotypes group for 3 parameters were considered, those results as below: level of triglyceride ($P < 0.001$) and total protein ($P < 0.0001$) were statistically significant; while level for cholesterol blood ($P < 0.066$) not significant but it approximately significant. The AA genotype resulted in a significant increase in triglyceride (29.91 mg/dL), total protein (9.961 mg/dL) and AQ genotype significant decrease in triglyceride (18.45 mg/dL), total protein (7.075 mg/dL). No significant difference was observed between the genotypes in and glucose blood ($P < 0.633$) . These results indicate that new marker associated with blood parameters can be used in marker-assisted selection in fat-tailed sheep.

Key Words: blood parameter, transferrin, polymorphism

TH190 Association of polymorphisms in the transferrin with carcass traits in Makoei fat-tailed sheep. A. H. F. Khaltabadi[1], H. M. Shahrbabak*[2], and H. Mohammadi[3], *[1]Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran, [2]Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Alborz, Iran, [3]Department of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Iran.*

Transferrin is a glycoprotein responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization by binding 2 Fe^{3+} ions in association with the binding of an anion, usually carbonate. It is expressed by the liver and secreted into plasma. The objective of this study was to evaluate the association transferring genotypes with carcass quantity traits in Makoei sheep. Blood samples were collected from a total 576 sheep of both sexes in Iranian fat-tailed breed, Makoei sheep, from the jugular vein in tubes containing EDTA, kept refrigerated during the transport and centrifuged at 4°C. Separate aliquots of plasma and erythrocytes were stored at −20°C until they were analyzed. Transferrin (TF) typing was performed using the polyacrylamide gel electrophoresis (PAGE) as described by Tucker and Clarke (1980). The relationship was studied between selected carcass quantity traits and the transferrin (TF) genotype. In the Makoei sheep, the transferring genotypes are associated with an increase in slaughter weight ($P < 0.001$), total carcass weight ($P < 0.0001$) and carcass weight without fat-tail ($P < 0.0001$). Animals of BC genotype showed a significantly heavier slaughter weight than those of genotype BB (25.939 vs. 25.212 kg). The carcass weights of animals with the BE genotype to be higher than those of the TT genotype (11.968 vs. 11.0008 kg). The carcass weight of animals with the AQ genotype was heavier than those of the CK genotype (10.994 vs. 10.279 kg). In conclusion, considering above result was shown, protein Tf^{B} might be associated with carcass characteristic.

Key Words: carcass trait, transferrin, Makoei

TH191 Expression of acetyl-CoA carboxylase alpha (ACC-α) in thin and fat tail sheep breeds associated with lipogenesis pathway. H. O. Mousapour*, A. Nejati-Javaremi, M. Moradi-Shahrbabak,

H. Moradi-Shahrbabak, and M. J. Najafpanah, *University Of Tehran, Karaj, Tehran, Iran.*

The objective of the current study was to evaluate the acetyl-coenzyme A carboxylase α (ACC-α) gene expression as a most important enzymes in the regulation of lipogenesis. In this research 2 independent resources have been investigated in thin and fat tail Iranian sheep breeds. Thus, Zel and Lori Bakhtiari sheep breeds were studied that are thin and fat tail kind of breeds, respectively. Eight lambs from both breed in 2 sex were selected for sampling. Selected sheep's have the same age and characteristics of racial purity that was managed in same condition and fed until the age of 6 mo. Samples from lipogenic tissues (fat tail / tail, visceral fat and liver) and also longissimus muscle tissue were taken when the breeds has 6 mo of age. Total RNA from tissue samples were extracted by using an isolation reagent kit (Tripure, Roch Applied Science). Extracted RNA was treated by DNase I enzyme for removing genomic DNA residues (Fermentas, Thermo Fisher Scientific). Rocket Script Reverse Transcriptase enzyme (Bioneer) was used to full length cDNA synthesis. Expression of the ACC-α gene was measured by using the Real-Time PCR. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) was used as internal standard. Results showed a significance difference of ACC-α expression levels between both breed ($P < 0.05$), also it was shown that sex of breeds has no effect on expression of ACC-α in studied tissues ($P > 0.05$). The minimum amount of gene expression levels was observed in longissimus muscle that is argued with regard to ACC-α gene function. The results of current trail confirmed that there is significance difference between relative gene expressions of ACC-α in thin and fat tail sheep breeds at liver tissue, which is a substantial result due to role of the liver tissue at lipogenesis process. With regard to the issue that So far no research has been done in this area, evaluating the expression of lipogenic genes can be introduces new insights in lipogenesis process at fat tail and thin sheep breeds that can to be effective in adjustment the mechanisms of fatty acids synthesis in sheep breeds.

Key Words: ACC-α, lipogenesis, gene expression