

at skeletal and cardiac muscles linked to the Z1-Z2 domains of titin. This protein is degraded into the *post mortem* period and influences the reduction of tenderness between 24 and 72 h after slaughter. The major objective of this work was genotyping the SNP AY428575.1:g.346G>A of the bovine *TCAP* gene by PCR-RFLP technique, and report its use for the first time. Using the forward primer 5' GGGAGTGAGCAGTCATCATGGC 3' and reverse primer 5' AGAGGCAGCACCCGCTGGT 3', amplification products of 517 bp were acquired. They were submitted to digestion with *BtsCI* enzyme, which resulted in the genotypes AA (approx. 177, 154, 128, and 58 bp), AG (approx. 305, 177, 154, 128, and 58 bp) and GG (approx. 305, 154 and 58 bp). A total of 118 Nelore (*B. indicus*) and 8 Angus × Nelore (*B. taurus* × *B. indicus*) animals were genotyped. The use of the PCR-RFLP for the genotyping of SNP of the bovine *TCAP* gene was inexpensive and robust, which will greatly facilitate analysis of this polymorphism by basic laboratory equipment and reagents when compared with the single-base extension method. There were slight variation among Nelore animals with just 1 genotype AG and 117 genotypes GG. In the same way, there were found 6 Angus × Nelore with genotype AG and 2 GG. These preliminary results suggest the worthlessness of SNP AY428575.1:g.346G > A of the bovine *TCAP* gene to association studies with traits of interest to Nelore breed and, probably, to the subspecies *B. indicus*. On the other hand, they show the viability of these studies with the crossbreed Angus × Nelore, with Angus and, possibly, to all subspecies *B. taurus*. Acknowledgments to FAPESP for financial support.

Key Words: beef cattle, candidate gene, meat quality

W67 Association study of heat shock protein 70 gene with serum biochemical indices in Sanhe cattle. Y. Wang^{*1}, L. Liu¹, Q. Xu², Q. Chu³, Y. Yu¹, H. Wu⁴, D. Wang⁴, P. Yuan⁴, and A. Liu⁵, ¹College of Animal Science and Technology, China Agricultural University, Beijing, China, ²College of Biology, Beijing Jiaotong University, Beijing, China, ³Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China, ⁴Xiertala Breeding Farm, Hailaer Farm Buro, Hailaer, Inner Mongolia, China, ⁵Hailaer Farm Buro, Hailaer, Inner Mongolia, China.

Resistance to extreme cold is one of the distinct characteristics of Sanhe cattle, a dual purpose breed developed in Northern China. To quantify the ability of cold resistance and explore the genetic mechanism of cold resistance, some physiological and biochemical indicators in the serum were chosen and polymorphism of Heat Shock Protein 70 gene (HSP70) were screened, and the association between those indicators and polymorphism of HSP70 was analyzed. Blood samples from 170 Sanhe cows were collected and 6 biochemical indicators-corticosteroid (CORT), adrenocorticotrophic hormone (ACTH), thyroxin (T4), triiodothyronine (T3), Glutathione peroxidase (GSH-Px) and erythrocyte potassium in the serum were tested. Pooled DNA sequencing method (36 unrelated Sanhe cows) was used for identifying the polymorphisms of promoter and exon in HSP70. Individual genotypes were detected using the MALDI-TOF-MS technique. For the association study, a fixed effect model considering parity, sire and genotype of each single SNP was employed. Descriptive statistics of CORT, ACTH, T4, T3, GSH-Px and erythrocyte potassium in Sanhe cattle were 277.79 ± 30.47 ng/mL, 23.81 ± 9.29 pg/mL, 66.43 ± 13.91 ng/mL, 1.18 ± 0.36 ng/mL, 777.73 ± 126.40 U/mL and 22.74 ± 2.48 mmol/L, respectively. Research showed that serum biochemical indices changes when animal are exposed to hot or cold environment, and variations were found in Sanhe cattle, so serum biochemical indices can be used as auxiliary indicators for assessing the degree of cold stress. Totally 13 SNPs (6 SNPs in promoter region and 7 SNPs in exons) were detected using pooled DNA sequencing method, and all were found polymorphic in the sampled population. Minimum

allele frequency of these SNPs was 0.027–0.423. The association study showed that parity significantly ($P < 0.05$) effected CORT level and sire significantly ($P < 0.05$) effected ACTH level in all situations. Three novel SNPs were found significantly ($P < 0.05$) associated with some biochemical indices, namely A1679G with ACTH level, C620G with GSH-Px activity and C1784T with erythrocyte potassium concentration. Current results provide evidence that HSP70 gene is an important gene associated with serum biochemical indices, therefore, assumed to have influence on cold resistance ability.

Key Words: HSP70 gene, Sanhe cattle, serum biochemical index

W68 Molecular characterization of constitutive androstane receptor (CAR) and its association with feed efficiency of Nelore (*Bos indicus*) cattle. P. Alexandre, M. H. A. Santana, R. C. Gomes, J. B. S. Ferraz,* and H. Fukumasu, College of Animal Science and Food Engineering - Animal Breeding and Biotechnology Group (USP/ FZEA/ZAB/GMAB), Pirassumunga, SP, Brazil.

The constitutive androstane receptor (CAR) was initially characterized as a key regulator of xenobiotic metabolism. CAR has also been implicated in various physiological pathways such as energy metabolism and homeostasis of lipids, triglycerides, cholesterol and other endogenous hydrophobic molecules. Here, our focus was to detect genetic polymorphisms (SNP) of CAR of Nelore beef cattle, predict their functional role and associate them to residual feed intake (RFI) and residual body weight gain (RIG), a recently proposed measure of feed efficiency. Genomic DNA was extracted from blood of 50 Nelore bulls and the entire CAR gene was amplified and sequenced with 8 pairs of primers. Molecular characterization was performed for polymorphism identification, phylogenetic analysis and prediction of functional consequences of SNPs. Also, statistical association with RIG was performed with PROC MIXED (SAS). We found 24 SNPs in CAR gene, being one in the promoter region, 8 exonic, 13 intronic and 2 SNPs after the 3' UTR. We did not find any SNPs in the DNA binding domain of the receptor (DBD); however, 2 SNPs were found between DBD and the ligand binding domain (LBD), both being synonymous: SNP10 (Leu→Leu) and SNP11 (Ser→Ser). The LBD was the most genetically variant region presenting 5 SNPs, being 4 synonymous: SNP14 (Asp→Asp), SNP17 (Ala→Ala), SNP18 (His→His) and SNP19 (Ala→Ala); and 1 non-synonymous: SNP13 (Ala→Treo). No SNPs were found in exons 8 and 9, which codes for 3'UTR. Phylogenetic analysis demonstrated that exons from CAR gene are highly conserved between *Bos indicus* and *Bos taurus* and are closer to primates than to dog or chicken. The single SNP found upstream of CAR gene (SNP01 c.-81–176G>A) changed the transcription factor binding sites due the variation of G to A. Interestingly, this SNP was the only one associated with RIG ($P = 0.0221$). These results lead us to consider that CAR expression might be associated with the complex physiology of feed efficiency in Nelore. Efforts to comprehend the role of CAR on molecular pathways related to feed efficiency and validate this marker for RIG in Nelore are under investigation by our group.

Key Words: Nelore, RFI, SNP

W69 Assessment of 16 candidate genes for growth and maternal ability traits in Mexican Charolais cattle. L. A. Meza-García, V. I. Pacheco-Contreras,* G. M. Parra-Bracamonte, and A. M. Sifuentes-Rincón, Laboratorio de Biotecnología Animal, Centro de Biotecnología Genómica, Instituto Politécnico Nacional, Reynosa, Tamaulipas, México.

Maternal ability, birth and weaning weights, are some of the most important traits considered as selection criterion in Mexican cattle. They are