

0892 Comparison of carcass and sensory traits and contents of fatty acids and volatile compounds in Longissimus dorsi of three cattle breeds.

M. Baik*, M. Y. Piao, H. J. Lee, H. J. Kim, S. J. Park, H. J. Kang, and C. Jo, *Department of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Seoul, The Republic of Korea.*

This study was performed to compare carcass and sensory traits, physicochemical composition, fatty acid (FA) contents, and volatile compounds in Longissimus dorsi (LD) of Korean cattle, Holstein, and American Angus. A total of 36 steer LD samples were obtained from Korean cattle ($n = 12$), Holstein ($n = 12$), and American Angus ($n = 12$) with quality grade (QG) 1+, QG 2, and Choice grade, respectively. Korean cattle had the highest ($P < 0.05$) contents of intramuscular fat and reducing sugar but the lowest ($P < 0.05$) shear force values. Korean cattle revealed the highest ($P < 0.05$) sensory traits (flavor, tenderness, juiciness, and overall acceptance), and these traits were positively correlated with fat ($0.95 \leq r \leq 0.99$; $P < 0.001$) and reducing sugar contents ($0.55 \leq r \leq 0.63$; $P < 0.001$). Korean cattle had the highest ($P < 0.05$) contents (g/100 g LD) of most of the FAs, including palmitic acid, stearic acid, oleic acid, saturated fatty acids, monounsaturated fatty acids, and unsaturated fatty acids, and these FA contents were positively correlated ($0.65 \leq r \leq 0.78$; $P < 0.001$) with all sensory traits. Korean cattle had the highest ($P < 0.05$) concentrations of several volatile compounds, including acetaldehyde, 2-methyl butanal, 3-methyl butanal, 2,3-butanedione, and 3-hydroxy-2-butanone, and these compounds were positively correlated ($0.56 \leq r \leq 0.81$; $P < 0.001$) with all sensory traits, whereas Angus had the highest ($P < 0.05$) concentrations of pentanal, hexanal, and n-pentane. In conclusion, the LD contents of fat, reducing sugar, and FAs, the concentrations of LD volatile compounds, and sensory traits varied among breeds of cattle. Sensory traits had positive correlations with contents of fat, reducing sugars, and most of the FAs, and these showed positive or negative correlations with several volatile compounds.

Key Words: cattle breed, reducing sugar, volatile compound

0893 Label-free MS^E proteomic analysis of the bovine skeletal muscle: New approach for meat tenderness evaluation.

M. D. Poleti*¹, R. C. Simas^{1,2}, A. S. M. Cesar¹, S. C. S. Andrade³, G. H. M. F. Souza⁴, L. C. Cameron⁵, L. C. A. Regitano⁶, and L. L. Coutinho¹, ¹*Animal Biotechnology Laboratory, ESALQ, University of São Paulo, Piracicaba, Brazil*, ²*Thomson Mass Spectrometry Laboratory, UNICAMP, Campinas, Brazil*, ³*Genetics and Evolutionary Biology Department, IB, University of São Paulo, São Paulo, Brazil*, ⁴*Waters Corporation, São Paulo, Brazil*, ⁵*Laboratory of Protein Biochemistry, Federal University of State of Rio de Janeiro, Rio de Janeiro, Brazil*, ⁶*Embrapa Southeast Livestock, São Carlos, Brazil.*

Meat tenderness is an important trait for beef consumer satisfaction and presents a large individual variation among animals. Meat from Nellore cattle is less tender, resulting in lower economic value. Although many biochemical factors associated with meat tenderness have been studied, the alterations in the muscle proteome profile that reflect the biological complexity of the tenderness process remain unclear. The aim of this study was to investigate pathways and biological mechanisms associated with meat tenderness in one Nellore steer population using label-free proteomic approach by high definition mass spectrometry with HDMS^E acquisition. We evaluated differential protein expression in the *Longissimus dorsi* muscle, collected at 20 min. postmortem, from 10 animals with lower and 10 with higher values of shear force at the seventh day postmortem. The proteome analysis was performed using the nanoACQUITY UPLC Synapt HDMS G2-S system (Waters, Manchester, UK), and the data were processed using Waters Progenesis QI for proteomics software. A Nellore transcriptome database build from RNaseq data from the *Longissimus dorsi* muscle was used to identify the proteins. A total of 5016 proteins were identified, of which 3311 were quantified and 1816 were present in at least 8 out of 10 biological replicates. Among these, 125 proteins were differentially expressed (DE, $P < 0.05$), 66 proteins presented as downregulated, and 59 as upregulated in the group of animals with lower values of shear force. Functional annotation analysis of the list of DE proteins using DAVID identified two pathways (KEGG): pyruvate metabolism and viral myocarditis; catabolic processes, such as glucose, hexose, carbohydrate, and monosaccharide; and molecular functions, such as actin binding, cytoskeletal protein binding, and calcium ion binding. These results provide a comprehensive protein profile of the skeletal muscle and indicate that changes in energy metabolism and cytoskeletal structure of muscle could influence meat tenderness.

Key Words: beef cattle, mass spectrometry, proteome