strategic application of multi-omic resources to discover functional SNP and obtain population-level genotype data provides opportunity to enhance EPD accuracy.

Key Words: cattle, growth, health, omics

TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM

0785 Muscle gene expression patterns associated with differential intramuscular fat in cattle and markers for skeletal muscle growth rate and major cell types.

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Growth rate, intramuscular fat content (IMF%), and IMF composition influence the value of individual animals. However, for IMF, there are many different pathways to the final common process of triacylglyceride (TAG) synthesis and storage in intramuscular adipocytes. Gene expression data from a number of cattle and sheep experiments was used to identify the pathways involved in the synthesis of IMF and the genes correlated with growth rate and as markers of cell populations. The data sets were from a time course of longissimus muscle (LM) development in Piedmontese (PxH) and Wagyu cross Hereford (WxH) cattle, from the LM of a group of 48 Brahman cattle of similar age and from the LM of a group of 20 sheep of similar age. The differential expression of genes between WxH (high marbling) and PxH (high muscling) cattle and the correlation of gene expression with measured IMF in the Brahman and sheep data sets was integrated with known biochemical pathways. Expression of genes encoding proteins involved in the synthesis and deposition of TAG was most correlated with IMF%. In well-fed immature animals, TAG deposition rate (estimated by TAG gene expression) was proportional to current IMF%. By comparing TAG gene expression and IMF%, we identified a small number of animals with unexpectedly low or high rates of IMF deposition for their IMF%. The genes in the fatty acid synthesis pathway were less correlated with IMF%, presumably as IMF TAG can contain preformed fatty acids from circulation as well as those synthesized de novo by intramuscular adipocytes. By comparing changes in expression of the TAG and fatty acid genes, we estimated the relative contributions of synthesized and preformed fatty acids to IMF deposition on different diets. The expression of two groups of genes in the LM of the Brahman steers, significantly enriched for “cell cycle” and “ECM (extracellular matrix) organization” GO terms, was correlated with ADG per kilogram liveweight. However, expression of the same genes was only partly related to growth rate across the development time course in (PxH and WxH). *K*-means clustering of genes with similar expression profiles to the ECM genes was undertaken. Analysis of the clusters and published markers of different cell types in muscle suggested that the “cell cycle” and “ECM” signals were from the fibro/adipogenic lineage. The increase in ECM remodeling required for increased IMF deposition probably altered the relationship between the expression of these genes and animal growth rate.

Key Words: cattle, lipid

0786 Factors influencing bovine intramuscular adipose tissue development and cellularity.

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Appearance, distribution and amount of intramuscular fat (IMF) or marbling are highly variable depending on nutrition, gender, and environmental and genetic factors. On the molecular level, the concerted action of several factors, including hormones, receptors, transcription factors, etc., determines where clusters of adipocytes arise. Therefore, the aim remains to identify biological markers of IMF to increase the ability to identify animals that deposit IMF early in age to ensure the competitiveness of meat products and increase efficiency of high-quality meat production. In an attempt to unravel the cellular development of marbling, we investigated on the one hand the abundance of markers for adipogenic differentiation during fattening of cattle and on the other hand the transcriptome of muscle and dissected IMF from different breeds. Markers of different stages of adipogenic differentiation are well known from cell culture experiments. However, early markers are transiently expressed and late markers may reflect the number of mature adipocytes in the sample rather than gene activity in a tissue. On the cellular level, the development of marbling requires recruitment, proliferation, and differentiation of adipogenic cells. Hypertrophy of adipocytes is limited and hyperplasia occurs to store excess energy in the form of lipids in new cells. Within muscles, hyperplasia and hypertrophy of adipocytes can be observed throughout life. In a recent study, we investigated the localization and abundance of delta-like homolog 1 (DLK1) and CCAAT/enhancer-binding protein β (CEBPB), early markers of adipogenic differentiation, in bovine muscle tissue. Cell culture models demonstrated high expression of DLK1 in preadipocytes and complete disappearance during differentiation to adipocytes. Accordingly, we could demonstrate an inverse relationship between IMF content and number of DLK1 positive cells in bovine muscle. Considering the cellular environment of differentiating adipocytes in muscle and accepting mature adipocytes and myocytes as secretory cells, it becomes obvious that cross talk between cells via adipokines and myokines may be important for IMF development. Secreted proteins can act on other cells, inhibiting or stimulating their development via autocrine and paracrine actions. Among them, agouti signaling protein and thrombospondin 4 were further investigated. Thromospondin 4 is a potential myokine with supposed impact on IMF development, which has been identified in a cross species comparison of muscle transcriptomes and secretomes. Furthermore, results from transcriptome analysis suggest involvement of genes that are not directly related to adipogenesis and lipid metabolism providing new candidates for future research.

Key Words: intramuscular adipogenesis, adipokines, myokines

0787 Growth and growth rate influences bovine intramuscular adipose tissue gene expression in a differential manner.

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Intramuscular (IM) adipose tissue is the last adipose depot to mature in the growing bovine, and nutrition and management practices that influence growth and growth rate can influence IM adipose tissue deposition. Diet leading to changes in rumen VFA profile can influence substrates utilized for fatty acid synthesis, but diet has a greater effect on subcutaneous (SC) than IM adipose tissue. Subcutaneous adipose tissue has a greater ability to utilize glucose and lactate to produce reducing equivalents and to use lactate and acetate for lipid synthesis than IM adipose tissue regardless of diet. The greater ability of SC adipose tissue to utilize glucose to produce reducing equivalents and acetate and lactate for fatty acid synthesis indicates limited ability to manipulate site of fat deposition through changes in rumen fermentation. Our data suggest that differentiation and lipid synthesis in IM adipose tissue are primarily related to BW whereas differentiation and lipid synthesis in SC and perirenal (PR) adipose tissue are influenced by energy intake and rate of gain. It is perplexing as to why differentiation and lipid synthesis of IM adipose tissue is not affected by rate of gain as in SC and PR adipose tissue. The close proximity of IM adipose tissue to muscle tissue during development suggests that intercellular signaling between these 2 tissues might be crucial for development of IM adipose tissue. Early in the development of IM adipose tissue, changes in gene expression in muscle that effect remodeling of the extracellular matrix along with angiogenesis appear to be critical for development of IM adipose tissue. The strong correlation of angiogenic growth factors in LM with angiogenic growth factors and markers of adipocyte differentiation in immature IM adipose tissue suggest that there is a highly coordinated change that occurs between skeletal muscle and IM during the early stage of adipose development. However, the mechanisms of IM adipose tissue development are still not fully clear and more in vitro and in vivo studies are needed to further elucidate the pathways and mechanisms involved in IM adipose tissue development. Further understanding the interactions between skeletal muscle and adipose tissue during IM development could allow for development of management strategies that optimize carcass quality in bovine.

Key Words: bovine, growth, intramuscular adipose tissue

0788 Molecular mechanisms of bovine intramuscular fat deposition.

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Intramuscular fat (IMF) content in the longissimus dorsi muscle (LM), also known as marbling fat, is one of most important factors that determine beef quality in Korea and Japan as well as in the United States. Intramuscular fat deposition is influenced by both genetic (e.g., breed, genotype) and nongenetic factors (e.g., gender, castration, nutrition, stresses, age). Castration markedly increases IMF deposition, resulting in improved beef quality in Korean cattle. We present a comparative approach in gene expression between bulls and steers in bovine tissues. The marling trait has relatively higher heritability compared with other phenotypes such as feed efficiency and BW and is quantitative, being influenced by variety of genes involved in nutrient metabolism. The identification of genes associated with IMF deposition is an important area for elucidating mechanisms of IMF deposition. Intramuscular fat deposition is determined by a balance between fat deposition and fat removal in the LM. Fat deposition is determined by lipogenesis, fatty acid uptake and transport, and fatty acid esterification and fat removal is regulated by lipolysis and fatty acid oxidation. Studies on these lipid metabolic gene expression patterns provide understanding of role and relative significance of lipid metabolic genes in IMF deposition. Several peripheral tissues, including LM and adipose as well as the liver, are involved in lipid metabolism. Therefore, understanding of significance of the tissue network on lipid metabolism is important. Our studies with several peripheral tissues provide involvement of many lipid metabolic genes in the IMF deposition as well as body fat deposition in beef cattle. Application of newly developed functional genomic tools is very efficient for elucidation of molecular aspect of metabolism. We present detailed molecular events associated with IMF deposition through the application of functional genomics tools, including microarray, RNA sequencing analyses, and bioinformatics. Expression of gene is also influenced by epigenetic factors such DNA methylation and histone modification. Possible involvement of DNA methylation levels in regulating bovine gene expression will be discussed. New information on molecular mechanisms of bovine IMF deposition could be applicable to design nutritional or genetic methods to increase IMF deposition and to modify fatty acid composition in the LM of beef cattle.

Key Words: beef quality, intramuscular fat, functional genomics

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0789 Dedifferentiated fat cells: Potential involvement in intramuscular adipogenesis.

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Intramuscular adipogenesis and the dynamics of lipid metabolism by mature adipocytes have been investigated primarily due to the importance of altering marbling to enhance meat quality. Knowledge regarding intramuscular fat development has relied on the conversion of a variety of preadipocyte-like cells (such as stromal vascular cells) and their differentiation into lipid-assimilating adipocytes, which was thought to be the end of their cell cycle. However, a great number of studies have demonstrated the ability of the mature adipocyte to dedifferentiate into a population of a proliferative-competent cells known as the dedifferentiated fat (DFAT) cells. As early as the 1970s, in vitro studies have shown that DFAT cells may be obtained by ceiling culture, which takes advantage of the buoyancy property of lipid-filled cells. It is documented that DFAT cells may acquire a phenotype similar to mesenchymal stem cells and may redifferentiate into multiple cell lineages. From an animal science/meat science perspective, the main question that arises from the current knowledge of DFAT cells is how do DFAT cells contribute to intramuscular fat accumulation? What regulation causes the intramuscular mature adipocytes to dedifferentiate or resume their capability to proliferate? Moreover, are DFAT cells controllable so that they differentiate into lipid-assimilation cells (and perhaps other cells) and thus contribute to overall increase of intramuscular fat in vivo? Considering the fact that marbling fat accumulation is the last step in meat production, a (muscle and fat cell) intercellular regulation might trigger the differentiation of intramuscular adipocytes (regardless of origin). For example, feed restriction followed by realimentation may lead to dedifferentiation of mature adipocytes followed by its redifferentiation of proliferative competent (DFAT) progeny cells (as well as other preadipocytes/adipofibroblasts) into lipid-assimilating cells on realimentation, which may be one of the causes of changing the body composition and increase of fatness. Dedifferentiated fat cells originating from different adipose depots possess different rates of redifferentiation, whereas those originated from intramuscular fat depot are more active in adipogenesis than other fat depots. In summary, although the mechanisms of dedifferentiation of mature adipocytes have not been well defined, DFAT cells may contribute to intramuscular adipogenesis. Dedifferentiated fat cells may lead to the adoption of strategies in livestock production to enhance fat deposition in specific (desired) depots.

Key Words: adipose tissue, ceiling culture, marbling

0790 Metabolic programming and intramuscular adipogenesis.

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The study was conducted to clarify how early nutrition as metabolic programming events affected intramuscular adipogenesis of Japanese Black cattle fattened with only roughage. As a control group, the roughage group (R; $n = 11$) was fattened on only roughage ad libitum from 4 to 31 mo of age (mo) after nursing at standard level (replacer milk intake of 0.6 kg/d) until 3 mo. As a treatment group, the high-energy group of metabolic programming events (MP; $n = 12$) was also fattened on only roughage ad libitum from 11 to 31 mo after intensively nursing and feeding a high-energy diet until 10 mo. The intramuscular fat content in longissimus muscle was significantly larger in MP (13.2%) than in R (9.4%) at slaughter (Soxhlet analysis). Expression of the adipogenic genes, C/EBPb, PPARγ, C/EBPa, FASN, SCD, LEP, FABP4, ADIPOQ, IGFBP4, PPARγ2, and PRMT5, was investigated at each stage by quantitative real-time PCR analysis by using longissimus muscle biopsy samples. At 3 mo, the expression levels of PPARγ, C/EBPa, PPARγ2, ADIPOQ, IGFBP4, and PRMT5 were significantly higher in the MP than in the R. At 10 mo, the expression levels of PPARγ, C/EBPa, FASN, SCD, and LEP were significantly higher in the MP. At 14 mo, only PPARγ and LEP in the MP showed significantly higher expression. PPARγ, PPARγ2, and C/EBPa and other adipogenesis markers such as LEP, ADIPOQ, FABP4, IGFBP4, and PRMT5 were expressed at higher levels in the MP compared with the R at 30 mo. This effect may involve several factors including metabolic additivity and response to nutritional stimulus and the unstable nature of expression of these genes. Conversely, at 20 and 30 mo, FASN and SCD were expressed at significantly lower levels in the MP. Nevertheless, according to investigation of fatty acid composition of intramuscular adipose tissue, early metabolic programming events positively affected the relatively higher amounts of C18:1, MUFA, and the US:S ratio in MP at slaughter compared with R. It may be concluded that metabolic programming through high nutrition at neonatal ages can positively change adipogenic gene expression at the molecular level. These effects stimulate the early development of adipocytes at an early age and these changes were maintained over the study period. These suggest that early nutrition affects final meat quality and that early metabolic programming has potential to advance the field of meat sciences and support the meat industry.

Key Words: cattle, metabolic programming, intramuscular adipogenesis, grass-fed beef cattle

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0791 Genetics and breeding for intramuscular fat and oleic acid content in pigs.

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Total fat and fatty acid content affect both food quality and human health, and therefore, they are becoming increasingly important to industry and consumers. The intramuscular fat (IMF) and oleic acid (C18:1) content have been favorably related to pork quality, particularly in dry-cured products. This has triggered the interest of including them in the breeding goal of pig lines producing for high-valued markets. It is known that IMF responds to selection, but there is little evidence on the opportunities for genetic change in fatty acid composition. Based on research conducted on a Duroc line, we showed that C18:1, like IMF, has a moderate heritability and is genetically associated with increased IMF, BW, and backfat thickness. Despite this correlation structure, we proved that there exist selection schemes leading to response scenarios where C18:1, IMF, and lean content can be simultaneously improved. A limitation for implementing direct selection for C18:1 is that phenotypes are costly to obtain and cannot be measured on selection candidates themselves. Furthermore, results may depend on the reference tissue used for genetic evaluations. Deoxyribonucleic acid markers and genomic selection provide a complementary approach to overcome this problem. A genomewide association study was performed on Duroc pigs genotyped with a 60,000-SNP chip to detect genomic variants exhibiting influence on fat content and composition. We detected strong associations with IMF and C18:1 for two chromosomal regions colocalizing with the *SCD* (SSC14) and *LEPR* (SSC6) genes, which were then validated using a set of data from around 1,000 pigs. The DNA variant at the *SCD* gene affected the oleic to stearic desaturation index (C18:1/C18:0), C18:1, and SFA and MUFA and was consistently detected in several muscles and subcutaneous fat and both in raw and dry-cured pork. The association of *LEPR* with fatty acid composition was detected in muscle and was, at least in part, a consequence of its effect on overall fatness, with increased IMF resulting in more SFA, less PUFA, and greater SFA:PUFA ratio. With the benefits of genomic selection needing further assessment, selection combining pedigree-connected phenotypic data on IMF and C18:1 and some singled-out genetic markers is presented as a suitable alternative. However, if adopted, the response on lean growth is expected to be reduced. The extent to which it is affordable relies on how much consumers are prepared to pay for high-IMF and C18:1 pork products.

Key Words: fatty acid, intramuscular fat, meat

0792 The genetic landscape of intramuscular fat content and composition in pigs.

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Intramuscular fat content and composition are relevant selection goals in pig breeding schemes because of their significant influence on meat tenderness, juiciness, and flavor. Muscle lipid phenotypes are determined by both nutritional and genetic factors, displaying moderate heritabilities and a polygenic architecture. In this way, genome scans with microsatellites have revealed the existence of more than 200 intramuscular fat content QTL scattered throughout the pig genome. Unfortunately, experimental limitations related with population size and marker density have prevented the identification of mutations with causal effects. The comparison of QTL maps among muscles and fat depots has evidenced a modest positional concordance, suggesting that the penetrance of polymorphisms with causal effects on lipid metabolism is modulated by tissue-specific factors. This is an important consideration that should be kept in mind when implementing gene-assisted or genomic selection schemes aimed to improve intramuscular fat content and composition in swine. Gene expression studies based on microarrays have also provided valuable clues about the biology of muscle fat deposition in pigs, showing that it is modulated by a complex network of pathways related with lipid (lipogenesis, lipolysis, and PPAR signaling) and carbohydrate (insulin signaling) metabolism. However, microarrays have a limited power because they do not allow exploring transcript structure or the expression patterns of noncoding RNA. The recent advent of high-throughput genotyping and sequencing technologies has made it possible to circumvent many of these limitations. Now, genomewide association studies take advantage of the information provided by tens of thousands of SNP markers to fine map genomic regions associated with intramuscular fat content and composition in pigs. In parallel, the RNA-seq technology is expanding the analysis of differential expression to mRNA splicing variants as well as to many noncoding RNA with functions yet to be discovered. Particularly powerful are those approaches integrating genomewide polymorphism and expression data, because they can offer an unprecedented view about the molecular mechanisms that regulate lipid deposition in the porcine skeletal muscle.

Key Words: intramuscular fat, pig, genomics

0793 Statistical models and tools for integration of omics data to uncover the genetic control of pork quality and growth traits.

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Next-generation sequencing is drastically changing the way we study the interactions between genomes, transcriptomes, and phenomes. The next generation of animal genomics data sets should be matched by the next generation of analysis models. Those models should be flexible and adaptable to complex designs pervasive in animal genomics, statistically sound to test hypotheses and estimate parameters that are important for animal genomic research, and computationally efficient and able to accommodate massive multilayer data sets that are typical of animal genome research. The goals of this presentation are to 1) propose models for genomewide association (GWA) that can be used for expression QTL (eQTL) and phenotypic QTL (pQTL) mapping and to show their properties using simulations and real data analyses. As part of the analysis, we specify significance thresholds to control type I error rate, we compute confidence intervals of QTL positions using cross-validation, and we demonstrate under simulation that intervals have the intended coverage. Finally, we derive a meta-analysis procedure to integrate results of several independent GWA. We use plasmode simulations to show that our proposed method has a series of desirable properties for implementation of high-throughput association analyses: 1) computational cost linearly scales with the number of markers allowing rapid GWA with massive data sets, 2) genetic substructure and relationships among animals are fully accounted for, and 3) type I error rates are controlled at nominal levels. Finally, we present graphical and descriptive summary tools to represent results of massively parallel GWA analyses. To illustrate the usefulness and computational efficiency of proposed models, we present results from several projects: 1) GWA analysis of over 50 pork quality, carcass composition, and growth traits for almost 1,000 Duroc × Pietrain F_2 pigs; 2) GWA of over 40,000 gene expression phenotypes from backfat and longissimus muscle tissues of 176 individuals of the same population; and 3) meta-analysis of five meat quality traits across three divergent pig populations. We show that using our proposed methods, we can map eQTL overlapping pQTL and confirm their joint association. More importantly, we demonstrate that such mapping can be performed and represented in an unsupervised way (with minimal human input) by integrating genomewide expression and genotyping as well as high-throughput phenotyping data through proper data analysis models and tools.

Key Words: expression quantitative trait loci, genetical genomics, genomewide association

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0794 Marbling: Management of cattle to maximize the deposition of intramuscular adipose tissue.

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Consumers in the United States, Japan, and Korea have valued highly marbled beef for nearly a century. In the United States, most consumers prefer beef that is reasonably marbled and juicy. Early studies demonstrated that the more oleic acid in beef, the greater the overall palatability of the beef. Scientists have taken a two-prong approach to understand the biology of marbling development. Biochemists, molecular biologists, and geneticists have worked to gain a better understanding of the intracellular and extracellular factors that regulate the development of marbling adipose tissue (also known as intramuscular tissue), whereas beef cattle nutritionists have worked to optimize diets and time on feed to provide high-quality beef carcasses without exacerbating carcass adiposity. Marbling adipose tissue preferentially uses glucose as the carbon source for fat synthesis, whereas subcutaneous adipose tissue preferentially uses acetate. Early weaning of beef steers promotes greater marbling development at slaughter than normal weaning of steers, and this may be caused by increased glucose availability (from the grain-based rations) at the early stages of marbling development. In addition to providing carbon for marbling adipose tissue development, grain-based diets also increase MUFA such as oleic acid in marbling by stimulating the expression of stearoyl CoA desaturase (SCD). There is a significant correlation between the concentration of MUFA and amount of intramuscular lipid in longissimus muscle in cattle with the genetic propensity to marble that are fed grain-based diets for extended periods of time. Marbling adipose tissue can be distinguished from other fat depots by its location within perimysial connective tissues alongside muscle fibers. However, in longissimus muscle from Japanese Black A5 cattle, marbling adipocytes have been observed within muscle bundles, suggesting that muscle satellite cells can be induced to differentiate into marbling adipocytes. To date, the mechanisms responsible for this *trans*-differentiation of satellite cells to adipocytes in beef cattle have not been identified, as this process is quite difficult to measure in situ. Marbling adipose tissue from Japanese Black cattle are exceptionally high in oleic acid, and recent cell culture studies have demonstrated that oleic acid promotes *trans*-differentiation of muscle cells to marbling adipocytes. The results of these studies indicate that grain-based diets are necessary to promote the development of marbling. Furthermore, grain-based diets increase the healthfulness and juiciness of beef by promoting the production of oleic acid in marbling and other fat depots.

Key Words: beef, marbling, oleic acid

0795 Linking from the farm to the table.

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Genomics promises tremendous opportunity to the beef industry; however, that opportunity is currently stymied by the structure of the industry and the limited use of long-standing traditional genetic evaluations. Industry segmentation and poor, or in some cases lack of, market signals can be seen in the industry response of the past decade to a demand for more highly marbled beef. From 2005 to 2015, the feeding sector simply overfed animals to achieve higher marbling at the very great expense of excess fat, poor carcass yield, and poor feed efficiency. Although a logical decision in itself at the finishing level, this approach ignored the potential of "supply-chain" genetics to meet an end goal. A further persistent need that the beef supply must address is inconsistency of tenderness of beef at the consumer level. Beef is a premium protein product and, as such, must meet a higher standard for consumer satisfaction. Considering the heritability of tenderness, it would seem obvious as a supply-chain breeding goal. And yet no selection has been attempted, due in part to the nature of the trait: difficult to measure on breeding animals. This is an area of particular interest to make use of genomics. A simple DNA test can give an estimate for tenderness, which, applied to three generations of sire selection, could have a dramatic impact on consumer satisfaction. A third trait that should be of interest to every beef producer is feed efficiency. Although a great deal of focus has been placed on residual feed intake and affordable panels have been developed, little selection pressure has been brought to bear. Again, this is due, in large part, to the segmentation of the beef industry. Genetic improvement in the beef industry will only reach its potential following a fundamental shift in outlook. Current segmentation by sector and "ranch-level" genetics must be replaced with a more holistic approach in which information and market signals flow up and down the supply chain. Only then will producers and, more importantly, consumers benefit from the promise of genomics.

Key Words: beef genomics, breeding goals, industry structure

HORSE SPECIES: MANAGEMENT

0796 Stress responses in horses tied with overchecks.

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Little information is available on the welfare of horses used for transportation. It is common to observe horses wearing a complete harness, hooked to horse-drawn vehicles, tied up for extended periods of time where horse-drawn transportation is popular. An observational survey of 305 horses at 7 locations in northeast Ohio found 29.5, 51.5, and 13.8% of the horses were tied wearing harnesses with high, low, or no overchecks. Six Standardbred mares were used in a Latin square (treatment × period) designed experiment to evaluate the effects of tying horses wearing overchecks. All horses were acclimated to harness and tying before testing. Three 90-min test periods (May and June 2015) were used, and horses were randomly assigned to treatment groups: high overcheck (HC), low overcheck (LC), or no overcheck (NC). Each test period was followed by a 2-wk recovery period. Heart rate was measured before the test; during the test at 15 (T15), 45 (T45) and 90 (T90) min; and after the test at 45 (P45) and 90 (P90) min. Plasma cortisol (ELISA) was measured before the test and at T45, T90, P45, and P90. Muscle soreness and tightness at 20 sites—(right and left) rhomboideus, trapezius, deltoideus, latissimus dorsi, triceps, biceps femoris, longissimus, gluteus, hamstrings, and tensor fascia lata—were scored by a trained professional (Powel et al. 2008. J. Equine Vet. Sci., 28(1):28–33) before testing and 24 h after testing. Heart rate tended to be higher (45 ± 2.5 bpm; $P = 0.098$) at T15 in all horses compared with pretesting values (40 ± 2.5 bpm), regardless of treatment. Plasma cortisol was higher ($P < 0.001$) in HC at T45 and T90 (159.7 and 166.3 ng/mL, respectively) compared with both LC (106.4 and 105.2 ng/mL) and NC (116.1 and 93.5 ng/mL) at T45 and T90, respectively. There was no treatment effect on muscle soreness and tightness. Overall, muscles were more sore ($P < 0.05$) and more tight ($P < 0.001$) following the test compared with pretest values in all horses. The rhomboideus ($P < 0.001$), latissiumus dorsi ($P < 0.05$), and longissimus ($P < 0.05$) showed significant changes in both muscle soreness and tightness whereas the trapezius, deltoideus, and biceps femoris were only tighter ($P < 0.05$). We recommend loosening or removing overchecks while horses are tied and advocate additional studies on the common practice of tying up horses.

Key Words: horse, welfare, cortisol

0797 Effect of prerace behavior on performance in racing quarter horses.

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It is purported that prerace behavior of a race horse can diminish their performance, known as "washing out." This study observed prerace behaviors of 1,040 Quarter Horse (QH) race horses that competed in 137 races over a 14-night duration at Delta Downs Racetrack (Vinton, LA). A total of 46 variables were recorded by experienced horsemen. The prerace period was divided into four different subsections: before saddling (BSAD), which was the time when the horse walked across the track's infield to right before they entered the stall to be saddled; during saddling (SAD), which was the time while the horse was being saddled; after saddling (ASAD), which was the time from when the horse was finished being saddled to when the jockey mounted the horse; and after the parade (POSTP), which was the time from when the jockey mounted