

## Nutrition: Oral Presentations

### Relating sensory characteristics with biochemical analyses of hays fed to horses

S. Julliand<sup>1</sup>, C. Omphalius<sup>2</sup>, M. Orard<sup>2</sup>, O. Parodi<sup>2</sup>, C. Villot<sup>2</sup>, H. Warren<sup>3</sup>, and V. Julliand<sup>4</sup>

<sup>1</sup>Lab to Field, France, <sup>2</sup>AgroSupDijon, France, <sup>3</sup>Alltech Bioscience Centre, Ireland, <sup>4</sup>Uranie NCA, AgroSup Dijon, France

Forages form the basis of horse diets. However in the field, forage nutritive value calculated from biochemical analyses is not commonly used. Horse people evaluate forage quality as “good” or “bad” based on their own quality indicators. The present study aimed at comparing the nutritive value of hays with their sensory characteristics using a descriptive analysis. Twenty hay buyers (equine breeders, trainers, owners and riding school proprietors) were interviewed. While trainers, owners and riding school proprietors said that they looked firstly at the origin of the hay, breeders focused on timing of harvest. All buyers looked at organoleptic qualities as the second major indicator. Among organoleptic qualities, odour and colour were the most frequent indicators mentioned. Twenty-one meadow hays originating from 12 different administrative regions of France were then collected for sensorial and biochemical analyses. For each hay, 2 kg were randomly hand-sampled from one opened bale in 10 different locations. Part was sent for biochemical analysis and part was used for sensorial analysis. The sensorial descriptive analysis was run in three separate workshops with 54 untrained subjects to sort hays by appearance, odour or texture. Subjects were asked to group hays by similarity of view, smell or touch and then to describe the groups with their own qualifying terms (with a maximum of five terms per group). Multidimensional scaling analyses were carried out in order to provide a hierarchical clustering of hays based on their description similarities and to map each group of hays in correlation with the associated description terms. Appearance was separated into four statistically distinct groups and described as “grassy-dark-green”, “mixed-thin”, “heterogenic-medium”, “yellow-strawy-moldy”. Odour characteristics were also separated into four groups: “dry-smell of farm-persistent”, “sweet-pleasant”, “spicy-aromatic-flowered”, “unpleasant-acid-moldy-smell of urine”. Texture characteristics were separated into three groups: “matted-long-pleasant-soft-homogeneous”, “unpleasant-strawy”, “mix-short-lightened”. Hay digestible energy (DE) varied from 1.56 to 2.32 Mcal/kg DM and crude protein (CP) from 63 to 163 g/kg DM. The appearance “grassy-dark-green” group had a higher DE than the “yellow-strawy-moldy” group ( $p < 0.05$ ). Predictive energetic values for “yellow-strawy-moldy” hays were lower ( $p = 0.001$ ) than for “grassy-dark-green” hays (1.7 versus 2.1 Mcal/kg DM, respectively). The odour “sweet-pleasant” group appeared higher than the “unpleasant-acid-moldy-smell of urine” group with respect to DE ( $p < 0.05$ ).

Predictive energetic values for hays that smell “sweet-pleasant” were higher ( $p = 0.005$ ) than for other hays (2.1 versus 1.8 Mcal/kg DM, respectively). No significant difference has been noticed for DE among the texture groups. Additionally, no significant difference in crude protein appeared among the groups. This study shows a link between appearance and odour of hays and their DE, which needs further investigation.

### Reference

- [1] Faye P, Brémaud D, Durand M, Courcoux P, Giboreau A, Nicod H. Perceptive free sorting and verbalization tasks with naive subjects: an alternative to descriptive mappings. *Food Quality and Preference* 2004;15:781-91.

### Identifying the role of a “caloric restriction mimetic”, resveratrol, in Equine Metabolic Syndrome and its implications for targeted therapy

A.A. Adams, M.H. Siard, S.E. Reedy, C. Stewart, A. Betancourt, M.G. Sanz, and D.W. Horohov  
M. H. Gluck Equine Research Center, Department of Veterinary Science, University of Kentucky, Lexington, KY 40546

Equine Metabolic Syndrome (EMS) is a complex disorder that affects a variety of horse breeds and is characterized by increased adiposity, systemic chronic inflammation, insulin resistance, and a predisposition toward developing laminitis. The common recommended treatment and management of EMS is decreasing caloric intake and increasing exercise. While caloric restriction in some horses can improve EMS by increasing insulin sensitivity and decreasing inflammation, it can take months to achieve this improvement and is not always successful. Therefore, we propose to investigate the effects of a polyphenolic compound, resveratrol, to improve conditions of EMS. Resveratrol has been shown to activate key cellular enzymes, causing beneficial downstream signaling events that mimic protective mechanisms induced by caloric restriction. Our working hypothesis is that administration of resveratrol supplementation to EMS horses will increase insulin sensitivity, decrease inflammation and adiposity. A total of 15 EMS horses (mean age 15 +/- 5 yrs) of mixed sex and breeds were used in this study. Horses were blocked by age and basal insulin levels to receive one of two treatment groups: group 1 (resveratrol) (n=8) or group 2 (placebo) (n=7). Treatment lasted 6 weeks and sampling occurred at week 0 and 6, consisting of measurements of body condition, metabolic and immune parameters. There was no significant change in body weight (BW) ( $P = 0.982$ ), body condition score (BCS) ( $P = 0.972$ ), neck crest score (NCS) ( $P = 0.865$ ) or percent body fat ( $P = 0.711$ ) in either treatment group after the six week period. There was a significant decrease in serum leptin ( $P = 0.012$ ) and triglycerides

( $P=0.010$ ) for the resveratrol treated group when compared to the placebo after the six weeks. Further, there was a significant ( $P=0.021$ ) decrease in insulin (mU/L) levels post an oral glucose sugar test at the six weeks post treatment compared to week 0 in the resveratrol treated group compared to the placebo group. There was a significant decrease ( $P=0.034$ ) in serum tumor necrosis factor- $\alpha$  (TNF $\alpha$ ) in the resveratrol treated EMS horses compared to the placebo. There was no significant ( $P=0.805$ ) difference in the percentage of lymphocytes producing TNF $\alpha$  protein measured by flow cytometry between the resveratrol and placebo treated horses, nor was there a difference in gene expression of IL-6 ( $P=0.651$ ) or interferon-gamma (IFN $\gamma$ ) ( $P=0.416$ ) in these cultures. Whole blood cytokine gene expression data revealed that there was a significant ( $P=0.009$ ) increase in IL-6 levels in the resveratrol group compared to placebo, however no difference in IFN $\gamma$  ( $P=0.693$ ) or TNF $\alpha$  ( $P=0.986$ ) at six weeks post treatment. In conclusion, 6 weeks of resveratrol therapy modulated both metabolic and inflammatory changes in EMS horses.

### Acknowledgements

The AQHA Young Investigator Award grant partially funded this study. Dr. Patrick Lawless, EquiThrive,<sup>TM</sup> supported the efforts of this research by providing the resveratrol and placebo compounds.

### Effect of ideal protein on muscle mass development

P.M. Graham-Thiers, and L.K. Bowen  
Department of Equine Studies, Virginia Intermont College,  
Bristol, VA 24201

Twelve geldings of light horse type weighing  $570 \pm 35$  kg were divided into two groups (standard protein, SP and ideal protein, IP) to evaluate the effect of ideal protein on muscle mass. Both groups were fed a 12% CP sweet feed but the IP group CP was formulated to provide ideal protein for horses as proposed by Bryden, 1991. Both groups received grass hay. Horses were out of work for 14 weeks and began a 12 week training program consisting of 1-2 hr of light to moderate exercise 5 days a week. Body weight and BCS were evaluated weekly. A 4 day total urine and feces collection period was conducted prior to the start and at the end of the study. Urine and feces samples were frozen for later analysis of nitrogen (N) to calculate N balance. Muscle biopsies were also obtained from the semitendinosus muscle prior to the start and at the end of the study. Muscle tissue was immediately frozen in liquid N for later histological analysis of fiber types, fiber areas and free amino acid concentrations. An ANOVA was done using the Proc MIXED function of SAS (2006) evaluating the effect of diet, time and any interactions between diet and time. The SP group consumed  $2.3 \pm 0.1$  kg grain mix and  $8 \pm 0.3$  kg hay while the IP group consumed  $2.2 \pm 0.1$  kg grain mix and  $8.2 \pm 0.4$  kg hay. There were no differences for any N

balance parameters. Muscle free concentrations of amino acids were not affected by diet except for leucine and phenylalanine which were higher in the IP group compared to the SP group ( $P = 0.045$  and  $0.05$  respectively). There was an effect of time on concentrations of threonine, valine and histidine which decreased for the SP group comparing pre and post samples ( $P < 0.05$ ). An interaction between diet and time was observed for concentrations of valine, methionine, leucine, phenylalanine and arginine which increased in the IP group compared to the SP group at the conclusion of the study ( $P < 0.05$ ). Histological analysis of the muscle biopsies found an initial difference in average fiber areas which were greater for the SP group compared to the IP group. Using these initial differences as a covariate revealed a decrease in muscle fiber size for the SP group compared to the IP group at the end of the study ( $P = 0.001$ ). Specifically, a decrease in muscle fiber size was observed in Type II fibers for the SP group as compared to an increase in muscle fiber size for Type II fibers in the IP group ( $P = 0.009$ ). While changes did not appear evident between groups at the "whole body" level, changes at the tissue level appear more evident.

### Reference

- [1] Bryden, W.L. 1991. Amino acid requirements of horses estimated from tissue composition. Proc. Nutr. Soc. Aust. p 53.

### Assessment of equine fecal microbial profiles during and after a colic episode using pyrosequencing

E.B. Venable<sup>1</sup>, M.S. Kerley<sup>2</sup>, and R. Raub<sup>3</sup>  
<sup>1</sup> Purina Animal Nutrition, Gray Summit, MO 63039,  
<sup>2</sup> University of Missouri-Columbia, Animal Science  
Research Center, Columbia, MO 65203, <sup>3</sup> US Feed  
Operations – Ridley, Inc., Mankato, MN 56001

Effects of colic on the equine microbiome are poorly understood. Therefore, 454 pyrosequencing was performed to characterize shifts in the microbial populations of the equine gut during and after a colic episode. Rectal grab samples were collected from nine horses admitted to veterinary teaching hospitals for large intestinal, non-surgical colic and stored in 50 ml sterile containers at  $-70$  C. Samples were frozen for a minimum of 24 hours and shipped on ice via UPS overnight mail. Follow-up samples were collected 30 – 90 days following discharge. Each sample was analyzed for concentration and purity of DNA using Nanodrop (Thermo Fisher Scientific, Waltham, MA). Libraries of amplicons compatible with 454 sequencing chemistry were generated using a loci specific primer pair that amplifies the V<sub>1</sub>, V<sub>2</sub>, and V<sub>3</sub> hyper-variable regions of the 16S ribosomal RNA gene. Emulsion PCR was performed to obtain enriched beads for massively parallel pyrosequencing. High quality reads were separated based on Multiplex Identifier tag and analyzed for phylogenetic origin by comparison to reference databases. Samples generated 1,241,844 reads (base pair sequences) and approximately 65% of the reads were unassigned (no assigned operational taxonomic unit). Thus, they were