

## Nonruminant Nutrition: Feedstuffs & Methodology

**W62 Comparison of classical and marker method, using three different markers and two analytical techniques, for the measurement of apparent digestibility in swine.** L. L. Oetting\*<sup>1</sup>, A. L. Abdalla<sup>1</sup>, J. D. F. Gomes<sup>2</sup>, A. R. A. Nogueira<sup>3</sup>, and C. E. Utiyama<sup>1</sup>, <sup>1</sup>Universidade de São Paulo, Piracicaba-SP, Brazil, <sup>2</sup>Universidade de São Paulo, Pirassununga-SP, Brazil, <sup>3</sup>Empresa Brasileira de Pesquisa Agropecuária-Centro de Pesquisa de Pecuária do Sudeste, Sao Carlos-SP.

Use of markers for the measurement of digestibility is a less intensive labor method than total fecal collection. Little is known about the use of rare earth as dietary markers in digestibility assays with swine. The aim of this work was (1) to compare the digestibility coefficient obtained by the classical method (CM) with the marker method (MM), using three dietary markers simultaneously: chromium (Cr), lanthanum (La) and ytterbium (Yb), and (2) to compare two analytical techniques (Inductively Coupled Plasma Atomic Emission Spectrometry - ICP-OES, and Energy Dispersive X-Ray Fluorescence - ED-XRF) of marker analysis. Twelve finishing gilts were housed in individual metabolism crates. The experimental diet consisted of a corn-soybean meal diet added with 0.3% of Cr and 60 mg/kg of La and Yb. Comparison between the digestibility coefficients (DC) of gross energy (GE), dry matter (DM) and crude protein (CP) are shown below. There were differences between analytical techniques in determination of Cr and La. Comparison between the MM with the CM showed that Cr+ICP-OES and La+ED-XRF provided similar results ( $P>0.01$ ) for energy and protein digestibility coefficients. The differences between the two methods can be explained by the low percentage of recovery of the markers in feces (80.97, 66.38, 57.43, 58.22, 82.32 and 46.19% for Cr+ICP, La+ICP, Yb+ICP, Cr+ED, La+ED and Yb+ED, respectively). It can be suggested that La+ED-XRF can be an alternative marker for Cr in digestibility studies with swine and it can be used at lower concentrations without affecting accuracy.

(%)	Classical method	Cr+ICP -OES	La+ICP -OES	Yb+ICP -OES	Cr+ED -XRF	La+ED -XRF	Yb+ED -XRF	SE
GE	87.27	87.07	83.77	80.91	81.65	87.01	84.36	1.09
DM	90.55	86.43	82.98	79.97	80.75	86.37	83.58	1.02
CP	85.58	85.36	81.61	78.38	79.24	85.30	82.29	1.27

**Key Words:** Apparent Digestibility, Swine, Rare Earth

**W63 Comparison of the single dose and withdrawal method for measuring the rate of passage of swine basal diets using multiple markers and alternative analytical techniques.** L. L. Oetting\*<sup>1</sup>, A. L. Abdalla<sup>2</sup>, J. D. F. Gomes<sup>3</sup>, A. R. A. Nogueira<sup>4</sup>, and C. E. Utiyama<sup>1</sup>, <sup>1</sup>Escola Superior de Agricultura "Luiz de Queiroz" da Universidade de So Paulo, Piracicaba-SP, Brazil, <sup>2</sup>Centro de Energia Nuclear na Agricultura da Universidade de So Paulo, Piracicaba-SP, Brazil, <sup>3</sup>Faculdade de Zootecnia e Engenharia de Alimentos da Universidade de So Paulo, Pirassununga-SP, Brazil, <sup>4</sup>Empresa Brasileira de Pesquisa Agropecuária - Centro de Pesquisa de Pecuária do Sudeste, Sao Carlos-SP, Brazil.

There are few studies on the determination of the rate of passage of diets in swine. Multiple markers can be used simultaneously to determine different rates of passage in the same animal. Rare earth elements offer some advantages in terms of cost, quantitative analyses and total recovery in faeces. Four finishing gilts were used to determine the rate of passage by single dose and withdrawal method of a basal diet (corn-soybean meal) using the combination of the three markers (chromium, lanthanum and ytterbium) and two analytical techniques: Inductively Coupled Plasma Atomic Emission Spectrometry (ICP-OES) and Energy Dispersive X-Ray Fluorescence (ED-XRF). The Cr was added directly to the diet, but the La and Yb were primarily incorporated to the maize. In the withdrawal method, the markers were administered in diet for 5 d and then were withdrawn. The concentration of markers in faeces was transformed to their natural logarithmic values and simple regression analysis was performed to establish the relationship between the natural log of marker concentration with time. The slopes of the regression lines ("b"), which represents the rate of marker disappearance, were compared for both methods and each marker by Tukey's test. There were no statistical differences between the two methods, with exception for the treatment Cr+ICP-OES. The mean of the slopes of the regression lines for Cr+ICP-OES, Cr+ED-XRF, La+ICP-OES,

La+ED-XRF, Yb+ICP-OES and Yb+ED-XRF was 0.087, 0.086, 0.021, 0.049, 0.032 and 0.046 (SE=0.015), respectively. The difference in the rate of passage found for La and Yb, in relation to Cr, was, probably, a result of the lower rate of passage of the maize in relation to the diet.

**Key Words:** Swine, Rate of Passage, Rare Earth

**W64 International Life Sciences Institute crop composition database: documenting natural variability in crop composition.** W. P. Ridley\*<sup>1</sup>, R. D. Shillito<sup>2</sup>, and L. Kurtyka<sup>3</sup>, <sup>1</sup>Monsanto Company, St. Louis, MO, <sup>2</sup>Bayer CropScience, Research Triangle Park, NC, <sup>3</sup>International Life Sciences Institute, Washington DC.

An understanding of the natural variability in nutrient composition of maize and soybeans is an important consideration in the development of diets that promote the healthy growth of swine, poultry, beef cattle and other livestock animals. Most existing publicly available crop composition data sources have relied on data that were 20 or more years old. In many cases the methods used for the generation of these data were not known or their performance parameters were not available. In May 2003, the International Life Sciences Institute (ILSI) released Version 1.0 of an online comprehensive crop composition database ([www.cropcomposition.org](http://www.cropcomposition.org)) that provides up-to-date information on the natural variability in the composition of conventional crops. The database is a compilation of over 53,000 data points on 102 nutritionally important analytes for maize and soybean samples obtained from controlled field trials in multiple worldwide locations between 1995 and 2001. All data can be traced back to their source and every data point is identified with its analytical method. The database is searchable, via a web-browser-based interface, on a number of attributes including analyte, matrix, year of harvest and field location. Information about the database has been shared with regulators, scientific/academic institutions, FAO, OECD, other ILSI task forces, and the US National Academy of Sciences. The ILSI Task Force responsible for the database plans to release Version 2.0 in the spring of 2004 that will contain over 70,000 data points and include data for cottonseed plus additional data sets for maize and soybeans.

**Key Words:** Crop Composition, Nutrients, Crop Composition Database

**W65 Comparison of corn grain from biotech and non-biotech counterparts for grow-finish pig performance.** H. H. Stein\*<sup>1</sup>, T. Sauber<sup>2</sup>, D. Rice<sup>2</sup>, M. Hinds<sup>2</sup>, D. Peters<sup>1</sup>, G. Dana<sup>2</sup>, and P. Hunst<sup>3</sup>, <sup>1</sup>South Dakota State University, Brookings, <sup>2</sup>Pioneer Hi-Bred International Inc., Johnston, IA, <sup>3</sup>Dow AgroSciences LLC, Zionsville, IN.

An experiment with 96 growing pigs (initial BW 23.5 kg) was conducted with the objective of testing the hypothesis that the inclusion of a genetically modified corn in diets for swine does not compromise pig performance or carcass quality. Four corn sources were used in the experiment. Corn 1 was bin-run obtained from the SDSU feed mill. The remaining three corns were obtained from Pioneer Hi-Bred International Inc. Corn 2 was grain produced from hybrid Pioneer<sup>®</sup> brand 33J56, corn 3 was grain produced from hybrid Pioneer<sup>®</sup> brand 33P66, while corn 4 was grain produced from hybrid Pioneer<sup>®</sup> brand 33P66 containing the TC1507 event. TC1507 is an event that contains the Cry1F gene from *Bacillus thuringiensis* var. azawai. This gene encodes the Cry1F protein that has been shown to have insecticidal activity towards several insects including European corn borer and black cutworm. The trade name for this corn is Herculex#8482 I. This trait was developed through collaboration between Pioneer Hi-Bred International, Inc. and Dow Agrosciences LLC. Diets based on each of the four corns were formulated using a single source of soybean meal. Pigs were assigned to four different treatment groups at approximately 23.5 kg based on ancestry, gender, and BW. There were three pigs per pen and eight replicate pens per treatment. A three phase feeding program was used with diets containing 1.0, 0.8, and 0.63% LYS within each phase. At 120 kg BW, pigs were harvested and carcass measurements recorded. During the first phase of the experiment, pigs fed the diet based on corn 3 had greater ( $P \#8804 0.05$ ) ADFI than pigs fed the other corns, however, there were no treatment differences in ADG or G:F. During the second and third phases and overall, no differences in ADG, ADFI, or G:F were observed. Likewise no differences in dressing percentage, 10th rib back fat, loin-eye area, fat

free lean, or lean meat percentage were detected. It is concluded that no negative effects on pig performance, dressing percentage, or carcass quality are associated with the use of corn produced from seed containing the Herculex#8482 I trait.

**Key Words:** Genetically Modified Corn, Performance, Pigs

**W66 Digestive fate of a *gdhA* gene from a genetically modified corn fed to growing pigs.** X. Qiu\*<sup>1</sup>, G. A. Apgar<sup>1</sup>, K. E. Griswold<sup>2</sup>, J. M. Beagle<sup>1</sup>, M. P. Martin<sup>1</sup>, K. L. Jones<sup>1</sup>, M. J. Iqbal<sup>1</sup>, and D. A. Lightfoot<sup>1</sup>, <sup>1</sup>*Southern Illinois University, Carbondale*, <sup>2</sup>*Penn State University Extension, Lancaster*.

Eight female PIC pigs (initial BW, 47.5 ± 1.8 kg) with an additional all-time negative control pig were utilized in a two period switchback design to evaluate the digestive fate of a transgenic corn. Pigs were fed diets comprised primarily of a genetically altered corn or a non-altered isogenic corn grown in the same locations. The genetically altered corn (*gdhA*+) contained a glutamate dehydrogenase gene isolated from *Escherichia coli*. Pigs were surgically fitted with steered ileo-cecal valve cannulas for collection of ileal digesta. Pigs were limit fed at 8% of metabolic body weight (BW<sup>0.75</sup>), in two equal feedings at 0600 and 1800 each day throughout the experiment. The study consisted of two 15-d periods. Each period was comprised of a 7-d acclimation period, a 3-d total collection of feces and urine, and two 12-h ileal collections separated by a 3-d adjustment period to assure adequate hydration. Samples of corn, diets, ileal digesta and feces were frozen immediately upon collection. Total genomic DNA was extracted, underwent PCR, and was visualized using agarose gel electrophoresis. Primers were designed to yield a 456 bp PCR product expanding from a rice-ubiquitin gene to the *gdhA* gene within the transgenic cassette. These primers were selected to eliminate the potential of replicating the *gdhA* gene from resident gastrointestinal tract bacteria. While the PCR product was detected from *gdhA*+ corn, *gdhA*+ diets, and even a mixture of the two corn sources containing only 1% *gdhA*+ corn, it was not detected from *gdhA*- corn or diets, or from ileal digesta or feces of any pigs, no matter if they were fed *gdhA*+ or *gdhA*- diets. In conclusion, the recombinant DNA fragment from *gdhA*+ corn appears to be digested and is not detected by regular PCR analysis.

**Key Words:** *gdhA* Gene, Genetically Modified Corn, Pigs

**W67 Herbicide-tolerant rice versus conventional rice in diets for growing-finishing pigs.** G. L. Cromwell\*<sup>1</sup>, B. J. Henry<sup>2</sup>, and D. W. Fletcher<sup>3</sup>, <sup>1</sup>*University of Kentucky, Lexington*, <sup>2</sup>*Bayer CropScience LP, Research Triangle Park, NC*, <sup>3</sup>*Genesis Midwest laboratories, Neillsville, WI*.

Genetically-modified (GM), herbicide-tolerant rice (LibertyLink<sup>®</sup>, event LLRICE62), a near-isogenic (NI) conventional medium-grain rice, and a commercial long-grain, brown rice (CM) were assessed in diets for growing-finishing pigs. The GM and NI rice were grown in year 2001 under similar agronomic conditions. The GM rice was from fields treated (GM+) or not treated (GM-) with Liberty<sup>®</sup> herbicide. The GM+, GM-, NI, and CM rice were similar in composition (DM: 86.4, 85.5, 86.1, 86.6%; CP: 9.7, 10.3, 9.0, 9.2%; NDF: 3.5, 3.9, 3.6, 3.6; ADF: 1.4, 1.6, 1.9, 2.0%; Fat: 2.6, 2.7, 2.6, 3.4%; P: 0.33, 0.37, 0.32, 0.37%; lysine: 0.34, 0.36, 0.33, 0.33%; GE: 3.81, 3.82, 3.78, 3.94 Mcal/kg). Pigs (n = 96) were fed fortified rice-soybean meal diets containing the four rice grains from 25 to 106 kg BW. Diets contained 0.99% lysine initially, with lysine reduced to 0.80 and 0.65% when pigs reached 51 and 77 kg. The rice in diets was constant during each of the three phases (72.8, 80.0, 85.8%). There were six pen-replicates (three pens of barrows, three pens of gilts) and four pigs per pen. All pigs were killed at termination for carcass data. ADG, ADFI, and feed:gain were not different (P > 0.05) for pigs fed the GM vs conventional rice diets (0.86, 0.79, 0.81, 0.85 kg/d; 2.41, 2.49, 2.37, 2.45 kg/d; 2.80, 3.17, 2.95, 2.89 for GM+, GM-, NI, and CM rice, respectively). Carcass traits (adjusted for final BW) were not different (P > 0.10) among treatments (hot carcass yield: 73.5, 72.6, 72.6, 73.2%; 10th rib backfat: 23.0, 22.7, 21.3, 23.8 mm; longissimus area: 38.6, 38.0, 38.2, 38.1 cm<sup>2</sup>; estimated carcass fat-free lean: 50.5, 50.5, 51.2, 50.0%). Gilts grew slower (P < 0.01) and were leaner (P < 0.05) than barrows. Responses to type of rice were similar for the two genders with no evidence of a diet x gender interaction (P > 0.15) for any trait. The results indicate that the genetically-modified,

herbicide-tolerant rice was similar in composition and nutritional value to conventional rice for growing-finishing pigs.

**Key Words:** Pigs, Rice, Biotechnology

**W68 Ultrastructural-chemical makeup of canola seed tissues explored with synchrotron reflection FTIR microspectroscopy: A preliminary study.** P. Yu\*<sup>1</sup>, J. J. McKinnon<sup>1</sup>, R. W. Newkirk<sup>2</sup>, C. R. Christensen<sup>3</sup>, and D. A. Christensen<sup>1</sup>, <sup>1</sup>*College of Agriculture, University of Saskatchewan, Saskatoon, Canada*, <sup>2</sup>*Canadian International Grains Institute, Winnipeg, Canada*, <sup>3</sup>*Canadian Light Source, Saskatoon, Canada*.

The objective of this study was to use synchrotron reflection FTIR microspectroscopy to explore the chemical makeup (functional group and bonding characteristics) of ultra-structural tissues of yellow (*Brassica Rapa* cv. Klondike) and brown-seeded (*Brassica Napus* cv. Bounty) canola. The investigated chemical bonding and functional groups included the NH&OH group with a broad band at 3298, CH groups (CH<sub>3</sub>-asymmetric stretch at 2961; CH<sub>2</sub>-asymmetric stretch at 2925; CH<sub>3</sub>-symmetric stretch at 2871; and CH<sub>2</sub>-symmetric stretch at 2853), amide I at 1650, carbonyl C=O ester stretch at 1740, and hemicellulose at 1240 and total carbohydrates (CHO) at ca. 1180-900 cm<sup>-1</sup> as well as their ratios. The results showed IR absorbed intensities (absorbance unit) of CH<sub>3</sub>-asymmetric stretch of 0.060 and 0.056; CH<sub>2</sub>-asymmetric stretch of 0.090 and 0.087; CH<sub>3</sub>-symmetric stretch of 0.052 and 0.048; and CH<sub>2</sub>-symmetric stretching of 0.045 and 0.043 for the yellow- and brown-seeded canola, respectively. The ratios of total CH<sub>2</sub>:CH<sub>3</sub>, CH<sub>3</sub>-asymmetric:CH<sub>3</sub>-symmetric, CH<sub>2</sub>-asymmetric:CH<sub>2</sub>-symmetric and total CH-asymmetric:CH-symmetric were 1.06 and 1.13, 1.28 and 1.26, 2.90 and 3.08, 1.82 and 1.78, for the yellow- and brown-seeded canola, respectively. The absorbed intensities (absorbance unit) of the peak area of the NH&OH, total CH, carbonyl C=O, amide I, hemicellulose, and total CHO were 101.623 and 87.123; 8.522 and 7.406; 0.387 and 0.414; 39.200 and 31.045; 1.445 and 1.329; 36.450 and 24.199 for the yellow and brown-seeded canola, respectively. The above results indicate the two varieties are potentially different in terms of ultrastructural-chemical makeup. The results also highlight the fact that synchrotron based reflection FTIR microspectroscopy can be used to determine the microstructural chemical bonding and functional group characteristics of canola tissue. Such information can be used for canola breeding programs for selecting superior varieties of canola for both oil and feed purposes and for prediction of canola quality and nutritive value for humans and animals.

**Key Words:** Synchrotron Infrared Microspectroscopy, Ultrastructural-Chemical Makeup, Canola

**W69 Proximate and amino acid composition in different sources of rice bran for pigs.** C. Kaufmann<sup>1</sup>, W. Sauer<sup>1</sup>, M. Cervantes\*<sup>2</sup>, M. Rademacher<sup>3</sup>, and J. He<sup>1</sup>, <sup>1</sup>*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada*, <sup>2</sup>*Instituto de Ciencias Agrícolas, Universidad Autónoma de Baja California, Mexicali, BC, Mexico*, <sup>3</sup>*Degussa-Huls AG, Hanau-Wolfgang*.

A study was conducted to determine the proximate and amino acid (AA) composition of five samples of rice bran (RB), as well as the relationship between their crude protein and AA content. Five different sources of RB were evaluated: RB 1, Canadian source; RB 2, Riceland Foods Inc., Stuttgart, AR; RB 3, Agribrands International, Italy; RB 4, North Luzon Region, Philippines; and RB 5, Agribrands/Tradico, Greenville Feed Facility, Greenville, MS. The contents of crude fat (CF), NDF, ash, and CP in RB 1, 2, 3, 4, and 5 were (%): 23.4, 4.1, 24.4, 5.4, and 20.7; 26.4, 26.0, 34.3, 2.1, and 25.5; 21.0, 12.7, 11.0, 4.8, and 16.3; 15.6, 21.0, 15.8, 13.6, and 18.1, respectively. There were considerable variations in the contents of CF, NDF, ash, and CP. The indispensable AA composition (%) in RB 1, 2, 3, 4, and 5 were: Arg, 1.32, 1.73, 1.29, 0.99, and 1.45; His, 0.44, 0.61, 0.44, 0.34, and 0.50; Ile, 0.51, 0.68, 0.56, 0.44, and 0.59; Leu, 1.05, 1.38, 1.14, 0.94, and 1.22; Lys, 0.69, 0.88, 0.75, 0.45, and 0.76; Met, 0.30, 0.40, 0.33, 0.31, and 0.34; Phe, 0.65, 0.86, 0.71, 0.60, and 0.76; Thr, 0.56, 0.75, 0.62, 0.46, and 0.65; Val, 0.80, 1.04, 0.87, 0.64, and 0.89; Trp, 0.20, 0.28, 0.20, 0.17, and 0.22, respectively. Arg and Leu were the most abundant indispensable amino acids in RB, whereas His, Met, and Trp were the least abundant. The relationships between the content of CP (Y) and each AA (X) were: Arg, Y = 0.0825 - 0.1958X (R<sup>2</sup> = 0.96); His, Y = 0.0308 - 0.1088X (R<sup>2</sup> = 0.98); Ile, Y = 0.0271 +

0.0347X ( $R^2 = 0.96$ ); Leu,  $Y = 0.0502 + 0.1611X$  ( $R^2 = 0.97$ ); Lys,  $Y = 0.0449 + 0.134X$  ( $R^2 = 0.79$ ); Met,  $Y = 0.0114 + 0.1025X$  ( $R^2 = 0.85$ ); Phe,  $Y = 0.0298 + 0.1259X$  ( $R^2 = 0.97$ ); Thr,  $Y = 0.0324 + 0.0104X$  ( $R^2 = 0.93$ ); Val,  $Y = 0.0439 + 0.0085X$  ( $R^2 = 0.91$ ); Trp,  $Y = 0.0116 + 0.0093X$  ( $R^2 = 0.96$ ). There was a linear increase in the content of all AA as the content of CP increased ( $P < 0.05$ ). This study shows that there is considerable variation in the proximate and AA composition in the RB. This also indicates that the AA content in RB can be predicted on the basis of its CP content.

**Key Words:** Pigs, Rice Bran, Amino Acid Digestibility

**W70 Maturity zone effects on composition of soybean meals sampled from 55 U.S. processing plants.** L. K. Karr-Lilienthal\*, C. M. Grieshop, J. K. Spears, and G. C. Fahey, Jr., *University of Illinois, Urbana.*

Variation in soybean meal (SBM) composition can affect nutrient digestibility of SBM by swine. To quantify variation in U.S. SBM, samples were collected from 55 U.S. processing plants three times at two week intervals (sampling times 1, 2, or 3). These samples were analyzed for crude and acid hydrolyzed fat as well as oligosaccharide and amino acid concentrations. Comparisons were made among SBMs according to maturity zone (1-7) where the SBMs were prepared and sampling times (1-3). Acid hydrolyzed fat concentrations were 1.5 to 3.3 times higher than crude fat concentrations, were greatest ( $P < 0.05$ ) at the second sampling time, and increased for processing plants located in the southern U.S. (3.9 to 4.3% for zones 1 and 7, respectively). Oligosaccharide concentrations varied depending on sampling time and maturity zone. Raffinose concentrations decreased ( $P < 0.05$ ) over time from 12.66 to 11.92 mg/g and verbascose concentrations were lowest for collection 3 (1.70 vs. 1.90 mg/g for collections 1 and 2), while stachyose concentrations increased over time from 51.78 to 53.52 mg/g. Concentrations of stachyose were highest for SBM prepared in zones 3 (55.6 mg/g) and 4 (55.2 mg/g), while verbascose concentrations were highest for samples collected in the southern U.S. Total essential amino acid (TEAA) and total amino acid (TAA) concentrations increased over time from 22.0 to 23.5% and 51.1 to 53.1%, respectively. For the processing plants located in the southern U.S., TEAA concentrations increased (22.3% for zone 1 vs. 23.7% for zones 5 and 6). The lowest TAA concentrations were noted for SBMs prepared in zones 1 (50.8%) and 2 (51.0%). Soybean meals produced in southern maturity zones contained higher concentrations of acid hydrolyzed fat and TEAA. There was variation in oligosaccharide and amino acid concentrations over time, probably due to variation in composition of soybeans arriving at the processing plant.

**Key Words:** Amino Acids, Oligosaccharides, Soybean Meal

**W71 Sensory tests reveal that the efficacy on masking capacity of a strawberry flavor changes with different protein sources and their level in feed.** I. Pérez-Portabella, C. Puyuelo, C. Ibáñez, J. Solà, and E. Roura\*, *Lucta SA, Barcelona, Spain.*

In piglet diets several types of protein sources are included and often subsequently substituted. Flavors are used to mask these and other dietary changes, thus avoiding olfactory cues that could depress feed intake. Sensory-based procedures were developed to assess the effect of some protein sources and their in-feed level on the efficacy of a strawberry flavor. Firstly, the detection threshold on a salt base for fishmeal, animal plasma and soybean meal was measured by a 15-member expert panel (7 women and 8 men) according to the standard practice (ASTM-E679). In a second step, each one of the three protein sources were mixed at 0, 3, 6 and 12% with corn meal, and 400 ppm of a strawberry flavor was added to all samples. Flavor intensity and masking capacity for each sample was evaluated by 8 panelists and results analyzed by the Tukey B test for differences in type of protein source and level of inclusion. The results of the first study show that fishmeal had the lowest detection threshold at only 5 ppm, animal plasma was detected at 162 ppm and soybean meal at 288 ppm. Women were capable of detecting lower levels than men in all three feedstuffs. Regardless of the protein, the higher the level the lower the flavor intensity. Particularly the level of fishmeal inclusion linearly affected both intensity of the strawberry flavor ( $y = -2.3x + 76.4$ ,  $R^2 = 0.77$ ) and its masking capacity ( $y = -4.1x + 76.2$ ,  $R^2 = 0.89$ ), while the effect of plasma levels ( $R^2 \leq 0.6$ ) and soybean meal ( $R^2 \leq 0.3$ ) did not appear to follow linearity.

Differences due to the protein source on both intensity and masking capacity were significant ( $P < 0.05$ ) at 6% and 12% inclusion, with fishmeal affecting more than plasma and plasma more than soybean meal (but not at 3%). It is concluded that the lower the detection threshold of fishmeal, animal plasma and soybean meal the higher the impact on the flavor intensity and its masking capacity. Flavor responses to the protein inclusion rate was linear only for fishmeal.

**Key Words:** Protein Sources, Odor Detection Threshold, Strawberry Flavor

**W72 An improved method for the rapid determination of phytase activity in animal feeds.** T.W. Kim\* and X.G. Lei, *Cornell University, Ithaca, NY.*

The current direct colorimetric assay for phytase activity in feeds is interfered by high phosphorus background and other factors. The objective of this experiment was to develop a rapid and reliable spin column method to accurately determine phytase activity in feed ingredients or complete diets. After the feed sample was extracted in 0.2 M citrate buffer, pH 5.5, for 30 min at room temperature, the oily layer of the supernatant was removed by passing an acrodisc syringe filter (0.45  $\mu$ m HT Tuffryn membrane, Gelman Laboratory, Ann Arbor, MI). The filtrate was then loaded onto a spin column (MW cutoff 30,000, Millipore, Bedford, MA) to remove free inorganic phosphate prior to the phytase activity assay. Compared with the direct assay, this new procedure improved both accuracy and reproducibility. When diets contained phytase at 0-1,000 units/kg, the coefficients of variation for multiple assays of the same samples ( $n = 6$ ; dietary enzyme levels = 5) by the new method ranged from 1.3 to 4.1%, but 10 to 39% by the direct method. There was a linear regression between the added phytase activity and the actual activity measured by the new method ( $R^2 = 0.997$ ;  $P < 0.001$ ). By concentrating the sample during spin column filtration, the new method could be used to accurately detect low levels of phytase in diets (10 units/kg). In conclusion, this spin column method is considered an improved assay for phytase activity in animal feed, and may be used for quality control of phytase supplementation.

**Key Words:** Phytase, Phosphorus, Feed enzyme

**W73 The effect of dietary calcium on indicators of bone turnover in mares.** B. D. Cassill\*, S. Hayes, J. Ringler, K. Janicki, and L. Lawrence, *University of Kentucky, Lexington.*

Preliminary studies in our laboratory have found that serum ICTP (carboxy-terminal pyridinoline cross-linked telopeptide region of type I collagen), an indicator of bone turnover, is increased shortly after foaling suggesting mares mobilize bone mineral during lactation. This study was conducted to determine whether dietary calcium and phosphorus concentration would affect indicators of bone turnover in mares during late lactation and after weaning. The study used 12 mares (average age  $10 \pm 4.8$  y) split into 2 groups. Groups were balanced for age and parity. The control group was fed to meet all NRC (1989) requirements. Group H was fed to meet all NRC (1989) requirements, plus enough dicalcium phosphate to increase calcium intake to 150% of the recommended level. The study was initiated at 2.5 mo of lactation and lasted for 16 wk which included 56 d of lactation and 56 d after weaning. Body weights were obtained every 14 d and blood samples were collected every 28 d for the duration of the study. Milk samples were collected every 28 d for the first 56 d. Calcium concentrations of milk were determined using atomic absorption spectrophotometry. Serum was analyzed for ICTP using radioimmunoassay. ICTP concentration in serum decreased over time ( $P = 0.057$ ) but was not affected by diet ( $P = 0.363$ ). Calcium concentration in milk decreased over time ( $P = 0.005$ ) but was not affected by diet ( $P = 0.236$ ). Average daily gain of the foals was not different between groups ( $P = 0.675$ ). Increasing dietary calcium and phosphorus intake by mares did not affect milk calcium or serum ICTP concentrations during late lactation or in the first 2 mo after weaning.

**Key Words:** Horse, Lactation, Calcium

**W74 Partitioning of metabolizable energy by rainbow trout and Atlantic salmon using a multivariate approach: species and diet effects.** P.A. Azevedo\*, S. Leeson, C.Y. Cho, S. Birkett, and D.P. Bureau, *University of Guelph, Ontario, Canada.*

A study was conducted to investigate how the allocation of energy to growth and maintenance differs between rainbow trout and Atlantic salmon and how the diet affects energy allocation. Rainbow trout and Atlantic salmon were handfed to satiation four isoenergetic diets (DE = 20 MJ/kg) with different digestible protein/digestible energy ratios (DP/DE), i.e., 24, 22, 20, and 18 g/MJ, achieved through reduction of DP level (53 to 39%) and increase of lipid level (19 to 26%). Intake of metabolizable energy (ME), protein (PD), and lipid (LD) gain were determined. Data were analyzed by multivariate analysis of PD and LD on ME. Maintenance energy requirements (ME<sub>m</sub>) and efficiency of ME utilization for PD (k<sub>p</sub>) and LD (k<sub>l</sub>) were estimated. The fraction of ME intake above maintenance for PD (X) was defined as linear function of body weight with slope (d) and intercept (c) estimated simultaneously with the above parameters. The ME<sub>m</sub> did not differ (P > 0.05) be-

tween rainbow trout and Atlantic salmon (20 kJ/day/kg<sup>0.8</sup>). On the other hand, K<sub>p</sub>, c, and d were significantly different (P < 0.05) between the two species, independently of the diet. The ME intake above ME<sub>m</sub> channeled towards PD (c) was higher in salmon than trout (57 vs. 55%; P < 0.05). The change in partitioning of ME toward PD due to the change in body weight was negative for trout (d = -0.18) while it was positive for salmon (d = 0.16). The values of d agreed well with the increase of LD/PD with body weight for trout and the decrease of LD/PD with body weight for salmon which may have been related to the maturation status of this fish and the associated loss of lipid observed with maturing salmon. The K<sub>p</sub> was significantly higher for salmon compared to trout (0.52 ± 0.06 vs. 0.43 ± 0.06; P < 0.05) and independent of the diet while K<sub>l</sub> was 0.81 ± 0.13 irrespective of species or diet. Lower cost of protein deposition for salmon compared to trout suggests differences in protein metabolism between these two species. Studies on protein turnover rates and metabolic utilization of nutrients for PD are required to gain insight on k<sub>p</sub> differences between salmon and trout.

**Key Words:** Rainbow Trout, Atlantic Salmon, Energy Allocation

## Nonruminant Nutrition: Sow & Gilt Nutrition

**W75 Ideal protein to improve lactation performance of multiparous sows.** F. Ji\*<sup>1</sup>, Y. G. Kim<sup>2</sup>, and S. W. Kim<sup>1</sup>, <sup>1</sup>Texas Tech University, Lubbock, <sup>2</sup>CJ Corporation, Seoul, Korea.

The objective of this study was to validate the ideal dietary amino acid pattern in lactation diets to improve the performance of multiparous sows during lactation. Thirty two (20 second and 12 third parity Camborough-22) sows and their litters were used for this study. On d 109 of gestation, sows with a similar body weight were grouped and allotted to one of four dietary treatments representing: low protein (LC), low protein with ideal protein (LI), high protein (HC), and high protein with ideal protein (HI). Low protein diets contained 17.5% CP and high protein diets contained 19.5% CP. Ideal amino acid patterns among lysine, threonine, and valine were 100:63.0:78.1 (lys:thr:val) for the LI diet and 100:62.3:77.5 for the HI diet when it was calculated based on ileal digestible amounts. To match amino acid pattern to ideal ratios, crystalline amino acids were supplemented. Crude protein contents in the diets with ideal protein pattern were matched to the control diets by adjusting SBM content as crystalline amino acids were added. Weight and backfat thickness of sows as well as the weight of each piglet were measured at farrowing and weekly until weaning at d 21 of lactation. All sows had free access to feed and water during lactation. The body weight of sows after farrowing (224.5±4.5 kg) and litter size at farrowing (10.2±0.2 pigs) were the same (P=0.361 and 0.779, respectively) among the treatments. Voluntary feed intake of sows (5.63±0.22 kg/d) did not differ (P=0.911) among the treatments. Sows fed the low protein diets had greater (P<0.05) weight loss than sows fed the high protein diets. Sows fed the diets with ideal protein tended to have smaller (P=0.051) weight loss than sows fed the control diets. For the second parity sows, there were no differences in backfat loss, litter size at weaning and litter weight gain among the treatment. However, weight loss of the HI sows was smaller (P<0.05) than the LC sows. For the third parity sows, there were no differences in lactation performance among the treatments.

**Key Words:** Lactation, Multiparous sows, Ideal protein

**W76 Utilization of seaweed (*Macrocystis pyrifera*) meal in wheat-based diets for lactating sows.** J. Baeza<sup>1</sup>, M. Cervantes\*<sup>2</sup>, J. L. Figueroa<sup>1</sup>, E. Chi<sup>1</sup>, M. Cuca<sup>1</sup>, and N. Torrentera<sup>2</sup>, <sup>1</sup>Ganadería, Colegio de Postgraduados, Montesillos, Mexico, <sup>2</sup>ICA, Universidad Autónoma de Baja California, Mexicali, BC, Mexico.

There is interest in alternative ingredients to enhance productive performance of animals without damage to the environment. Therefore, an experiment was conducted to evaluate the addition of seaweed (*Macrocystis pyrifera*) to wheat-based diets for lactating sows on milk production and composition, daily litter gain, and wean to first oestrous interval of sows. Thirty two multiparous sows (Landrace x Duroc x Yorkshire) were fed four diets with eight replicates. Treatments were: T1) wheat-soybean meal, basal diet; T2) T1+1.5% seaweed; T3) T1+3.0% seaweed; and T4) T1+4.5% seaweed. Litters were standardized to eight piglets

and milk production was estimated at 6, 13, 20, and 27 d by the double-weight method; milk protein concentration was determined at 13 and 27 d. Piglet weights at weaning and daily weight gain, sows milk production, and number of weaned piglets for treatments 1 to 4 were: 7.30, 7.22, 7.21, 7.01 kg; 201, 196, 196, 186 g/d; 5.98, 5.35, 5.75, 6.13 kg/d; 7.86, 7.71, 7.38, 7.87, respectively. Seaweed addition did not affect the analyzed variables. A linear effect was observed (P < 0.05) between productive variables (litter daily gain, milk production, sows feed intake) and days on lactation. The peak of milk production was observed between the third and fourth weeks of lactation. The litter weight gain and feed intake were highest in the fourth week. These results suggest that seaweed addition to lactating sow diets does not affect productive and reproductive performance of lactating sows and their litters.

**Key Words:** Sows, Lactation, Seaweed

**W77 The importance of dietary selenium on antioxidant status and hormonal profile in post-pubertal gilts.** M.-É. Fortier\*<sup>1</sup>, H. Quesnel<sup>2</sup>, A. Giguère<sup>3</sup>, J.-F. Bilodeau<sup>1</sup>, J.-P. Laforest<sup>1</sup>, and J. J. Matte<sup>3</sup>, <sup>1</sup>Université Laval, Quebec, Canada, <sup>2</sup>Institut de la Recherche Agronomique, St. Gilles, France, <sup>3</sup>Agriculture and Agri-Food Canada, Lennoxville, Quebec, Canada.

This project aimed to determine the effect of selenium (Se) as inorganic Na-selenite (MSe) or organic Se-yeast (OSe) on antioxidant status and hormonal profile, after puberty and in early gestation of gilts. Forty-nine gilts were allocated to one of the 3 feeding treatments at first estrus: control (C: basal diet (Se=0.2 ppm) without added Se) (n=16), MSe (C+0.3 ppm Se) (n=16) and OSe (C+0.3 ppm Se) (n=17). Treatments started at the day after the first pubertal estrus and lasted up to 30 d post-AI (AI at the fourth estrus). Blood was collected from all gilts on the day after each estrus and on d 30 post-AI. Blood was also collected daily from d -4 until d +4 of the third onset of estrus (d 0) in 8 C, 9 MSe and 8 OSe canulated gilts. Blood Se was lower (P<0.01) in C than in Se groups and higher in OSe than in MSe (P<0.01) (C:249±6, MSe:273±6 and OSe:316±8 µg/L on d 30 post-AI). Blood Se-GSH-Px tended to be lower (P<0.06) in C than in Se groups starting at third estrus and was higher (P<0.01) in MSe than in OSe starting at AI (C:2078±74, MSe:2594±84 and OSe:2392±105 mU/mg hemoglobin on d 30 post-AI). Plasma T3, a Se-related hormone, was not altered by treatments (P>0.12) prior to AI but, during gestation, T3 decreased markedly (P<0.03), values for MSe being lower (P<0.02) than for OSe on d 30 of gestation (C:90±2, MSe:79±5 and OSe:94±3 ng/100mL). In canulated gilts, plasma FSH was lower (P<0.04) for MSe than for C on d +2 and d +3. On d +4, FSH (C:0.88±0.12, MSe:0.94±0.19 and OSe:1.27±0.20 ng/mL) and T3 (C:88±12, MSe:75±7 and OSe:97±16 ng/100mL) values became higher (FSH, P<0.05) or tended to be higher (T3, P<0.07) for OSe than MSe. There was no treatment effect (P>0.10) on the profile of LH or E2 during the third estrus. In summary, the Se status response to dietary Se was not reflected on Se-GSH-Px which responded to Se supplements but, in a different way, to the type of Se supplements. Taking into account the role of T3 in FSH synthesis, the FSH and T3 effects after estrus merit