679 Effects of dbcAMP on the proliferation, differentiation and adipogenesis-related genes of porcine adipocytes. L. Wang*[1,2], Z. Y. Jiang[1], Y. C. Lin[1], X. Y. Ma[1], and X. G. Lei[2], [1]*Institute of Animal Science, Guangdong Academy of Agricultural Sciences*, *Guangzhou, Guangdong, China*, [2]*Department of Animal Science, Cornell University*, *Ithaca, NY*.

We investigated the roles of dbcAMP (N^6, 2′-O-dibutyryl adenosine 3′, 5′ cyclic monophosphate) on adipogenesis of porcine adipocytes. Adipocytes were derived from freshly dissected back subcutaneous fat of 7-d Duroc × (Large White × Landrace) crossbred pig and incubated for 1d to 6d in DMEM/F12 media containing 10% fetal bovine serum and dbcAMP (0, 0.001, 0.01, 0.1, 1, 10, 100 and 1000 μmol/L). The proliferation and differentiation of adipocytes were measured by the MTT assay and Oil Red O staining, respectively. The mRNA expression of peroxisome proliferator-activated receptor γ_2 (PPARγ_2), adipocyte fatty acid binding protein (A-FABP) and CCAAT/enhancer binding protein α (C/EBPα) were measured by semiquantitative RT-PCR using β-actin as an internal standard. All data were analyzed by ANOVA using the GLM procedure of SAS 8.2. Supplementation with dbcAMP inhibited porcine preadipocytes proliferation in a dose-dependent manner with significance ($P < 0.05$) reached at 1000 μmol/L. The differentiation of porcine preadipocytes changed quadratically with increasing concentration of dbcAMP, and minimal differentiation at 0.1 or 1 μmol/L ($P < 0.05$). PPARγ_2 and A-FABP mRNA expression were decreased significantly ($P < 0.05$) by supplementation with 1000 μmol/L dbcAMP, while C/EBPα mRNA expression was unchanged. Above-mentioned results indicated dbcAMP supplementation in porcine preadipocytes inhibited proliferation and differentiation.

Key Words: dbcAMP, adipocytes, adipogenesis

680 DbcAMP increased lean percentage and protein deposition in finishing pigs. Z. Y. Jiang, L. Wang*, Y. C. Lin, C. T. Zheng, and X. Y. Ma, *Institute of Animal Science, Guangdong Academy of Agricultural Sciences*, *Guangzhou, Guangdong, China*.

This study was conducted to investigate the effects of dbcAMP (N^6, 2′-O-dibutyryl adenosine 3′, 5′ cyclic monophosphate) on growth performance and muscle growth in finishing pigs. Seventy-two Duroc × (Landrace × Large White) barrows (57.3 ± 0.6 kg) were randomly allotted to 3 treatments with 6 replicate pens (4 pigs per pen). The pigs were fed corn-soybean diets containing 0 (control), 10 and 20 mg/kg dbcAMP (purity, 98%), respectively, and allowed ad libitum access to feed and water, until the final slaughter weight of approximately 90 kg. Lean percentage was calculated by dissecting lean, fat and bone. Cryostat sections were stained with hematoxylin and eosin to determine fiber diameter and density of longissimus dorsi muscle (LDM). The concentration of cAMP (3′, 5′-cyclic adenosine monophosphate) and activities of cAMP dependent protein kinase A, adenylate cyclase (AC) in LDM were measured by ELISA. The mRNA expression of myogenic determinative factor (MyoD), myostatin, α-actin and myosin heavy chain (MHC) were measured by semiquantitative RT-PCR using β-actin as an internal standard. All data were analyzed by ANOVA using the GLM procedure of SAS 8.2. The ADG were 808, 836 and 832 g/d separately, but there were no significant differences among treatments ($P > 0.05$). Lean percentage in pigs fed 10 mg/kg dbcAMP was 5.64% greater ($P < 0.05$). No difference in fat percentage, bone weight percentage and in fiber density of LDM were detected ($P > 0.05$) among treatments. Compared with the control, fiber diameter of LDM tended to increase 8.61 ~26.17% ($P = 0.06$). Supplementation with 10 mg/kg dbcAMP elevated significantly AC activity, and MyoD, α-actin, MHC mRNA expression in LDM ($P < 0.05$). These results indicated that supplementation with dbcAMP in the diet could promote muscle growth and increase protein deposition in finishing pigs.

Key Words: dbcAMP, protein deposition, finishing pigs

681 The impact of dietary long chain fatty acids on bone and cartilage in swine. C. I. O'Connor-Robison*[1], J. D. Spencer[2], and M. W. Orth[1], [1]*Michigan State University*, *East Lansing,* [2]*JBS United, Inc.*, *Sheridan, IN*.

Dietary long chain polyunsaturated fatty acids (LCPUFA) including arachidonic acid (AA), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) can regulate the production of certain inflammatory mediators. The objective of this study was to characterize the effects of dietary LCPUFA on cartilage fatty acids and bone density and morphology. Sows and gilts were fed either control corn/soybean meal based diets, or the control diet supplemented with 1.0% protected LCPUFA from Fertilium (JBS United, Sheridan, IN). Sows had completed an average of 5.5 parities while gilts reached an average BW of 111 kg at time of slaughter. The cartilage was biopsied from the right and left humeral-ulnar joints of 14 sows (7/trt) and 16 gilts (8/trt) within 30 h of slaughter for fatty acid analysis. The right fused radius/ulna was saved for analysis via computerized topography (CT). Cartilage was pulverized in a freezer mill then fatty acids were extracted, methylated, and analyzed by GLC. Bones were cleaned and then analyzed with CT where 1 cm slices were acquired through the distal radius, central radius, and proximal ulna. Cortical width and density were measured and trabecular density was measured at the distal radius. Sows fed LCPUFA had increased DHA ($P < 0.01$), decreased C20:1 ($P < 0.01$), and an overall decrease in the omega-6 to omega-3 ratio ($P < 0.05$) in cartilage. Gilts fed LCPUFA had increased EPA ($P < 0.10$), DHA ($P < 0.01$), C22:1 ($P < 0.01$), and C22:5 ($P < 0.10$) in cartilage. CT scans of the radius/ulna from gilts revealed no differences for cortical width and bone density. Sows fed LCPUFA had greater cortical width of the proximal ulna ($P < 0.05$) and decreased cortical width of the distal radius ($P < 0.05$). Although the LCPUFA diet did increase omega-3 incorporation into chondrocytes the biological significance is unclear since concentrations of AA were at least 9-fold higher than EPA or DHA. Also, bone density was not affected by a LCPUFA enriched diet. Changes in cortical width were interesting but cannot be explained at this time. Thus, if omega-3 fatty acids can mitigate inflammation in joints, the benefit would likely be the result of systemic changes in inflammatory mediators.

Key Words: swine, omega-3, cartilage

682 Cannabinoid receptor type 1 (CB1) antagonist, SR141716 suppresses hepatic carnitine palmitoyltransferase 1 (CPT1) gene expression in rat. T. Wu*, Z. Yuan, and Y. Wang, *Institution of Feed Science*, *Hangzhou, Zhejiang province, China*.

SR141716 is the antagonist of cannabinoid receptor type 1 (CB1). The study was conducted to investigate the effects of SR141716 on body weight gain, hepatic fat deposit and carnitine palmitoyltransferase 1 (CPT1) expression in obese Sprague-Dawley (SD) rats induced by high fat diet (HFD). Twenty-four SD rats were randomly allocated to 3 groups: the normal diet (ND) as control group, the high fat diet (HFD) and SR141716 treated HFD-diet (SFD) animals as experimental

groups. Plasma was collected immediately for following plasma indexes determination. Liver samples were flash frozen in liquid nitrogen and stored at –80°C until use for following experiments. Compared with the ND group, HFD significantly increased the body weight gain (ND: 158.5 ± 4.14g, HFD: 173.8 ± 2.58g, $P \leq 0.05$), total viscera fat pad (ND: 2.38 ± 0.14 g/100g BW, HFD: 2.52 ± 0.11 g/100g BW, $P \leq 0.05$) and hepatic triglyceride (TG) (ND: 5.74 ± 0.58 mg/100g tissue, HFD: 10.71 ± 1.05 mg/100g tissue, $P \leq 0.05$) in rats, while SR141716 significantly suppressed these effects (154.6 ± 5.96g; 2.04 ± 0.10g/100g BW; 7.76 ± 0.52mg/100g tissue, $P \leq 0.05$). Furthermore, hepatic CPT1 mRNA level was significant decreased by HFD (24.78%, $P \leq 0.05$). Hepatic CPT1 and PPARgamma mRNA level were significantly suppressed by SR141716 accompanied with a decrease in expression of CB1 mRNA (19.52%, $P \leq 0.05$). The results indicated that SR141716 can significantly suppress the excess hepatic adipose deposit induced by HFD in rats. During this process, the pivotal role of CB1 in hepatic fat deposit may be due to modulation of CPT1 expression through PPARgamma. However, the accurate mechanism remains to be elucidated in the future.

Key Words: SR141716, Hepatic fat deposition, CPT1

683 Is the effect of dietary energy levels on feed intake of broiler chickens affected by bird age? M. Cho*[1], R. L. Payne[2], and H. L. Classen[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [2]*Evonik-Degussa Corporation*, *Kennesaw, GA*.

It is historically known that chickens are able to adjust their feed intake according to the dietary energy content. However, broiler chickens may not be able to adjust their feed intake due to intense genetic selection and/or limited gut capacity at a young age. Hence, 2 experiments were conducted to clarify the relationship between dietary energy level and feed intake in broiler chickens and how it is affected by bird age. Trial 1 was conducted to determine the AME of Western Canadian feedstuffs using 5 and 21 d old broilers. Differences were found between 5 and 21 d old chickens for AMEn of some ingredients and therefore the determined values were used to formulate diets for trial 2 using age appropriate values. Trial 2 was conducted to investigate the effect of age on the feed intake response of broiler fed diets with a range in dietary energy content (2700, 2833, 2966 and 3100 kcal/kg). Diets in this energy range were fed for the entire experiment (SGF), for the grower and finisher periods (GF) or only in the finisher period. (F). Starter, grower and finisher diets were fed from 0 to10, 11 to 25 and 26 to 35 d, respectively. Amino acid levels in diets met or exceeded the primary breeder recommended values. Overall, birds did not adjust their feed intake based on the energy level of the diet. Switching from 3100 kcal/kg diets to lower energy had no impact on feed intake when started at the grower phase. A similar switch at the finisher phase caused a temporary (25 to 30 d) decrease in feed intake and consequently growth rate. Growth rate of birds fed the 2700 kcal/kg diet was lower than other treatments. The data suggest that modern broilers do not or cannot change feed intake in response to dietary energy when dietary amino acid requirements are met and this response is relatively consistent through-out the broiler growth period.

Key Words: nutrient density, poultry nutrition, AME

684 Estimation of net energy values of feedstuffs by simulation of biochemical reactions in broiler chicks. S. Cerrate* and C. Coon, *University of Arkansas*, *Fayetteville*.

A computer program is proposed which simulates energy metabolism in the growing broiler chicken for the estimation of net energy (NE) values of feedstuffs. This approach is based on a quasi-steady-state system which measures reactants and products in major metabolic pathways for carbohydrates, protein and fats. The input variables were digestible carbohydrates, amino acids and fatty acids and the output variables were 1) estimated net energy needs for maintenance and 2) net energy for tissue gain. Adenosine triphosphate was used to quantify the energy from chemical reactions obtained from oxidative metabolism of nutrients and then utilized for maintenance and gain by anabolic reactions. Simulations of a basal diet and 10 experimental diets (basal + feedstuff), were formulated to estimate their NE values. For each diet an estimation of NE value was simulated and then calculated for each feedstuff. The simulated NE values for each feed ingredient were compared with determined NE values of feedstuffs reported by past studies. A high correlation was observed between simulated and determined NE values for feed ingredients. The data indicates that the proposal model can be used to predict net energy values of feed ingredients.

Key Words: broiler, net energy, biochemical reactions

685 Energy determination of corn co-products fed to broiler chicks from fifteen to twenty-four days of age and use of composition analysis to predict AME_n. S. J. Rochell*[1], B. J. Kerr[2], and W. A. Dozier, III[1], [1]*Auburn University*, *Auburn, AL*, [2]*USDA-ARS Agroecosystems Research Unit*, *Ames, IA*.

Fifteen co-products collected from various wet and dry milling plants were fed to broiler chicks to determine AME_n and to generate an equation to predict AME_n based upon each ingredient′s chemical composition. Co-products included: DDGS (6), high protein dried distillers grain (HP-DDG) (2), dehydrated corn germ (2), corn germ meal, corn bran, corn gluten meal, corn gluten feed, and dehulled degermed corn. A control diet was fed containing corn, soybean meal, dextrose (15%), dicalcium phosphate, limestone, salt, vitamins, and trace minerals. Test diets were formulated by mixing the control diet with 15% of a co-product at the expense of dextrose. Nineteen hundred and 20 Ross × Ross 708 chicks (10 per pen; 5 males and 5 females) were randomly assigned to 15 dietary treatments (12 replicate pens). Broilers were fed experimental diets from 15 to 22 d of age followed by a 48 h total excreta collection period. Ingredients were analyzed for GE, CP, DM, crude fat, crude fiber, ash, total dietary fiber, NDF, and ADF, and hemicellulose was determined by difference. Gross energy was determined on the feed and excreta to calculate AME_n for each ingredient. The corn-soybean meal portion of the basal diet averaged 3,037 kcal AME_n/kg DM, with dextrose having an assumed value of 3,640 kcal/kg DM. For the 6 samples of DDGS, AME_n ranged from 2,146 to 3,098 kcal/ kg DM, averaging 2,676 kcal/ kg DM. The AME_n values for dehydrated corn germ, corn germ meal, HP-DDG, corn gluten meal, corn gluten feed, corn bran, and dehulled, degermed corn were 3,308, 1,991, 2,820, 3,182, 1,746, 3,030, and 3,442 kcal/kg DM, respectively. Stepwise regression resulted in the equation: AME_n, kcal/kg DM = 3,517 + (46.02 × % crude fat, DM basis) – (82.47 × % ash, DM basis) – (33.27 × % hemicellulose, DM basis) ($R^2 = 0.89$; SEM = 191; $P \leq 0.01$). These results determined that wide variability exists among corn co-products produced from dry and wet milling plants, and that the best predictors of AME_n are crude fat, ash, and hemicellulose.

Key Words: corn co-products, metabolizable energy, chicks

686 Apparent metabolizable energy (AME_n) content and standardized ileal amino acids digestibility of wheat, wheat-corn and corn distillers dried grains with solubles (DDGS) for broilers. A.

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In Exp. 1, the apparent metabolizable energy (AME_n) contents of 2 samples of wheat distillers dried grains with solubles (DDGS), 3 samples of wheat-corn DDGS, and 3 samples of corn DDGS were determined. A total of 225 broiler chickens were assigned to 9 dietary treatments, each consisting of 5 pens of 5 birds each, and were fed a basal starter diet or the basal diet plus 30% of DDGS from 14 to 19 d of age. All diets contained titanium dioxide (0.3%) as an indigestible marker. On average and in comparison with corn DDGS, wheat DDGS had lower AME_n content (2,872 vs. 3,177 kcal/kg DM) which is a reflection of its lower fat (4.5 vs. 10.7% DM) and carbohydrate (7.1 vs. 10.5% DM), including residual starch (1.6 vs. 6.6% DM), contents. The wheat-corn DDGS samples had intermediate values for AME_n contents which averaged 2,975 kcal/kg DM. As blending of wheat and corn is a common practice in bio-ethanol production in western Canada, a prediction equation for energy availability was developed and demonstrated a strong relationship between the amount of wheat and corn grain used and the AME_n content ($R^2 = 0.95$). The AME_n values corresponded well with the TME_n values, which averaged 3,160 for wheat DDGS, 3,238 for wheat-corn DDGS, and 3,488 kcal/kg DM for corn DDGS. In Exp. 2, the standardized ileal digestibility (SID) of amino acids (AA) was determined for 2 wheat DDGS, 6 wheat-corn DDGS and 4 corn DDGS samples. A nitrogen-free diet was used to determine endogenous AA losses. The SID values averaged 59.0, 59.6 and 62.7% for Lys; 82.7, 79.8 and 82.7% for Arg, and 70.6, 64.4 and 68.3% for Thr, respectively, for wheat, wheat-corn and corn DDGS ($P > 0.05$). The SID for Met was lower ($P < 0.05$) in wheat-corn DDGS (73.3%) compared with wheat DDGS (81.2%) or corn DDGS (81.3%). Overall, there was no conclusive relationship between the SID of amino acids and the type of DDGS used.

Key Words: DDGS, AME_n, amino acid digestibility

687 Use of the precision-fed rooster TME assay and chick AME assay to quantify the energy value of Nutridense corn. T. Loeffler*, D. A. Neves, and A. B. Batal, *University of Georgia*, *Athens*.

To determine the energy value of Nutridense corn, 2 precision-fed rooster TME assays and 2 conventional chick AME digestibility trials were conducted. The TME and AME values were compared within each experiment for both the Nutridense corn and the control corn, and the same experimental design was used for each study. The rooster assays were traditional precision-fed rooster assays in which 10 birds per diet were fasted for 24 h, crop intubated with 35 g of the test diet containing 92.25% control corn or 92.25% Nutridense corn, and excreta was then collected for 48 h. For the chick studies, 288 one-day-old Cobb 500 by product male broiler chicks were placed in Petersime battery brooders with raised wire floors. There were 12 replications of 12 chicks per replication assigned to the 2 corn diets. Chicks were fed a standard corn-soybean meal starter diet until 13 d of age, and on d 14, the chicks were allowed ad libitum access to the corn diet. Excreta were collected on d 17, dried, weighed, ground and analyzed for gross energy and crude protein. The determined AME values were 3.1% higher in study 1 (3096 vs. 3003 kcal/kg) and 2.3% higher in study 2 (2974 vs. 2907 kcal/kg) for the Nutridense as compared with the control corn. The determined TME values were also higher for the Nutridense corn as compared with the control corn; 2.2% increase (3463 vs. 3390 kcal/kg) and 1.2% increase (3446 vs. 3404 kcal/kg) for study 1 and 2, respectively. There was a larger difference in the ME values between the rooster TME and chick AME for study 1 than for study 2, but the Nutridense always had a higher ME than the control corn. Although the results for energy digestibility are not in agreement between the chicks and roosters in these studies, analysis of the data indicates that Nutridense corn has higher metabolizable energy than the control corn.

Key Words: Nutridense, corn, ME

688 Evaluation of energy digestibility among and within feedstuffs for swine using an in vitro digestibility technique. L. F. Wang*[1], P. R. Regmi[1], N. S. Ferguson[2], A. Pharazyn[2], and R. T. Zijlstra[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Nutreco Canada*, *Guelph, ON, Canada*.

The DE content of feedstuffs varies; thus, rapid and accurate evaluation of apparent total tract digestibility (ATTD) of energy is required for accurate swine feed formulation. Previously, a 3-step in vitro energy digestibility technique using pepsin, pancreatin and Viscozyme predicted ATTD of energy accurately among single samples of 8 feedstuffs ($R^2 = 0.97$). Within feedstuff variability was predicted well for grains and poorly for canola meal and corn DDGS. The objective was to expand the feedstuff matrix to multiple samples of corn, pulse crops, soybean meal and wheat; and to compare the accuracy of predicting ATTD of energy between in vitro digestibility and data from proximate analyses (fiber, ether extract, CP). The ATTD of energy was determined for 60 samples of 7 feedstuffs using 148 grower pigs with the indicator method. For multiple samples per feedstuff, in vitro energy digestibility was the best single predictor ($R^2 = 0.71$) compared with proximate analyses ($R^2 = 0.63$). Prediction accuracy of the in vitro technique was similar to using proximate analyses ($R^2 = 0.71$ vs. 0.75; SE of prediction [SEP] = 5.5 vs. 5.0; respectively). The prediction residuals from both methods were highly correlated (r = 0.88); the SEP for in vitro was highest for corn (5.1), then pulse (4.0), soybean meal (4.2), and lowest for wheat (1.3). Among feedstuffs, combining in vitro digestibility and proximate data reduced the error (SEP = 4.6). However, within feedstuff, the SEP of in vitro digestibility data was higher than for multiple chemical data (corn, 2.8 vs. 0.9; pulse crops, 2.6 vs. 1.7; soybean meal, 2.3 vs. 0.6; wheat, 1.4 vs. 0.1). In conclusion, in vitro energy digestibility and proximate analyses resulted in similar prediction accuracy for the ATTD of energy among feedstuffs. In contrast to grains, other feedstuffs revealed difficulty in achieving an accurate prediction of ATTD of energy within feedstuff using current procedure of in vitro energy digestibility.

Key Words: energy digestibility, in vitro, pig

689 The ontogeny of intestinal carbohydrate digestive, absorptive and nutrient sensing proteins in pigs. M. Al-Rammahi*[1], A. Moran[1], D. Batchelor[1], P. Sangild[2], C. Ionescu[3], D. Bravo[3], and S. Shirazi-Beechey[1], [1]*University of Liverpool*, *Liverpool, UK*, [2]*University of Copenhagen*, *Frederiksberg, Denmark*, [3]*Pancosma*, *Geneva, Switzerland*.

In the small intestine, dietary carbohydrate is hydrolysed ultimately by intestinal brush border membrane hydrolases, sucrase, lactase and maltase, to glucose, galactose and fructose. Glucose and galactose are transported across the luminal membrane of enterocytes by the Na^+/glucose cotransporter 1, SGLT1, which is upregulated by luminal sugars via the sweet taste receptor, T1R2/T1R3, expressed in enteroendocrine cells. Na^+-independent transporters, facilitate transport of fructose across the luminal membrane (GLUT5) and all 3 monosaccharides across the basolateral membrane (GLUT2). Aim: To determine the developmental profile of these key carbohydrate digestive-related gut functions in pigs before and after birth. Methods: Intestinal tissues were removed from pre-term (fetal age 105 d, n = 4), full-term (115 d, n = 4), suckling (15 d, n = 4) and weaned (28 d, n = 8) piglets following

euthanasia under ethical approval. Results: By immunohistochemistry, we showed presence of SGLT1 (on enterocytes luminal membrane), GLUT2 (on enterocytes basolateral membrane) and the glucose sensor (in enteroendocrine cells) both before and after birth; GLUT5 protein was only present after weaning. By functional assays and qPCR, we demonstrated highest expression of SGLT1 in weaned animals (on 60% carbohydrate diet). The expression level of SGLT1 was weaned > suckling > term > pre-term. A similar pattern of expression was observed for sucrase and maltase, while the developmental profile of lactase expression showed maximal levels in suckling animals. The presence of carbohydrate digestive/absorptive and nutrient sensing proteins in the intestine during pre-natal life indicates that a pre- programming of intestinal functions occurs before birth to prepare the gut for its post-natal functional demands. A better understanding of both ′hard wired′ and diet- induced functions of the gut in early life allows the design of rational and innovative approaches to formulate feed and feed additives to ensure the health and well-being of the young animal.

Key Words: gut development, sugar transporters, disaccharidases

690 Quality characteristics and fatty acid composition of eggs from hens fed *Camelina sativa* (camelina meal). R Kakani*[1], A Haq[1], J Fowler[1], E Murphy[2,3], T Rosenberger[3], M Berhow[4], and C. A. Bailey[1], [1]*Texas A&M University*, *College Station,* [2]*University of North Dakota*, *Grand Forks,* [3]*Agragen, LLC*, *Cincinnati, OH*, [4]*National Center for Agricultural Utilization Research, USDA*, *Peoria, IL*.

Camelina sativa or false flax is an oilseed producing plant rich in essential omega-3-fatty acids. Camelina meal is the by-product of oil extraction, and has a crude protein content (40%) similar to that of rapeseed meal. Camelina meal is a rich source of essential n-3 and n-6 fatty acids that can be incorporated in laying hen diets to enrich eggs with n-3 fatty acids. In this study, the effects of feeding camelina meal to commercial laying hens on egg production, egg quality characteristics and fatty acid composition of eggs was determined. Twenty-nine-week old Lohmann White Leghorn hens were randomly allocated to 3 dietary treatments (n = 25 per treatment) and data collected over a 12 week production period. All the treatment groups were fed a corn soy based experimental diets containing 0% (CON), 5% (CAM5) and 10% (CAM10) extruded camelina meal. Feed and water were offered ad libitum. There were no significant differences in % hen day egg production among the treatment groups. Egg weight was significantly lower in CAM5 (58 ± 4 g) relative to CON (60 ± 4 g), whereas no significant difference was detected between CAM10 (60 ± 5 g) and control. Egg shell strength (Instron) was significantly higher in CAM5 (5.0 ± 1.1 kg) and CAM10 (4.7 ± 1.1 kg) than in CON (4.5 ± 1.0 kg). Total cholesterol content in the yolk was unchanged between groups. Total egg n-3 fatty acid content was nearly doubled in CAM5 (117 ± 24 mg/yolk) and tripled in CAM10 (161 ± 20 mg/yolk) when compared with CON (60 ± 8 mg/yolk). The n-6 to n-3 ratio was significantly different between groups, 12.4 ± 0.8 (CON), 6.0 ± 0.2 (CAM5), and 4.3 ± 0.1 (CAM10). There were no detectable glucosinolates in the eggs of CAM5 and CAM10 treatment groups. Significant accretion of n-3 fatty acids was observed in the yolk of hens fed 5% and 10% camelina meal. These results indicate that camelina meal is a viable dietary source of n-3 fatty acids for poultry and its inclusion results in eggs enriched with n-3 fatty acids, including a 2.5-fold increase in DHA.
Funded by Great Plain Oil and Exploration

Key Words: camelina meal, egg quality characteristics, n-3 fatty acids