

For the consumer and the meat industry variation in meat tenderness is a well known problem. Although it is an area with high attention the mechanisms leading to tender, and sometimes unexpectedly tough, meat are not fully understood. Meat tenderizes during post mortem storage and it is well established that post mortem protein degradation plays a major role in the tenderization process. During the post mortem proteolytic processes several muscle proteins are degraded, but the number and identity of the proteins that are degraded is partly unknown. Moreover, it is still unclear which proteolytic enzymes are involved and how they are regulated.

We apply proteomics to study the mechanism involved in the tenderization process in meat and to identify specific markers for the post mortem proteolytic processes. Several protein fragments that result from post mortem proteolysis have been identified and it has also been possible to assign which part of the full-length proteins the fragments were revealed from. This information was used to construct the cleavage pattern of some of the proteins involved in meat tenderization. More importantly, some of the identified fragments were significant correlated to meat texture. We also apply proteomics to study the regulation of the calpain-system, which takes part in the tenderization process.

Key Words: Proteomics, Meat, Tenderness

Nonruminant Nutrition: Weanling Pig Nutrition and Methodology

179 Fermented soybean meal as a protein source in nursery diets replacing dried skim milk. S. W. Kim*, R. D. Mateo, and F. Ji, *Texas Tech University, Lubbock, TX.*

Two studies were conducted to evaluate if fermented soybean meal (FSBM) successfully replace the use of dried skim milk (DSM) in nursery diets. Fermentation of soybean meal was done by *Aspergillus Oryzae GB-107*. Previous studies demonstrated that this fermentation process reduces trypsin inhibitor contents and the size of soybean peptide. In Exp. 1, 192 newly weaned pigs (21.5 ± 0.1 d, 6.35 ± 0.10 kg) were allotted to one of four dietary treatments by increasing FSBM (0, 3, 6, and 9%) whereas reducing DSM (25, 22, 19, and 16%). Each treatment had six pens with eight pigs per pen. All diets contained 1.53% lysine, 0.87% methionine+cysteine, 1.03% threonine, 0.28% tryptophan, and 3.40 Mcal/kg ME. Pigs were fed the diets for two weeks. Body weight and feed intake were measured weekly. Diarrhea score was recorded daily during the entire feeding period. Average daily gain and feed intake were the same ($P > 0.05$) among the pigs fed the diets with 0, 3, and 6% FSBM. Pigs fed a diet with 9% FSBM had a lower ($P < 0.05$) ADG and ADFI than pigs with 0% FSBM. Diarrhea scores were the same ($P > 0.05$) among the treatments. In Exp. 2, 144 newly weaned pigs (22.1 ± 0.1 d, 6.52 ± 0.11 kg) were allotted to one of three dietary treatments by increasing FSBM (0, 5, and 10%) while reducing DSM (40, 32.4, and 24.8%). Lactose was added at 0, 3.8, and 7.6%, respectively, in order to match lactose content equal to 23.5% for all diets. All diets contained 1.58% lysine, 0.91% methionine+cysteine, 1.03% threonine, 0.29% tryptophan, and 3.51 Mcal/kg ME. All detailed procedure was identical to Exp. 1. Pigs fed a diet with 5% FSBM had a greater ($P < 0.05$) ADG and gain/feed than pigs with 0% FSBM when lactose contents were the same among the treatments. Pigs with 10% FSBM had the same ADG and gain/feed to those with 0% FSBM and 10% FSBM. Diarrhea scores were the same ($P > 0.05$) among the treatments. Fermented soybean meal can be used up to 10% in a nursery diet successfully replacing the use of dried skim milk when the lactose contents were matched.

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Key Words: Fermented Soybean Meal, Dried Skim Milk, Nursery Pigs

180 Comparative efficacy of plant and animal protein sources on the growth performance, nutrient digestibility and intestinal morphology of the early-weaned pigs. J. H. Yun, I. K. Kwon, J. D. Lohakare, W. T. Cho, and B. J. Chae*, *Kangwon National University, Chunchon, Kangwondo, Korea.*

The present study was conducted to evaluate and compare the effects of various animal and plant protein sources on piglet's performance, digestibility of amino acids and gut morphology in the weaned pigs till 28 days after weaning. Two hundred seventy weaned pigs of 17 ± 3 days of age (Landrace × Yorkshire × Duroc) were allotted to five treatments with three replicates, comprising 18 pigs in each replicate. The plant protein sources used were soybean meal (SBM), fermented soy protein (FSP), rice protein concentrate (RPC); and animal protein sources tested were, whey protein concentrate (WPC) and fish meal (FM). Iso-proteinous (21%) diets were formulated and lysine (1.55%) content was same in all the diets. The level of each protein source added was 6% by replacing SBM to the same extent from the control diet containing 15% SBM. The

ADG was higher ($P < 0.05$) in the groups fed animal proteins as compared with plant proteins at all the levels of measurement, except during 15-28 days. The highest ADG was noted in WPC and FM fed diets and lowest in SBM fed diet. The feed intake was higher in animal protein fed groups than plant proteins at all phases. The digestibilities of gross energy, dry matter and crude protein were higher in animal protein fed groups than to plant protein fed sources. The apparent ileal digestibilities of essential amino acids like Leu, Thr, and Met were significantly higher ($P < 0.05$) in animal proteins fed animals as compared with plant protein fed groups. But the apparent fecal digestibilities of essential amino acids like Arg and Ile were significantly higher ($P < 0.05$) in plant protein diets than animal protein sources. The villous structure studied by scanning electron microscope were prominent, straight finger-like, although shortened and densely located in FM fed group as compared with others. Overall, it could be concluded that animal protein sources in the present study showed better effects on growth performance, nutrient digestibility and gut morphology than plant protein sources.

Key Words: Plant Protein, Animal Protein, Pigs

181 Growth performance, gut health and digestive function in newly weaned pigs fed fermentable proteins and carbohydrates. E. A. Jeaurond* and C. F. M. deLange, *University of Guelph, Guelph, Ontario, Canada.*

Feeding fermentable carbohydrates (FC) may reduce the negative impact of enteric proteolytic fermentation in pigs. A total of 144 newly weaned pigs (6.23 kg BW; six pens per treatment; six pigs per pen) were used to determine the interactive effects of feeding fermentable protein (FP) and FC on growth performance, indicators of digestive function and intestinal health. Dietary treatments were: (1) basal diet (control), (2) control + 10% poultry meal (PM) as FP source, (3) control + 5% beet pulp (BP) as FC source and (4) control + PM and BP. Diets were formulated to be similar in digestible energy and digestible amino acid contents. In general, no interactive effects of FC and FP were observed ($P > 0.10$). During the 3-week post-weaning period, feeding FP reduced ADG (269 vs. 242g/d; SE, 7), while feeding FC increased ($P < 0.05$) ADG (243 vs. 269 g/d; SE, 7). Overall feed intake did not differ between treatments ($P > 0.10$). Based on PCR-DGGE, feeding FC and FP appeared to increase microbiota diversity in colon contents. On d 14 and 28 post-weaning, Clostridia sp. counts in colon contents, White Blood Cell counts and segmented blood Neutrophils were lowered ($P < 0.05$) by feeding FC, suggesting lower bacteriological stress. Blood urea nitrogen was increased by feeding FP (6.5 vs. 9.5 mg/dL; SE, 0.5), while ammonia concentration in colon contents was lowered ($P = 0.06$) by FC (193 vs. 154 µg/mL; SE, 14.2). Among biogenic amines, levels of tyramine (304 vs. 140 nmol/g DM; SE, 38) and spermidine (219 vs. 174 nmol/g DM; SE, 14) in colon contents were lowered by feeding FC ($P < 0.05$). Acetic, propionic and butyric acid contents in colon contents were increased by feeding FC, while valeric acid content was decreased by feeding FP ($P < 0.05$). Feeding FC and FP had no effect ($P > 0.10$) on colon histology, pH of colon contents, fecal consistency score and organ weights. Results suggest that FP and FC have independent effects on newly weaned pigs, while effects appear to be partly related to changes in gut micro flora.

Key Words: Pig, Gut Function, Fermentation

182 The interaction of net energy concentration and feeding level in weaned pigs. I. Growth, nutrient digestibility and energy utilization. T. F. Oresanya^{1,2}, A. D. Beaulieu¹, and J. F. Patience^{*1}, ¹Prairie Swine Centre Inc., Saskatoon, Saskatchewan, Canada, ²University of Saskatchewan, Saskatoon, Saskatchewan, Canada.

The simultaneous evaluation of the impact of dietary energy concentration and feed (energy) intake is important for an accurate understanding of energy metabolism in weaned pigs. Surprisingly, there is very little information on this subject. This study investigated the interaction of dietary net energy concentration (NE) and daily feed intake on growth, nutrient digestibility and energy utilization in weaned pigs. Individually penned PIC barrows ($n = 81$; 31.5 ± 0.3 d; initial BW = 9.5 ± 1.0 kg) were allotted to one of nine treatments (trt) in a 3×3 factorial arrangement ($n = 9/\text{trt}$). Factors were formulated NE (low, 2.21; medium, 2.32; and high, 2.42 Mcal NE/kg) and feeding level (FL: 100%, 80% or 70%). NE was increased by a simultaneous decrease and increase of CP and fat, respectively. BW was determined twice per wk and daily feed allowance adjusted per pig on a BW basis, relative to the ad libitum intake of pigs on each diet. Pigs remained on test until they reached 25 ± 1 kg BW. ADG, ADFI and G/F were unaffected by NE (572 g/d, 781 g/d and 0.732, respectively; $P > 0.05$). ADG and ADFI increased ($P < 0.05$) with FL but not G/F ($P > 0.05$). Apparent fecal digestibility of GE, DM, fat, CP and ash increased ($P < 0.05$) with increasing NE but declined with increasing FL ($P < 0.05$) while that for crude fiber declined ($P < 0.001$) with increasing NE and FL. Estimated NE from digestible nutrients were determined to be 2.15, 2.26 and 2.37 Mcal NE/kg for the low, medium and high NE diets, respectively. Energy intake increased with increasing NE and FL ($P < 0.001$) whereas energy efficiency for growth (Mcal NE/kg BW gain) became poorer with increasing NE and FL ($P < 0.001$). In conclusion, weaned pigs were able to consume sufficient energy for growth within the range of NE investigated herein. There was no benefit of increased energy intake with increased NE concentration on growth and feed efficiency. The effects of NE concentration and feed intake on growth are additive.

Key Words: Weaned Pigs, Net Energy, Growth

183 The interaction of net energy concentration and feeding level in weaned pigs. II. Body composition, nutrient deposition rates and plasma IGF-I concentration. T. F. Oresanya^{1,2}, A. D. Beaulieu¹, and J. F. Patience^{*1}, ¹Prairie Swine Centre Inc., Saskatoon, Saskatchewan, Canada, ²University of Saskatchewan, Saskatoon, Saskatchewan, Canada.

The effects of simultaneously increasing energy concentration and changing daily energy intake through the control of feed intake in weaned pigs have not been examined. This study evaluated the interactive effect of increased dietary net energy concentration (NE) and feeding level (FL) on body composition, nutrient deposition rates and plasma IGF-I concentration. Individually penned PIC barrows ($n = 60$; 31.5 ± 0.3 d; initial BW = 9.4 ± 1.1 kg) were allotted to one of nine treatments (trt) in a 3×3 factorial arrangement or an initial slaughter group (ISG; $n = 6/\text{trt}$ or ISG). Factors were formulated NE (low, 2.21; medium, 2.32; and high, 2.42 Mcal NE/kg) and FL (100%, 80% or 70%). Pigs were bled twice (d 7 and d 21) and remained on test until they reached 25 ± 1 kg BW, at which time they were sacrificed for carcass analysis. Carcass and empty body (EB, carcass plus organ) protein and lipid content and deposition rate (PD and LD) were determined. Carcass and EB lipid content increased (interaction, $P < 0.01$) while water content decreased in pigs with ad libitum intake on the high NE diet. Carcass and EB protein content declined with increasing NE ($P < 0.05$) but were not affected by FL ($P > 0.05$). Carcass and EB PD increased with increasing FL ($P < 0.001$) but not with NE ($P > 0.05$). Carcass and EB LD and LD/PD ratio increased (interaction, $P < 0.01$) in pigs with ad libitum intake on the high NE diet (EB LD = 44, 51 and 86 g/d and LD/PD = 0.41, 0.47 and 0.76 for ad libitum pigs on the low, medium and high NE diets, respectively). Plasma IGF-I concentration increased with increasing FL and day (interaction, $P < 0.001$) but not with NE ($P > 0.05$). In conclusion, the effects of NE concentration and feed intake on PD and plasma IGF-I are additive. In contrast to PD, the interactive effects of NE concentration and feed intake on EB lipid content, LD and LD/PD ratio indicates that increasing energy concentration is not desirable for optimal lean growth in weaned pigs.

Key Words: Weaned Pigs, Net Energy, Nutrient Deposition

184 Genetic background impacts growth performance and endocrine parameters during dietary phosphorus deficiency in young gilts. S. Cutler*, L. Grapes, M. Rothschild, and C. Stahl, Iowa State University, Ames.

Costs associated with inorganic phosphorus (P) levels in animal diets have driven research to more accurately define requirements in order to minimize P excretion while maintaining growth rate. We examined the influence of two sire lines, selected primarily for either meat quality (MQ) or growth performance (GP), on P utilization by 36 gilts (21 d of age, 6.63 ± 0.78 kg) from six litters (three pigs/litter) for each sire line. Pigs were allotted into three dietary treatment groups: P adequate (+P, 0.41% available P), P repletion (RP, 0.14% available P for wk 1, 0.41% available P for wk 2), or P deficient (-P, 0.14% available P) for 2 wk. MQ sired -P pigs had lower ($P < 0.05$) ADG compared to either RP or +P pigs, whereas this effect was not seen in GP sired pigs. Both MQ and GP sired -P pigs had lower ($P < 0.05$) G:F than their siblings in either the +P or RP groups. Plasma levels of inorganic P and plasma alkaline phosphatase activities were altered by -P diet but not genetic background. The RP group returned to normal levels after 1 wk on a +P diet. Pigs in the -P group had lower ($P < 0.05$) plasma IGF-1 concentrations than +P pigs. This difference in circulating IGF-1 levels was greater ($P < 0.05$) among the MQ sired animals than the GP sired animals. Gilts in the RP MQ group showed greatly increased plasma IGF-1 levels after being returned to the +P diet. This coincided with a sixfold increase in pituitary GH expression. The relative expression of IGF-1, IGFBP-1, IGFBP-2, and IGFBP-3, and IGFBP-5 mRNA in liver tissue was; however, not different between any of the treatment groups. Differential expression of thyroid receptor interaction protein 6 (TRIP-6) mRNA in the liver suggests that energy metabolism may be differentially regulated across these genetic backgrounds. These results suggest that genetic background dramatically influences inorganic P requirements and that genotype specific P supplementation could reduce the environmental impact of swine production without detriment to performance.

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Key Words: Phosphorus, IGF-1, Pigs

185 Dietary and ontogenetic regulation of digestive enzyme mRNAs in the small intestine of weanling pigs. J. Zhao*, X. Xiao, E. A. Wong, K. E. Webb, Jr., A. F. Harper, E. Gilbert, and D. M. Denbow, Virginia Polytechnic Institute and State University, Blacksburg.

Dietary and ontogenetic regulation of digestive enzyme mRNAs were evaluated in weanling pigs ($n = 54$, $17 + 2$ d of age, $6.2 + 0.3$ kg BW) along the horizontal axis of the small intestine. Experimental diets included a control soy protein diet, a diet containing 6% spray-dried plasma protein or a 0.5% commercial hydrolyzed marine protein source (Peptiva®, VITECH BIOCHEM, San Fernando, CA). Pigs were housed in double-deck nursery pens with continuous lighting at 29°C. Pigs were killed at weaning or 3 or 10 d after weaning for harvest of mucosa from duodenum, jejunum and ileum. The mRNA level of digestive enzymes aminopeptidase A (APA), aminopeptidase N (APN), dipeptidyl peptidase IV (DPPIV), and maltase-glucoamylase (MGA) were measured by Northern blotting and expressed as relative abundance to the housekeeping gene GAPDH. Significant diet \times intestinal region interactions ($P < 0.05$) were found for APA and APN. Aminopeptidase A was evenly distributed along the small intestine in the Peptiva® group, but decreased dramatically in the ileum in other groups. Aminopeptidase N increased from proximal to distal intestine in the soy protein and plasma groups, whereas in the Peptiva® group, expression was highest in the jejunum and lowest in the duodenum. The profiles of mRNA levels showed that MGA was expressed at higher level in the jejunum compared to duodenum and ileum ($P < 0.01$). Aminopeptidase A expression decreased from duodenum to ileum ($P < 0.01$), whereas APN and DPPIV showed the opposite expression pattern ($P < 0.01$). The mRNA levels of MGA increased with age, compared to APA and DPPIV which decreased ($P < 0.05$). The APN level was constant during the entire experimental period. In this study, protein source altered the expression pattern of APA and APN. Expression of APA, APN, DPPIV and MGA was differentially regulated along the length of the small intestine and varied as a function of age.

Key Words: mRNA, Digestive Enzyme, Weanling Pigs

186 Effect of oral N-carbamylglutamate (NCG) supplementation on growth and tissue protein synthesis in piglets. J. Frank^{*1}, J. Escobar¹, A. Suryawan¹, C. Liu¹, H. Nguyen¹, T. Davis¹, and G. Wu², ¹USDA/ARS CNRC, Baylor College of Medicine, Houston, TX, ²Texas A&M University, College Station.

Recent research indicates that oral supplementation of NCG, an analogue of N-acetylglutamate, increases plasma arginine concentrations and growth rate in sow-reared piglets. To investigate the mechanism involved in this response, nursing piglets (n = 14; BW = 2.75 kg) were orally administered 50 mg/kg BW of NCG or saline twice daily from 7 to 14 d of age. After an overnight (12-h) fast, 14-d old piglets were administered saline or NCG at time 0 and 60 min, then received a flooding dose of [3H]phenylalanine in order to measure protein synthesis. At 90 min, the piglets were euthanized and tissue samples were collected. NCG-treated pigs gained more weight during the 7-d trial than control pigs (1.63 ± 0.07 vs. 1.43 ± 0.06 kg, respectively; P < 0.001). Plasma arginine concentrations were 44% higher in NCG-treated pigs compared to control pigs (P < 0.01). NCG-treated pigs tended to have higher plasma insulin concentrations compared to control pigs (P < 0.06). Plasma glucose concentrations were not different between the treatments (P > 0.73). Fractional protein synthesis rate in longissimus dorsi muscle was 17% higher in NCG-treated pigs compared to controls (6.9 ± 0.5 vs. 5.9 ± 0.6 %/d, respectively), although this did not reach significance (P < 0.24). Fractional rates of protein synthesis in liver, kidney, and duodenum were not different between treatments (P > 0.49). We postulate that the sensitivity of muscle protein synthesis to NCG treatment in piglets may be reduced in the fasted state. Oral NCG administration increases growth rate of nursing piglets likely by increasing plasma arginine concentrations.

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Key Words: Pigs, N-Carbamylglutamate, Protein Synthesis

187 Evaluation of culture independent quantitative real-time PCR of *S. bovis* in weaning pig. H. B. Lee^{*}, C. S. Kong, M. S. Yun, L. G. Piao, and Y. Y. Kim, Seoul National University, Seoul, South Korea.

A culture independent quantitative real-time PCR method was evaluated for enumeration of the bacteria species *Streptococcus bovis* from intestinal samples of weaning pigs. Many of the earlier molecular techniques including real-time PCR were culture dependent or conducted with cultured samples, resulted in unaccurate analysis due to the fact that culture independent sequencing from intestinal samples showed less than 95% of similarity with culture dependent sequencing results. The intestinal microbiota of the pig is consisted mostly of anaerobic bacteria with little knowledge of its nutritional requirement, and consequently, it is hard to culture in the aerobic condition for further analysis. A total of 36 weaning pigs were sacrificed and samples from jejunum, cecum, colon and rectum were collected and immediately stored in liquid nitrogen, conserving the exact microbiota of the pig. Total DNA was extracted by bead-beating method using the UltraClean™ DRY Soil kit (MoBio). Primer set *S. bovis*_RT1, with CTAATACCGCATAACAGCAT (forward) and AGAACTTCCTATCTCTAGG (reverse) was designed and tested for species specificity. The standard for RT-PCR was established according to DNA concentration from pure cultured *S. bovis*. The quantification of DNA (as DNA copy/g samples) by RT-PCR was performed with ICycler® Optical Module (Bio-Rad) using the iQ™ SYBR® Green Supermix (Bio-Rad). The result showed 95.3% of PCR efficiency, providing reliable data on *S. bovis* quantity in samples from different regions of the intestine, collected by culture independent method. This experiment indicated the possibility of a culture independent quantification of the intestinal microbes with known DNA sequence.

Key Words: Weaning Pig, Quantitative Real-Time PCR, *Streptococcus bovis*

188 Validation of an in vitro analysis to determine energy digestibility of barley for grower pigs. R. T. Zijlstra^{*1}, W. C. Sauer¹, J. H. Helm², D. N. Overend³, and R. W. Newkirk⁴, ¹University of Alberta, Edmonton, AB, Canada, ²Field Crop Development Centre, Lacombe, AB, Canada, ³Ridley Inc., Mankato, MN, Canada, ⁴Canadian International Grains Institute, Winnipeg, MB, Canada.

In vitro analyses will be beneficial to characterize the existing variation in energy digestibility within specific feed ingredients such as grains and to develop procedures predicting nutritional value of grains for swine. Analytical procedures have been developed to determine in vitro energy digestibility and DE content for barley, but have not been validated for their suitability to predict in vivo values. First, 21 barley samples with a range in fiber content (5.7 to 12.1% ADF) and total-tract energy digestibility (51.9 to 78.5%) and DE content in grower pigs were subjected to an existing in vitro analysis in duplicate. Briefly, the procedure involved subsequent digestions with pepsin (6 h), pancreatin (18 h), and cellulase (24 h), and DM and GE analyses of the barley sample and residue. The in vitro energy digestibility ranged from 63.7 to 82.2% for the 21 barley samples and relative errors for samples ranged from 0.2 to 4.8%. In vitro energy digestibility was strongly related to swine in vivo energy digestibility content (R² = 0.81). Second, a subset of seven barley samples was subjected to quadruplicate in vitro analyses. In vitro energy digestibility ranged from 63.5 to 82.8% for the seven samples and the relative error was 4.2% for the barley sample with a low energy digestibility (63.5%) and ranged from 0.6 to 1.4% for the other six barley samples. For the seven barley samples, in vitro energy digestibility was strongly related to in vivo energy digestibility content (R² = 0.97). In summary, with quadruplicate analyses, in vitro energy digestibility was an accurate predictor of in vivo energy digestibility. In vitro energy digestibility can be successful as the core analytical procedure to calibrate rapid analytical equipment to predict energy digestibility and therefore DE content of barley for grower pigs.

Key Words: Pig, Grain, Analysis

189 Dietary strategy to suppress ochratoxicosis in piglets. G. Schatzmayr^{*1}, S. Nitsch¹, D. Schatzmayr¹, M. Mezes², and E. Binder¹, ¹Biomim GmbH, Herzogenburg, Austria, ²Szent István University, Faculty of Agricultural and Environmental Sciences, Gödöllő, Hungary, ³Erber AG, Herzogenburg, Austria.

Ochratoxin A (OTA) is a mycotoxin occurring in many food- and feed commodities. In swine, OTA affects the kidneys (tubular necrosis). Economic losses attributed to the presence of this compound in feeds are not only related to impaired animal health and productivity, but are partly due to the discharge of pig carcasses after slaughter. OTA has a long biological half life and is frequently found as residue in porcine meat and meat products intended for human consumption. A yeast strain (*T. mycotoxinivorans* = MTV) with the capability to degrade OTA was isolated for the development of an OTA-deactivating feed additive. This feed additive was tested in a trial where piglets were challenged with OTA (500 µg/kg). Seventy-two pigs (Hungarian Large White x Hungarian Landrace F1 genotype; sex ratio, 1:1) with an age of 5 to 6 weeks and an initial average live weight of 10 kg were used in this experiment. Treatments included negative control (without OTA and MTV), addition of OTA alone (500 µg/kg), OTA combined with MTV at three different levels (10⁴, 10⁵ and 10⁶ CFU/g of feed) and MTV alone (10⁶ CFU/g of feed). Results revealed that OTA had a negative impact on live weight (LW), average daily weight gain (ADWG) and feed conversion ratio (FCR) of weaning piglets. Addition of 10⁴ CFU of MTV did not show an improvement in live weight after 28 days but did show improved FCR (28 days) and live weight after 49 days. Higher concentrations of MTV already showed an improvement of live weight after 28 days. Compared to the toxin group the live weight after 49 days and FCR after 28 days were considerably improved. In all control and treated groups' losses of animals and cases of diarrhea were lower than in the toxin group. The ADWG in the toxin group was significantly lower than in all the other groups. From these results it can be concluded that *T. mycotoxinivorans* at a proposed concentration of 10⁵ CFU/g of feed can be used to alleviate negative effects of OTA on swine.

Key Words: Ochratoxicosis, Deactivation, *T. mycotoxinivorans*

190 Effect of feeding reduced crude protein and phosphorus diets on pig compartmental and whole body mineral masses and accretion rates. R. Hinson^{*1}, B. Hill¹, M. Walsh¹, D. Sholly¹, S. Trapp¹, J. Radcliffe¹, A. Sutton¹, A. Schinckel¹, B. Richert¹, G. Hill², and J. Link², ¹Purdue University, West Lafayette, IN, ²Michigan State University, East Lansing.

Pigs (Exp. 1 = 98 and Exp. 2 = 148) were allotted by sex and BW to determine the effects of feeding a control (CTRL), corn-SBM based diet or a low nutrient excretion (LNE) diet, with reduced CP + synthetic amino acids, low phytic acid corn, and phytase, on carcass, visceral, and blood mineral contents and masses. Pigs were split-sex phase fed, three nursery diets for a 5-wk nursery period (Exp. 2) and two grower and two finisher diets for a 16-wk grow-finish (G-F) period (Exp. 1 and 2). Pigs were housed two-five pigs/pen and five pens/sex/treatment (trt) in G-F. Individual pig weights and pen feed consumption were recorded bi-weekly. Five or six pigs/sex were harvested at the start of each experiment to determine initial composition and six pigs/sex/trt were harvested at the end of the nursery period (Exp. 2) and 10 pigs/sex/trt were harvested at wk 8 and 16 of the G-F period (Exp. 1 and 2) for determination of tissue pool compositions. Tissues were assayed for: DM, Ash, N, P, Ca, Zn, Fe, Cu, Mg, and Mn. There were no differences in nursery, grower, or finisher whole body tissue mass between treatments. However, total mass and accretion rates of P, Ca, and Mg decreased and Zn and Mn increased when LNE diets were fed during the nursery period (Exp. 2 only; $P < 0.05$). Grower period ash, P, Ca, Mg, and N (Exp. 2) masses and accretion rates of ash, P, Ca, Mg, Fe (Exp. 1), Zn (Exp. 2), Cu (Exp. 2) decreased when pigs were fed LNE diets ($P < 0.05$). During the finisher period, whole body ash (Exp. 2), P, Ca, Mg, N (Exp. 2) decreased and accretion rate of Zn (Exp. 2) increased ($P < 0.05$) when pigs were fed LNE diets. Overall, total tissue accretion rate was not different between treatments, however whole body accretion rates of ash (Exp. 2), P, Ca, Mg, and N (Exp. 2) were decreased when pigs were fed LNE diets from weaning to market. There were differences in individual mineral accretion rates by the different tissue pools at different phases of the pigs growth cycle, however, the carcass is the largest pool and has the greatest influence on the whole body mineral accretion rates.

Key Words: Pigs, Phosphorus, Whole Body Mineral Accretion

191 Pigs housed under deep litter and conventional housing systems have different growth paths to a similar carcass composition. D. Suster¹, D. J. Henman², D. J. Cadogan³, and F. R. Dunshea^{*1,4}, ¹Primary Industries Research Victoria, Werribee, Victoria, Australia, ²QAF Meat Industries, Corowa, NSW, Australia, ³Feedworks, Hamilton, Qld, Australia, ⁴University of Melbourne, Parkville, Victoria, Australia.

Three replicates of 120 boars and gilts were weaned into deep litter (rice hulls and straw) pens with an additional 60 pigs of each sex weaned into groups of 20 housed under conventional systems (raised weaner cots and then concrete flooring). All pigs were located in the same airspace with a stocking density of 0.65 pigs/m². Randomly allocated focus pigs were used for dual energy X-ray absorptiometry analyses at various time points to determine body composition. In the immediate post weaning period, conventionally housed pigs ate more (199 vs. 170 g/d, $P < 0.01$) and grew faster than deep litter pigs (189 vs. 154 g/d, $P < 0.05$). However, feed intake was higher ($P < 0.05$) in pigs housed in the deep litter system between 8 and 85 days of age. Over the final growth phase from 114 until 149 days of age, feed intake (2,726 vs. 2,551 g/d, $P < 0.05$) and daily gain (897 vs. 808 g/d, $P < 0.05$) were higher in conventionally-housed pigs. Over the finisher phase, gilts consumed more feed (2,379 vs. 2,289 g/d, $P < 0.05$) than boars probably because of social interactions between boars housed in groups. Pigs raised in deep litter systems deposited more ($P < 0.05$) lean and fat tissue than conventionally housed pigs up until about 60 and 80 days of age, respectively after which time the conventionally housed pigs deposited more of each tissue. The rate of lean tissue gain decreased in gilts but remained elevated in boars over the latter stages of the study. Hot carcass weight and backfat were not affected by either housing system. These data suggest that under the same relatively high stocking density there is little difference in the final carcass composition and overall growth performance of pigs housed under either conventional conditions or in deep litter. However, there were quite clear differences in the pattern of growth and tissue deposition with the deep litter pigs initially eating more and growing faster before slowing down.

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Key Words: Deep Litter, Pig, Body Composition

Physiology and Endocrinology II

192 Differential expression of superoxide dismutases (SODs) in bovine corpus luteum during estrous cycle and pregnancy. R. K. Putluru^{*}, C. N. Lee, and Y. S. Kim, *University of Hawaii at Manoa, Honolulu.*

In the tropics, lower conception rates are common in dairy cattle. While many factors contribute to a successful pregnancy, an important ingredient is a healthy functional corpus luteum (CL) for the maintenance of pregnancy. Previous studies in rabbits have shown that the generation of reactive oxygen species (ROS) including superoxides may play a role in the regression of CL and subsequent luteolysis. Studies in pregnant rats also showed that the up-regulation of superoxide dismutase (SOD), a ROS scavenging enzyme, is involved in the rescue of the CL from luteolysis. The objective of this study was to investigate the presence and expression of different types of SODs in the bovine CLs at different stages of the estrus cycle (1st, 2nd, 3rd and 4th) and pregnancy. CL samples (n=155) were collected from a local slaughter house and classified into different stages based on morphological classification. CL samples (0.25 gms) were homogenized in 20 ml of PBS buffer. Protein concentration of each CL was measured by Lowry method, and equal amount of protein from each sample was subjected to SDS-PAGE. The fractionated proteins were transferred onto a nitrocellulose membrane and immunoblotted against commercially available anti-MnSOD and anti-Cu/ZnSOD antibodies. The Mn-SOD and Cu/Zn-SOD were quantified using densitometry analysis. Mn-SOD was highly expressed in the pregnant CLs and 3rd and 4th stage CLs of the estrus cycle. In contrast, Cu/Zn SOD was equally expressed throughout the estrus cycle and pregnancy. Present results suggest that the Mn-SOD is probably involved in the maintenance of bovine pregnant corpus luteum.

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Key Words: Superoxide Dismutase, Bovine Corpus Luteum, Estrus Cycle

193 Effects of changes in systemic progesterone in the first few days after ovulation on uterine retinol binding protein and folate binding protein gene expression in cattle. R. McNeill^{1,2}, R. Fitzpatrick¹, J. Sreenan¹, and D. Morris^{*1}, ¹Teagasc, Research Centre, Athenry, Co. Galway, Ireland, ²National Diagnostics Centre, National University of Ireland Galway, Galway, Ireland.

Low systemic progesterone in the first week after AI is associated with a low probability of embryo survival in dairy cows. Progesterone may affect embryo survival by altering uterine gene expression and ultimately uterine function. The objective of this study was to establish the relationship between systemic progesterone during the first week after AI and bovine uterine gene expression. Heifers (n=24) were blood sampled twice daily from the day of ovulation (day 0) and on the basis of their systemic progesterone concentrations were divided into high or low groups on day four. Half of each group was, in turn, supplemented with exogenous progesterone (CIDR) from day 4 to day 8, resulting in a total of four groups, low control (LC), high control (HC), low supplemented (LS) and high supplemented (HS). Uterine endometrial tissue was harvested post mortem on day 6 or day 8 and snap frozen in liquid nitrogen. The effects of changes in systemic progesterone on uterine gene expression was measured using candidate and global gene approaches. Data were analyzed as a 2 x 2 factorial using analysis of variance. High systemic progesterone concentration up to day 4 was associated with increased ($P < 0.01$) uterine retinol binding protein (RBP) mRNA expression on day 6 but not on day 8. In contrast supplementation with exogenous progesterone between days 4 and 6 or days 4 and 8 did not alter RBP mRNA expression ($P > 0.05$). There was a positive ($P < 0.05$) linear relationship between progesterone and folate binding protein (FBP) mRNA expression on day 6 after ovulation but not on day 8. These results indicate that uterine gene expression is very sensitive to small changes in systemic progesterone.