pig is an important production species and biomedical model, however the mineral or trace element content of pig milk and mammary transport systems have not been well characterized. We analyzed the mineral and trace element content of porcine milk throughout lactation and compared it to bovine and human milk. Milk was obtained from three sows at farrowing (0 h), 12 h and d 1-4, 7, 14, 18, 21 and 24 postpartum. Human milk (n=8) was obtained between 1 and 3 months postpartum and bovine milk (n=3) from cows in midlactation. Milk samples were analyzed by atomic absorption (Ca, Mg, Na and K), colorimetric assay (P) and trace elements by Inductively Coupled Plasma Emission Spectroscopy (Cu, Fe and Zn). Longitudinal changes in porcine milk were analyzed by repeated measures ANOVA using the MIXED model within SAS and data are expressed at means ± SEM. All minerals and trace elements were affected ($p<0.001$) by stage of lactation, with the exception of Fe. Ca increased ($P<0.001$) 3-fold from porcine colostrum (563 ± 87 ug/L) to mature milk (1664 ± 96 ug/L). Mg (91 ± 4 vs. 121 ± 4 ug/L) and P (1252 ± 40 vs. 1562 ± 31 ug/L) also increased ($p<0.001$) from colostrum to mature milk. Milk K initially increased between 0 and 24 h, then declined from 1314 ± 46 ug/L in colostrum to 1035 ± 44 ug/L in mature milk ($p<0.001$). Na also decreased ($P<0.001$) from colostrum (651 ± 45 ug/L) to mature milk (329 ± 17 ug/L). Zn decreased from colostrum (10.2 ± 1.0 ug/L) to mature milk (5.3 ± 0.2 ug/L), as did Cu (2.6 ± 0.3 vs 1.1 ± 0.1; $P<0.001$). Compared to human milk, porcine milk contained 2- to 5-fold higher ($p<0.001$) concentrations of all minerals. Porcine milk was also higher in Ca, P, Cu, Fe and Zn than bovine. Mg was similar and Na and K were lower ($P<0.001$) between porcine and bovine. The high content of minerals and trace elements in porcine milk suggest high capacity transport systems in pig mammary gland that merit further investigation.

Key Words: Milk, Minerals, Pig

W130 Effect of vaccenic acid/conjugated linoleic acid-enriched butter on plasma lipoproteins in the cholesterol-fed hamster. A. L. Lock[1], C. A. M. Horne[2], D. E. Bauman*[1], and A. M. Salter[2], [1]*Cornell University*, *Ithaca, NY*, [2]*University of Nottingham*, *Sutton Bonington, LEICS, UK*.

Butter naturally enriched in *cis*-9, *trans*-11 CLA (rumenic acid; RA) and vaccenic acid (VA) has been shown to be an effective anticarcinogen; however, there has been no examination of the effects of a naturally-derived source of VA and RA on atherosclerosis-related biomarkers. The current study was designed to determine the effect of VA/RA-enriched butter (VA/RA-BT) on plasma lipoproteins and tissue fatty acid profiles in the cholesterol-fed hamster as the biomedical model. Male Golden Syrian hamsters were fed diets containing 0.2% cholesterol and 20% added fat as, treatment (TRT) 1: control (20% standard butter; STD-BT), TRT 2: 5% STD-BT + 15% VA/RA-BT or TRT 3: 15% STD-BT + 5% partially hydrogenated vegetable oil (PHVO). The content of RA and VA was 3.61 and 15.36 g/100 g fatty acid, respectively, in the VA/RA-BT and 0.44 and 1.39 g/100 g in the STD-BT. Diets were fed for 4 wk after which plasma lipoproteins were isolated, cholesterol quantified, and tissue fatty acid profiles determined. The concentration of RA in the liver and epididimal and perirenal fat depots was 0.33, 0.52, and 0.58 for TRT 1; 2.07, 3.35, and 2.98 for TRT 2; and 0.67, 0.85, and 0.80 g/100 g for TRT 3, respectively ($P < 0.001$). The concentration of VA was 0.32, 0.74, and 0.64 for TRT 1; 2.41, 5.11, and 4.53 for TRT 2; and 0.78, 1.66, and 1.51 g/100 g for TRT 3 for liver and epididimal and perirenal fat depots, respectively ($P < 0.001$). Total ($P < 0.001$) and LDL ($P < 0.01$) cholesterol concentrations were significantly reduced in TRT 2 and 3 compared to TRT 1. However, VLDL concentrations were significantly reduced in TRT 2 animals compared to those in both TRT 1 and 3 ($P < 0.01$). HDL was not different among TRT. The ratio of potentially atherogenic lipoproteins (VLDL+IDL+LDL) to anti-atherogenic HDL was lower in animals fed VA/RA-BT (0.60, TRT 2) than those fed either control diet (1.70, TRT 1) or the diet containing PHVO (1.04; TRT 3; $P < 0.001$). Thus, increasing the VA/RA content of butter results in a beneficial plasma lipoprotein profile that is associated with a reduced risk of atherosclerosis.

Acknowledgements: Supported by the National Dairy Council

Key Words: CLA, Vaccenic Acid, Atherosclerosis

Nonruminant Nutrition: Enzyme Supplementation and Methodology

W131 Nutrient digestibility in microbial phytase supplemented corn-soybean based diets in two phases of growing pigs. H. Krebs*[1], C. T. Kadzere[1], Z. Liu[1], and E. van Heugten[2], [1]*North Carolina A&T State University*, *Greensboro*, [2]*North Carolina State University*, *Raleigh*.

Phytate phosphorus (P) makes up 40 to 90% of P in cereal grains and in oilseeds and is unavailable to swine except when supplementary phytase is in the diet. In a 4 x 4 CRD study, 16 male castrated pigs were assigned to four homogenous groups of four animals each to evaluate the effects of microbial phytase on nutrient digestibility in pigs in Phase I (PI) and in Phase II (PII). Each group was fed one of four diets (DI to DIV) differing only in P, calcium (Ca), and phytase content. The average weights of pigs were 19 kg and 39 kg at the start of PI and PII collection periods, respectively. In PI, DI (negative control) contained 0.1% less P and Ca than DII and no phytase; DII (positive control) which had 0.6% P and 0.7% Ca as recommended for growing pigs (10-20 kg) by NRC and 0.0% phytase; DIII and DIV had both 0.1% less P and Ca than DII and had 0.0125% and 0.025% supplemental phytase, respectively. The amount of phytase in PII was similar to that in PI diets. PII diets had 0.1% less P and Ca in DI, DIII, and DIV than the NRC recommendation of 0.5% P and 0.6% Ca for growing pigs (20-50 kg) as in DII. A pig on DII in PI was removed from the study. Fecal samples were collected on d 25 to d 31 in PI and on d 60 to d 66 in PII and analyzed. There were no differences in nutrient digestibility in PI. There were differences ($P < 0.05$) in ash, protein, and fiber digestibility in PII. In PII, pigs on DIII had the highest (75.9%) and those on DI the lowest (65.8%) ash digestibility. Protein digestibility was highest (90.3%) in DIII pigs and lowest (83.0%) in DII. Fiber digestion was highest (68.6%) in DIII and lowest (57.8%) in DII. Nutrient digestibility was higher ($P < 0.05$) in PII than in PI. Microbial phytase in corn-soybean based diets did not influence nutrient digestibility in PI but did in PII. Data presented shows that phytase at the lower level improved digestibility of protein and fiber. It is hard to understand why this was not the case with the higher level.

Key Words: Phytase, Swine, Nutrition

W132 Effect of microbial phytase in corn-soybean based diets on total and soluble fecal phosphorus excretion in two phases of growing pigs. Z Liu[1], C. T. Kadzere*[1], H. Krebs[1], and E. van Heugten[2], [1]*North Carolina A&T State University*, *Greensboro*, [2]*North Carolina State University*, *Raleigh*.

The effect of microbial phytase in corn-soybean based diets on total phosphorus (TP) and soluble phosphorous (SP) excretion were evaluated in growing male castrate pigs in Phase I (PI) and Phase II (PII) in a 66-d 4 × 4 CRD study. Pigs (n = 16) were assigned to four equal groups of four pigs each and groups were fed one of four diets (DI to DIV) differing only in phosphorus (P), calcium (Ca), and phytase. The average pig weights were 19 kg and 39 kg at the start of PI and PII collections, respectively. In PI, DI (negative control) contained 0.1% less P and Ca and no phytase; DII (positive control) had 0.6% P and 0.7% Ca as recommended for growing pigs (10-20 kg) by the NRC and no phytase; DIII and DIV both had 0.1% less P and Ca than DII, and had 0.0125% and 0.025% supplementary phytase, respectively. Phytase levels in PII diets were the same for corresponding PI diets. PII diets had 0.1% less P and Ca in DI, DIII, and DIV than in DII with the NRC recommended level of 0.5% P and 0.6% Ca for grow-

ing pigs (20-50 kg). A pig on DII was removed from the study. Fecal samples were collected on d 25 to d 31 and on d 60 to d 66 in PI and PII. TP was determined after digestion in HNO_3 by ICAP spectrophotometry. Similarly, SP was obtained by the ICAP method after filtration through a 0.45 µm membrane. TP in PI was 17.3, 21.7, 14.8, and 14.5 mg/g for pigs on DI, DII, DIII, and DIV and was 19.3, 18.2 17.1 and 14.1 mg/g in PII for pigs on DI, DII, DIII and DIV respectively. TP excreted by pigs on DIII and IV was lower ($P < 0.05$) than DI and DII. The SP in PI was 3.8, 3.2, 3.1, and 3.2 mg/g for pigs on DI, DII, DIII, and DIV and was 1.8, 1.7, 2.1, 2.1 mg/g for pigs in PII on DI, DII, DIII, and DIV respectively. The values were not different ($P > 0.05$). Microbial phytase reduced TP excretion in PI and PII but did not influence SP in either phase.

Key Words: Phytase, Phosphorus, Excretion

W133 Effect of phytase activity of the diets on the faecal and urinary phosphorous excretion in adult roosters. J. Tossenberger[1], L. Babinszky*[1], and I. Kühn[2], [1]*University of Kaposvár, Department of Animal Nutrition*, *H-7400 Kaposvár, POB 16, Hungary*, [2]*AB-Enzymes GmbH*, *D-64212 Darmstadt, Germany*.

The effect of phytase on P excretion of poultry has been customarily determined in studies with intact birds based on collection of excreta. By using cannulation techniques, it is possible to measure faecal and urinary P excretion separately. The aim of our trials was to study how different dietary phytase activities influence faecal and urinary P excretion of adult roosters. The studies were conducted with a total of 16 adult Shaver Star Cross 288 roosters (four birds/treatment) in two replicates (n = 8/treatment). Prior to the trials a simple T-cannula was implanted in the terminal colon. Nutrient contents of the corn-soy based diets met the 1994 NRC recommendations. The Ca content of the basal diet was 4.9 g/kg, and its P content was 3.0 g/kg. The trial included four treatments. Treatment 1 diet contained no phytase supplementation. In treatments 2, 3 and 4 diets were supplemented with a bacterial 6-phytase (trichoderma reesei) at the rate of 125, 250 and 500 PPU/kg, respectively. Measured phytase activity of the diets was 0, 166, 311 and 695 PPU/kg. Trial data were analyzed by means of ANOVA. According to our data, 125 PPU/kg phytase supplementation led to a P digestibility increase from 31% (control) to 44% ($P \leq 0.05$). Higher phytase dosages did not improve P digestibility ($P \geq 0.05$). As a result of 125 PPU/kg phytase supplementation daily urinary P excretion was increased from 13 mg/kg$^{0.75}$ (control) to 23 mg/kg$^{0.75}$ ($P \leq 0.05$). Further increase of phytase dosages did not increase any further urinary P excretion ($P \geq 0.05$). From total phosphorous excretion 16.5, 28.4, 31.7 and 32.5% (treatments 1, 2, 3, and 4, respectively) was excreted via urine. As a result of 125 PPU/kg phytase supplementation P retention increased by 38%. Higher phytase dosages did not lead to an increase in retention ($P \geq 0.05$). Thus, our data also call the attention to the fact that adult roosters excrete their P surplus in the urine, similarly to pigs.

Key Words: Rooster, Phosphorous Digestibility, Urinary Excretion

W134 Effect of combination of phytase and xylanase on the growth performance and nutrient digestibility of growing pigs. O. A. Olukosi*[1], J. S. Sands[2], and O. Adeola[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*Danisco Animal Nutrition*, *Marlborough, UK*.

Growth performance and nutrient digestibility responses to an *E. coli* derived-phytase (ECP) and xylanase were investigated in pigs receiving corn, soybean meal, wheat middling and canola meal-based diet. Forty-eight 10-kg pigs were used in the 28-d feeding trial. They were blocked by weight and sex and randomly allocated to six dietary treatments. The six diets were a positive control (PC) with adequate level of non-phytate P (2.7 g/kg), a negative control (NC) with low non-phytate P (1.8 g/kg), the NC with ECP added at 500 or 1,000 FTU/kg, NC with xylanase added at 2,500 U/kg, and NC with a combination of xylanase and ECP added at 2,500 U/kg and 500 FTU/kg, respectively. Nutrient digestibility was determined during d 10 to 14 and 24 to 28. Low levels of non-phytate P in the NC treatment depressed final body weight (FBW) and daily gain (DG) of pigs but ECP linearly increased ($P < 0.05$) these to a level comparable with the PC diet. Xylanase alone had no effect on FBW or DG of pigs but the combination of xylanase and ECP increased ($P < 0.05$) these response criteria to that obtained in the PC diet. The treatments had no effect on feed intake or gain:feed. There was linear effect ($P < 0.01$) of ECP on digestibility of Ca, P and ash. Xylanase alone increased ($P < 0.05$) the digestibility of P but combination of ECP and xylanase increased the digestibility of P, Ca, and ash above the xylanase alone treatment. The treatments had no effect on the digestibility of nitrogen and energy. It is concluded from this study that addition of a combination of xylanase and *E. coli* phytase improved performance of pigs on a low non-phytate P diet but the effect was likely more from the phytase because when phytase alone was added, there was improved performance, whereas xylanase alone did not improve performance.

Key Words: Phtase, Xylanase, Pigs

W135 Effect of a multi-enzyme preparation administered through drinking water in broiler chickens. S. Maisonnier-Grenier, F. Rouffineau, P. Dalibard, S. Jakob*, and P.-A. Geraert, *Adisseo France SAS*, *Commentry*.

The effect of a fungal multi-enzyme preparation produced by *Penicillium funiculosum* (Rovabio™ Excel) upon the apparent metabolizable energy (AMEn) has been demonstrated in numerous trials. Up to now, NSP-enzymes were mainly incorporated into the feed to express its effect on the feed after ingestion. However, due to very high temperatures during special feed treatment (extrusion or expansion) other possibilities to distribute the enzyme have to be found in order to enlarge its use to all feeds. A simple method to supply the exogenous enzyme to poultry is the distribution through the drinking water. The present study was performed to prove the convenience and efficacy of enzyme distribution via the drinking water for broiler chickens. A trial was performed to validate the efficacy of enzymes in drinking water upon the AMEn. Thirty male Ross broiler chicks (d 12 to d 22) were fed a wheat-soy based diet (wheat, 597 g/kg; soybean, meal 260 g/kg; palm oil, 50 g/kg) and equally distributed to three different treatments: a control treatment (C) and two experimental treatments (E1 and E2). A multi enzyme preparation, Rovabio™ Excel, was sprayed either directly on the diet after pelleting (E1) or included in the drinking water (E2). The energy balance was performed between 19 and 22 d of age using the European Reference Method for AMEn. During the experiment, feed intake and growth was measured. Statistical analysis was performed using one way ANOVA. Both, the enzyme supplementation in feed and via water increased ($P < 0.05$) the AMEn and reduced the FCR between 12 and 22 d of age. The improvement was higher for chicks receiving the enzymes through drinking water as compared to the supplementation by feed. It can thus be concluded that Rovabio™ Excel can be supplied through the drinking water with the same efficacy on a wheat-based diet as when supplied through the feed.

	Control	+ Rovabio in diet	+ Rovabio in water	P
AMEn (MJ/kg)	11.73 ± 0.31	12.48 ± 0.26	12.74 ± 0.26	0.04
FCR	1.95 ± 0.05	1.90 ± 0.02	1.88 ± 0.04	0.38

Key Words: Enzyme, Drinking Water, Broiler

W136 Effect of an enzymatic compound in turkeys under two feeding systems on their productive performance. I. A. García-Galicia[1,2], A. L. Rentería-Monterrubio*[2], G. B. Galicia-Juárez[1], M. L. Gorostiola-Herrera[1], F. Salvador-Torres[2], and J. C. García-López[3], [1]*Dirección General de Educación Tecnológica Agropecuaria*, *Distrito Federal, México*, [2]*Facultad de Zootecnia, UACH*, *Chihuahua, Chih.,México*, [3]*Alltech de México*, *Distrito Federal, México*.

Two hundred White turkeys, nine weeks old, were randomly distributed in four poultry pens: (T1) 50 poults in confinement with no enzyme as the control group, (T2) 50 poults in grazing with enzymatic compound (Allzyme VegPro®), (T3) 50 poults in grazing without enzymatic compound, and (T4) 50 poults in grazing with enzymatic compound to determine the effects of the feeding sys-

tem and the addition of an enzymatic complex (0.1%) to the diet during 8 weeks on the productive performance. The commercial diet based on corn and soybean covered the 1994 NRC nutritional requirements, and the grassland used consisted of oat, barley alfalfa and native plants (30, 30, 30 and 10, respectively). The statistic analysis was based on a 2 x 2 factorial arrangement (enzyme x feeding system), analyzing the average daily gain (ADG), live weight (LW), feed intake (FI), forage intake (FGI), and carcass yield (CY). In LW, the interaction between the main effects ($P \geq 0.05$) was not found (see table below), while the effects of the enzyme and grazing showed higher values during the test. ADG and CY showed interactions ($P \leq 0.05$), with a positive effect of the enzyme only in confinement. The FI was not altered by the main effects or by its interaction, while the FGI was increased ($P \leq 0.05$) by the effect of the enzyme. It is concluded that the presence of exogenous enzymes in the turkey diet increases the LW and CFI, with a positive effect over ADG only in confinement. The grazing also has a positive effect on LW.

Productive performance of turkeys in finisher under two feeding systems, with or without an enzymatic compound in the diet

	Treatment				
Variable	T1	T2	T3	T4	P
ADG (g)	81 ± 3[a]	107 ± 3[b]	125 ± 3[c]	132 ± 3[c]	0.01
CY (%)	71.07 ± 0.33[a]	75.87 ± 0.36[b]	77.30 ± 0.35[c]	77.38 ± 0.36[c]	0.001

	Effect					
	Without enzyme	With enzyme	P	Confinement	Grazing	P
LW (kg)	10.282 ± 0.17[a]	10.885 ± 0.17[b]	0.016	9.850 ± 0.017[a]	11.316 ± 0.17[b]	0.001
FGI (g of DM)	38 ± 1[a]	31 ± 1[b]	0.008			

[a,b,c]Means differ ($P < 0.05$) within the same row.

Acknowledgements: Thanks to Alltech de México

Key Words: Turkeys, Enzymes, Grazing

W137 Development of an analytical method for the analysis of acid proteases in feed samples. P. Glenney* and K. Filer, *Alltech, Inc.*, *Nicholsville, KY.*

Exogenous enzymes can be added to poultry and swine diets to increase the nutrient availability of feed ingredients. Proteases are a common class of enzymes that are utilized for this purpose. Detection of acid proteases after they have been added to the feed is difficult. The purpose of this work was to develop a method for the detection of an acid protease after it was applied to poultry feed. The approach used for this work was to adapt an assay based on the hydrolysis of hemoglobin. A completely randomized design was utilized. Two treatments, 6 hours and 24 hours, were utilized with enzyme levels at 15,000; 7,500; 3,750 and 1,875 HUT/kg. The change in absorbance produced in the assay vs. enzyme activity was graphed and the R^2 value for each curve calculated and compared using Student's *t* test. The assay that produced the largest R^2 value and had a change in absorbance at 275 nm of at least 0.500 units for the sample that contained the highest enzyme activity would be utilized to estimate the activity of four poultry feeds containing protease. The samples were two commercial and two mixed in the lab. If the R^2 value for the curves were not different then the 6 hour assay would be used to estimate blind samples. The R^2 values for the 24 hour assay, 0.99517, and the 6 hour assay, 0.99437, were not different ($P > 0.05$). The range of the change in absorbance for the 6 hour assay was 0.143 ± 0.022 units at 1,875 HUT/kg to 0.534 ± 0.029 units at 7,500 HUT/kg. The 24 hour assay showed a range of 0.196 ± 0.015 units to 0.704 ± 0.037 units. Two blind samples in the lab were mixed to contain 7,500 HUT/kg and 15,000 HUT/kg. The estimated activity for each sample was 8,003 ± 152 HUT/kg (6.7% over) and 14,157 ± 322 HUT/kg (5.6% under). A commercial sample from North America was estimated to contain 2,512 ± 188 HUT/kg (33% less) and a sample from South America was estimated to contain 8,248 ± 1,495 HUT/kg (10% more). The results indicate that the assay can be useful in providing an estimate of the protease activity present in a poultry feed.

Key Words: Acid Protease, Enzymes, Feed

W138 New strategies guarantee success in mycotoxin control. U. Hofstetter*[1], V. Starkl[1], D. Schatzmayr[1], G. Schatzmayr[1], and E. M. Binder[2], [1]*Biomin GmbH*, *Herzogenburg, Austria*, [2]*Erber AG*, *Herzogenburg, Austria*.

Mycotoxins are toxic chemical products formed by fungal species that pose a potential threat to animal health as many of these toxins are immunosuppressive, estrogenic or genotoxic. Especially swine, are known to be affected with kidney problems (e.g., porcine nephropathy), increased water consumption, increased urine production and decreased feed consumption and daily weight gains due to Ochratoxin A (OTA). The most common approach to counteract mycotoxins is adsorption by minerals. But mycotoxins are completely different in their chemical structure, and thus it is impossible to deactivate all mycotoxins by using only a single strategy. One investigated solution is detoxification by biotransformation. Specific enzymes can change the toxic group of a mycotoxin into a non-toxic metabolite under intestinal conditions. For deactivation of trichothecenes, a strictly anaerobic bacterium *Eubacterium BBSH 797* has been isolated out of rumen fluid, and a newly-discovered yeast strain *T. mycotoxinivorans* is capable of detoxifying ochratoxins. As all mycotoxins are hepatotoxic agents and can cause immunosuppression in animals, plant and algae extracts were selected. A product based on the three above mentioned strategies proved to be a solution to help to counteract the diverse mycotoxin problems in swine. Its efficacy to alleviate the negative effects of OTA on weaning piglets was proven by several feeding trials (Table). Performance criteria like final weight, average daily weight gain (ADWG) and feed conversion ratio (FCR) were improved. Currently the most common mycotoxins like aflatoxin, zearalenone, ochratoxin A and all trichothecenes can be detoxified by a selected blend of minerals, *BBSH 797* and *T. mycotoxinivorans*.

Trial design and trial results (day 1-49)

	A	B	C	D
Product	-	-	+	+
OTA [ppb]	-	500	500	-
Final weight [kg]	32.65	30.78	32.07	33.10
ADWG [g]	457.7	379.8	445.4	465.5
FCR	2.44	2.35	2.30	2.24

Key Words: Mycotoxin, Biotransformation, Weaning Piglets

W139 Influence of weaning on caecal microbiota of pigs: use of real-time PCR and t-RFLP. M. Castillo*[1], S. M. Martín-Orúe[1], E. G. Manzanilla[1], M. Roca[2], and J. Gasa[1], [1]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*, [2]*Centre de Recerca en Sanitat Animal*, *Bellaterra, Barcelona, Spain*.

The development of the healthy microbiota in the young pig is determinant to avoid post-weaning disease and to reach an optimal growth performance. The objective of this trial was to monitor the microbial changes of caecal population associated with early-weaning. Twelve pigs (20 ± 2 days) from six different littermates were selected from a commercial source. Animals from the same littermates were divided in two groups: a control group (L) that remained with the sow and an experimental group (F) that was weaned and fed a commercial post-weaning diet. After one week, animals were sacrificed and samples from caecal digesta were taken and preserved in ethanol until analysis. Microbial counts for enterobacteria and lactobacilli were determined by quantitative-PCR using 16S rDNA specific primers and SYBR Green® dye. Microbial profiles

were assessed by terminal restriction fragment length polymorphism (t-RFLP) using fluorescently labeled 16S rDNA forward primer (FAM0008) and restriction enzyme *HhaI*. Dendograms, according to the similarity of the community profiles, were constructed using UPGMA method and the Fingerprinting II® software. Weaning promoted a decrease in lactobacilli population that resulted in a significant increase in enterobacteria:lactobacilli ratio (0.27 vs. 1.67 log/log 16S rDNA copy number; $P = 0.05$). Biodiversity of microbial ecosystem (number of bands) was similar between both experimental groups (49.34 for L and 53.40 for F, respectively; $P = 0.22$), however the band patterns were clearly grouped in two different clusters by dendogram analysis. Some particular bands were consistently present or absent in each of the groups. Results obtained showed weaning as a challenging point on the process of establishment of the indigenous microbiota in the caecum. Changes consisted primary of a substitution of some microbial species by others.

Key Words: Microbiota, Weaning Pig, PCR

W140 Available energy from fermentation in the hindgut in growing pigs fed with different levels of dietary fiber. M. Anguita[1], N. Canibe[2], J. F. Pérez*[1], and B. B. Jensen[2], [1]*Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*, [2]*DIAS, Research centre Foulum*, *Tjele, Denmark*.

An experiment, combining in vivo and in vitro ethodologies, was carried out to asses the available energy to the pig from hindgut fermentation. Six male pigs (Danish Landrace x Yorkshire x Duroc) were fitted with a simple T-shaped cannula at the terminal ileum and offered, following a Latin-square design, three diets with increasing levels of non-starch polysaccharides (NSP): Low fiber diet (LFD, 7.7% NSP), standard fiber diet (SFD, 16.0% NSP) and high fiber diet (HFD, 24.0% NSP). After adapting the animals to the diet, samples from ileum and feces were collected and analyzed for dry matter, energy, crude protein and chromic oxide. Freeze dried ileal samples were fermented in vitro in a batch system for 48 hours. The pH was automatically adjusted to 6.0, and temperature was kept constant at 38°C. Anoxic conditions were maintained by sparing cultures of high purity N_2. Available energy (MJ/kg DM feed) from fermentation was calculated from the amount of SCFA produced in vitro and the in vivo ileal flow of DM. Results from the in vivo experiment, reflected that the inclusion of fiber promoted a decrease ($P < 0.001$) in the energy digested (MJ/kg DM feed) in the foregut (15.3, 12.32, and 10.93 for LFD, SFD, and HFD, respectively), and to an increase ($P < 0.001$) of the energy digested in the hindgut (1.61, 2.97 and 3.53 for LFD, SFD and HFD, respectively). The in vitro data showed that, although the amount of SCFA produced per gram of DM of ileal effluent was not different ($P = 0.26$), the calculated SCFA production per kg DM feed was higher ($P < 0.001$) with increased levels of fiber, due to the higher flow of DM at the terminal ileum. The results from the present study showed that growing pigs receiving diets with NSP levels between 7.7 and 24.0% obtained between 7.1 and 17.6% of their available energy from fermentation in the hindgut.

Key Words: Pigs, Energy, Fermentation

W141 An automated algorithm to estimate body protein and lipid deposition patterns in growing pigs from growth and feed intake curves. G. Vander Voort* and K. de Lange, *University of Guelph*, *Guelph, Ontario, Canada*.

The evaluation of alternative management strategies for growing-finishing pigs requires accurate estimation of nutrient accretion patterns. The objective of this research was to develop an automated algorithm to establish body protein (Pd) and body lipid deposition (Ld) curves in growing pigs. Daily BW gain and feed intake curves for 40 individual pigs (30 to 110 kg BW) were established using random regression methodology. Daily records of ad libitum feed intake and BW were obtained with computerized feed intake and BW recording equipment for individual pigs housed in groups. A dynamic nutrient partitioning model, with a 1-day iteration interval, was used to represent utilization of ME and lysine intake for growth, while three pig type parameters were varied: maximum Pd (Pdmax, g/d), which was assumed constant up to the BW at which Pdmax starts to decline (BWdecl, kg; thereafter maximum Pd declined as represented by a Gompertz function) and constraints on the ratio between whole body lipid and whole body protein (minBL/BP, MJ ME^{-1}; linearly related to daily ME intake). For each pig and based on the observed feed intake curve, 1,000 different growth patterns were generated by varying the pig type parameters. Best fit pig type parameters were chosen based on minimizing the sum of squared differences between simulated and recorded daily BW gain. Data from three pigs were not deemed reliable. The difference between observed and recorded daily BW gain was homogenous across BW with a mean of 10 g/d (SD, 10). In this group of pigs, Pdmax was 164 g/d (SD, 32), BWdecl was 76.7kg (SD, 15.2), while minBL/BP was 0.033 MJ ME^{-1} (SD, 0.013). The automated algorithm was effective in establishing Pd and Ld curves in individual pigs.

Key Words: Pigs, Protein, Deposition

W142 Dual-energy x-ray absorptiometry for determination of body composition in a porcine model of obesity development. C. A. Baldwin* and T. S. Stahly, *Iowa State University*, *Ames*.

The precision and accuracy of the Dual Energy X-ray Absorptiometry (DEXA) estimates of the weight and tissue (fat, lean and bone mineral) content of two body depots (carcass and internal organs) were evaluated in thirty-three heavy weight pigs (133-265 kg) serving as a model for obesity development. DEXA (Hologic, fan beam) scanning accurately estimated the carcass weight (+2%) relative to that determined by gravimetric weighing. DEXA underestimated the fat tissue contents of both the carcass and organ depots (-19 and -26%) and overestimated the lean tissue contents (13 and 27%) relative to those estimated from chemical analysis of the fat and protein contents of the depots. However, DEXA precisely detected changes in carcass and organ depot weights (R^2 = 0.99 and 0.99, respectively) and less precisely predicted changes in the depot′s chemically determined fat (R^2 = 0.95 and 0.73) and protein content (R^2 = 0.88 and 0.84). Specifically, for each 1 kg change in carcass and organ depot weights, DEXA predicted the changes with a 95% confidence (two SE of estimate) within ± 0.008 and 0.026 kg, respectively. For each 1 kg change in the two depot′s chemically determined fat content, DEXA predicted the change within ± 0.092 and 0.338 kg, respectively. In conclusion, DEXA precisely predicted changes in body depot weight and fat and lean tissue contents in large, heavy weight pigs being used in a model of obesity development. The precision was less in the internal organ depots than carcass depots.

Key Words: DEXA, Obesity, Pigs

W143 Hepatic gluconeogenesis and muscle intermediary metabolism in hybrid striped bass (HSB) determined by ^{13}C-mass isotopomer distribution analysis. B. J. Bequette*, S. L. Owens, N. E. Sunny, S. W. El-Kadi, and L. C. Woods, *University of Maryland*, *College Park*.

High dietary carbohydrate is not well tolerated by carnivorous fish, resulting in unregulated plasma glucose and enlarged and dysfunctional livers. The metabolic basis underlying this limited ability to use dietary glucose remains sketchy at best. Our aim was to generate a metabolic profile of the pathways of glucose synthesis and muscle glucose utilization in carnivorous fish. HSB (M. chrysops × M. saxatilis; 65 g; n=10) were fed (3% of BW) twice a day for 1 mo a diet of 39% crude protein (fish meal), 30% dextrin, and 9% fish oil. For the last 5 d, [U-^{13}C]dextrin replaced 18% of diet unlabelled dextrin. Fish were killed and tissues collected after 1 d (n = 4), 3 d (n = 3) and 5 d (n = 3) of feeding the tracer diet. Isotopomer steady-state labeling of plasma glucose, and various tissue (liver, muscle) amino acid (AA) pools (alanine, aspartate, glutamate) was attained by day 1 of tracer feeding. Absorbed glucose was 272 ± 24 mg/d, gluconeogenesis from AA was 321 ± 61 mg/d, and glucose recycling was 66 ± 15 mg/d. In the liver, 26.7% (± 1.7) of the 3-carbon pool derived from glucose catabolism. Here, the 3-carbon pool contributed to 60.4% (± 11.8) of acetyl-CoA and to 30.8% (± 5.2) of oxaloacetate fluxes, and thus only 16.6% (± 3) and 7.8% (± 0.7) of these fluxes, respectively, derived from glucose catabolism in the liver. In muscle, 28.9% (± 3.5) of the 3-carbon pool derived from glucose catabolism. Here, the

3-carbon pool contributed to 70.7% (± 7.2) of acetyl-CoA and to 2.2% (± 0.8) of oxaloacetate fluxes, with only 20.2% (± 1.5) and 0.7% (± 0.3) of these respective fluxes derived from glucose catabolism in muscle. In this study, despite high rates of dietary glucose absorption, gluconeogenesis (from AA) was maintained, and at rates similar to glucose absorption. In liver and muscle, glucose catabolism made a minor contribution to overall Krebs cycle metabolism, and thus fatty acids and (or) AA were the largest contributors to energy generation in these fish tissues.

Key Words: Striped Bass, Glucose, Stable Isotope

Nonruminant Nutrition: Minerals

W144 Genetic background and phosphorus nutrition affect bone strength and gene expression in young pigs. L. Hittmeier, R. Lensing, L. Grapes, M. Rothschild, and C. Stahl*, *Iowa State University*, *Ames.*

Phosphorus (P) is essential to bone growth and turnover; however, little research has focused on the genetic mechanisms controlling P utilization. In this study, 36 gilts (6.63 ± 0.78 kg) from six litters (three gilts/litter) were sired by two lines known differ in bone structure [one considered heavier-boned (HB) and the other lighter-boned (LB)]. Pigs were assigned to three dietary treatments: P adequate (0.41% available P for 2 wk), repletion (0.14% available P for wk 1, 0.41% available P for 2 wk), or P deficient (0.14% available P for 2 wk). After 14 d, pigs were harvested and bone marrow was collected for analysis of gene expression by real-time PCR, and radial bones were collected for breaking strength analysis. In HB, but not LB pigs, the P deficient diet caused a decrease in ADG ($P < 0.01$) compared to the other treatments. In the LB line, repletion pigs had higher ADG ($P < 0.01$) than the other treatments. For both lines, P deficiency caused a reduction in radial bone strength ($P < 0.01$). The LB and HB lines responded similarly to P deficiency in the expression of *OXTR* and *IGF1*. In HB, but not LB pigs, diet affected the expression of *VDR* ($P < 0.04$), *CALCR* ($P < 0.05$), and *IGFBP3* ($P < 0.06$), and there was a trend of increased *IL6*, *Sox-9*, and *TFIIB* expression with P deficiency. Expression of *BGLAP*, *OPG*, *RANKL A-Raf-1* and *IGFBP5* was not affected by sire line or diet. Data were analyzed using a mixed model with line, diet, and line × diet fit as fixed effects. Based on this study, the HB pigs were more responsive to dietary P than LB pigs. Differences in growth and gene expression within the bone marrow suggest a difference in the homeorhetic control of P utilization between these genetic lines. In addition, a better understanding of the role genetics plays in P homeorhesis will enable selection for pigs that will require and excrete less P, as well as allow for the recommendation of specific genetic lines for producers with different waste management strategies.

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Key Words: Bone, Gene Expression, Phosphorus

W145 Effect of dietary phosphorus on the gene expression related to energy metabolism in porcine muscle. A. Qu*, L. Grapes, M. Rothschild, and C. Stahl, *Iowa State University*, *Ames.*

Phosphorus (P) plays a vital role in growth and development, however little research has focused on the genetic mechanisms controlling P utilization. We examined the influence of two sire lines, selected primarily for either meat quality (MQ) or growth performance (GP), and dietary P on the expression of a variety of genes related to energy metabolism in muscle. These genes were identified in a previous oligonucleotide microarray study. Thirty-six gilts (21 d of age, 6.63 ± 0.78 kg) from six litters (three pigs/litter) for each sire line 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. Using real-time PCR, we quantified the gene expression of glycogen synthase, succinate dehyrdrogenase, and the succinate dehydrogenase iron-sulfur protein in porcine muscle. The relative gene expression levels in muscle samples from all gilts were analyzed using a mixed-model which included the fixed effects of sire line, diet and sire line by diet interaction. Phosphorus deficiency caused an increase ($P < 0.05$) in the expression of glycogen synthase regardless of genetic background. However, the increase tended to be greater in the GP sired pigs. In MQ, but not GP, sired pigs fed the -P diet had lowered ($P < 0.05$) and those fed the RP diet tended ($P < 0.06$) to have lowered expression of the succinate dehydrogenase iron-sulfur protein. Also the MQ sired pigs in the -P group had higher ($P < 0.05$) levels of succinate dehydrogenase mRNA, while dietary P did not effect its expression in GP sired animals. Our results demonstrated that there are significant nutrition × genetic interactions that affect gene expression in porcine muscle. Elucidating these interactions may enable selection for pigs that will require and excrete less P, as well as allow for the recommendation of specific genetic lines for producers with different waste management strategies.

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Key Words: Phosphorus, Energy Metabolism, Gene Expression

W146 Phosphorus utilization is improved in the growing Enviropig™(Cassie line). A. Ajakaiye*, R. G. Meidinger, M. Z. Fan, D. A. Murray, J. Zhang, M. Mundia, J. P. Phillips, S. P. Golovan, J. M. Kelly, R. R. Hacker, and C. W. Forsberg, *University of Guelph*, *Guelph, Ontario, Canada.*

The objectives of this study were to determine phosphorus (P) utilization by the Enviropig™ (EP) during the growing phase and to compare the values obtained with that derived from the Yorkshire pigs (YK). Six of each EP and YK growing barrows, with average initial BW of 24 and 20 kg, respectively, were fed three diets according to a cross-over (split-plot design). The main plot was the breed and diet was the subplot. There were three diets, six pigs and three periods, with two pigs/diet/period for a total of six replicates/diet. The diets were formulated on the basis of available P with Ca:P maintained at 2:1. The diets consisted of diet A, a control diet with supplemental PO_4^{3-}; diet B, no supplemental PO_4^{3-}; and diet C, no supplemental PO_4^{3-} and 2% lower CP. Each experimental period consisted of 14 d with 10-d adaptation and 4-d collection of urine and representative fecal samples. Data collected were subjected to analysis of covariance using the mixed models procedure with initial BW as a covariate. Fecal P values were significantly reduced ($P < 0.05$) in EP by up to 39% on diet A, 70 % with the diet B, and 68% with the diet C compared to the YK. Apparent P digestibility was increased ($P < 0.05$) in EP than in the YK. Also, the total manure P excretion was reduced when EP was fed the diet with low P and low CP compared with YK (2.82 ± 0.99 vs. 4.56 ± 0.96 g/pig/day; 3.37 ± 1.05 vs. 4.28 ± 0.94 g/pig/day), respectively. The increase ($P < 0.10$) in urine P observed in the EP (4.13 ± 0.84 g/pig/day) vs. YK (-2.0 ± 0.96 g/pig/day) fed diet A is due to the supplemental inorganic P in the diet since the EP does not require supplemental inorganic P in their feed. These data support that the Enviropig™ breed would cost less to feed because neither supplemental P nor phytase enzyme needs to be included in the diet. Furthermore, the reduced P in the manure from the Enviropig™ is more compatible with stringent nutrient management legislation.

Key Words: Enviropig™, Yorkshire, Phosphorus