M246 Effect of T-2 toxin on growth of ruminal bacteria in batch culture. D. Srichana*[1,2], G. E. Rottinghaus[1], P. Srichana[1,3], J. H. Porter[1], M. S. Kerley[1], and J. N. Spain[1], [1]*University of Missouri*, *Columbia*, [2]*Thammasat University*, *Phathumthani, Thailand*, [3]*Charoen Pokphand Group Co., Ltd.*, *Bangkok, Thailand*.

T-2 toxin (T), a type-A trichothecene is a mycotoxin that has been found to contaminate feeds fed to dairy cattle. The effect of T-2 toxin on ruminal bacterial growth and fermentation was measured in a batch culture experiment. Feeds were incubated (39°C) in fermenters with buffer and ruminal fluid containing 0, 100, 200, 400 and 800 ppm T. Culture optical density (OD) was measured to estimate microbial populations. The cultures were sampled at 0, 6, 12 and 24 h to measure fermentation end products, pH and OD. The experimental treatments were arranged as a completely randomized design and analyzed with Proc MIXED procedures of SAS. Differences were identified at P<0.05. Optical density increased over time with no differences among treatments. Culture pH decreased over time and was significantly higher at 12 and 24 h for the cultures with T at 800 ppm compared to all other treatments. The pH at 24 h was 6.08b, 6.10b, 6.09b, 6.10b and 6.18a for 0, 100, 200, 400 and 800 ppm T, respectively. Total concentration of VFA increased overtime with differences at 12 h, but VFA concentration was similar after 24 h (P>0.05). Propionic acid increased over time with feed containing no T having lower propionic concentration than other treatments at 24 h (19.8b, 24.8a, 24.9a, 24.4a and 24.7a mM for 0, 100, 200, 400 and 800 ppm T). Feed containing no T supported higher concentration of butyric acid at all time points, including 24 h (19.6a, 17.3b, 17.8b, 17.9b, 17.8b mM) and ammonia at 24 h (31.5a, 29.2b, 27.0c, 28.2b, 26.9c mM) versus other treatments at 100, 200, 400 and 800 ppm. The results indicate that T-2 toxin altered ruminal microbial fermentation. The effect of these changes in rumen fermentation on animal performance should be investigated.

Key Words: T-2 Toxin, Ruminal bacteria, Batch culture

M247 *Lactobacillus acidophilus* isolated from cattle with potential to improve starch utilization. L. D. Early*, J. A. Nangle, and S. E. Gilliland, *Oklahoma State University*, *Stillwater*.

Starch is the major energy component of grains and is therefore a primary energy source in many diets. From enrichment cultures in which starch was the only source of carbohydrate, a total of 19 different strains of species of *Lactobacillus* were isolated from four samples of cattle fecal matter. These strains were compared for relative abilities to hydrolyze soluble starch. Of the 19, six were selected for testing on raw starch. The six cultures also were examined for bile tolerance. There were variations among the cultures with respect to both starch hydrolysis activity and bile tolerance. All six cultures hydrolyzed raw starch and were bile tolerant; but the culture that showed the best starch hydrolysis activity with regard to soluble starch has been identified as Lactobacillus *acidophilus* S893-3. Two strains *L. acidophilus* S893-1 and S893-3 were significantly better than the others for hydrolysis of raw starch. However, there was no significant difference between the two strains in either test. *Lactobacillus acidophilus* S893-3 was significantly more bile tolerant then *L. acidophilus* S893-1. Thus this strain appears to offer the best possibility for use as a direct fed microbial to enhance starch utilization in cattle. The data were analyzed as ramdomized blocks with repetitions being blocks and cultures being treatments. Least significant differences were used to separate means. Differences having P < 0.05 were considered significant.

Key Words: *Lactobacillus*, Starch, Probiotic

M248 Evaluation of rumen microbial fluctuations in response to sub acute rumen acidosis using 16S rDNA profiles. H. Purvis II*[1], S. Fernando[1], K. Rutz[1], F. Najar[2], B. Roe[2], and U. DeSilva[1], [1]*Oklahoma State University*, *Stillwater*, [2]*University of Oklahoma*, *Norman*.

Rumen acidosis is considered to be one of the most important nutritional disorders in the feedlot and dairy industries today. Additionally, the economic impact of the losses due to subacute rumen acidosis is estimated to be in the billions of dollars for both the beef and dairy industries. We evaluated the corresponding fluctuations in rumen microbial population dynamics as animals contracted subacute ruminal acidosis (SARA) in an experimental setting. Eight multi-cannulated beef steers (510 ± 20 kg) were utilized in a crossover design and randomly assigned to two treatment groups (n=4/trt); Control (2.5 % BW prairie hay,) and Concentrate (2.5% BW, 3.0 Mcal of ME/Kg of DM). Following adaptation to diets two animals on Concentrate were challenged with 1.2g/Kg body weight of ground corn to experimentally induce SARA. Rumen samples were collected every two h for 24 h period following the morning feeding (0800). A 800bp fragment of the microbial 16S rRNA gene was PCR amplified and the microbial population structure and diversity were assessed using Terminal Restriction Length Polymorphism (T-RFLP) and was analyzed using the Phylogenetic Analysis Tool (PAT) software. To identify the major contributors of sub acute rumen acidosis, 16S rDNA libraries were constructed from both animals with induced SARA and control animals on high energy diet during critical stages of pH change and were sequenced. The sequence analysis shows significant increases in Proteobacteria (0.8% to 23.1%) and Actinobacteria (0.3% to 7.3%) populations, and significant decreases in Firmicutes (36.1% to 21.9), Spirochaetes (4.4% to 0.0) Bacteroidetes (44.3% to 31.0%) populations. Overall, changes in rumen populations can be evaluated using T-RFLP and microbial populations are altered greatly by SARA.

Key Words: Subacute rumen acidosis, 16s rDNA, Beef cattle

M249 The negative effects of one cycle of eight hours at suboptimal pH on rumen fermentation are not reduced by splitting it into various cycles. M. Cerrato, S. Calsamiglia*, and A. Ferret, *Universitat Autonoma de Barcelona*, *Bellaterra, Spain*.

Previous studies indicate that the total amount of time (h) that ruminal pH is suboptimal may be more critical for ruminal fermentation than mean daily pH. We hypothesized that ruminal bacteria may resist short periods of low pH if pH is above 6.0 long enough to permit their regrowth. However, the negative effects of prolonged periods (12 h) of suboptimal pH were not reduced by splitting it into various cycles. Eight 1325-ml dual flow continuous culture fermenters were used in two consecutive periods to examine if the negative effects of 8 h at pH 5.5 on rumen fermentation can be reduced by splitting it in 2 periods of 4 h at pH 5.5. Temperature (39°C), diet (97 g/d of a 60 to 40 forage to concentrate diet; 16.6% CP, 30.0% NDF) and solid (5%/h) and liquid (10%/h) dilution rates were similar. Treatments were a constant pH 6.4 (CTR); 1 period of 4 h at pH 5.5 (P4); 1 period of 8 h at pH 5.5 (P8); 2 periods of 4 h at pH 5.5 (P2x4). Data were analyzed using PROC GLM of SAS (1996) and differences declared at P<0.05. Treatment P8 reduced DM (52.7 vs 61.9 %), NDF (20.5 vs 31.8 %) and CP (38.1 vs 52.8%) degradation, ammonia N concentration (5.7 vs 10.4 mg/dL) and acetate to propionate ratio (2.2 vs 3.8) compared with CTR. There were no differences in these estimates between P8, P4 and P2x4. The ADF digestion (33.5 vs 38.7 and 40.7%) and branch-chained volatile fatty acids proportion (1.0 vs 1.75 and 2.8 mol/100mol) were lower

in P8 compared with P4 and CTR, respectively, but there were no differences in these estimates between P4 and CTR. There were no differences between the treatments in OM digestion (47.9%), total VFA concentration (95.3 mM), the flow of total (3.20 g/d), bacterial (1.17 g/d) and nonammonia (3.00 g/d) N and in the efficiency of microbial protein synthesis (44.8 gN/kg OM truly digested). Results suggest that the negative effects of pH 5.5 are dependent of the total time that ruminal pH is suboptimal and are not reduced by splitting it into two cycles.

Key Words: pH, Acidosis, Rumen fermentation

M250 Effect of the magnitude of the decrease of rumen pH and its fluctuations on rumen microbial fermentation. M. Cerrato, S. Calsamiglia*, and A. Ferret, *Universitat Autonoma de Barcelona*, *Bellaterra, Spain*.

Ruminal pH below 6.0 has negative effects on rumen microbial fermentation. However, previous studies indicate that ruminal bacteria may resist short periods (4h) of pH below 6.0. It is not clear if the magnitude of the decrease is important. Eight 1325-ml dual flow continuous culture fermenters were used in two consecutive periods with similar temperature (39°C), diet (97 g/d of a 60 to 40 forage to concentrate diet; 19.2% CP, 30.0% NDF) and solid (5%/h) and liquid (10%/h) dilution rates to determine the effect of the magnitude of the decrease of rumen pH and its fluctuations on rumen bacterial fermentation. Treatments were a constant pH 6.4 (CTR); 1 period of 4 h at pH 5.6 (L); 1 period of 4 h at pH 5.1 (VL); 1 period of 2 h at pH 5.1 and 2 h at 7.1 (HL). Data were analyzed using PROC GLM of SAS (1996) and differences declared at $P<0.05$. Dry matter (62.5% vs 75.1%) and NDF (20.8% vs 33.8%) digestion were lower in VL compared with CTR, but there were no differences compared with HL or between CTR and L. Treatment VL reduced acetate proportion (54.0 vs 60.8 and 60.4 mol/100 mol), and increased propionate proportion (31.5 vs 20.9 and 17.7 mol/100 mol) and ammonia N concentration (9.6 vs 11.6 and 13.3 mg/100 mL) compared with L and CTR, respectively. There were no differences in these estimates between VL vs HL, and between CTR vs L. The branch-chained volatile fatty acids proportion (mol/100 mol) was lower in VL (1.06) compared to L (2.86) and CTR (4.19), but there were no differences compared with HL. There were no differences between treatments in the flow of total (3.38 g/d), bacterial (1.20 g/d) and nonammonia (3.06 g/d) N, and in the efficiency of microbial protein synthesis (27.4 gN/kg OM truly digested). Dietary N flow was higher (2.04 vs 1.66 g/d) and CP degradation lower (25.1 vs 38.9 %) in VL compared with CTR. Results indicate that bacteria are able to resist short periods (4 h) at suboptimal (5.6) pH, but the effects were negative if pH fell at 5,1 for 2 or 4h.

Key Words: pH, Acidosis, Rumen fermentation

M251 Conservation of fermentation energy and control of the VFA profile in the rumen. E. M. Ungerfeld* and R. A. Kohn, *University of Maryland*, *College Park*.

The objective of this analysis was to compare energy conservation as ATP in the different volatile fatty acid (VFA) pathways of ruminal fermentation and relate it to the VFA profile produced. It is well understood through stoichiometrical calculations and empirical evidence that a decrease in the acetate to propionate ratio results in less methane (CH_4) being produced per unit of fermented hexose. Because CH_4 is not an energy source for ruminants, a decrease in the acetate to propionate ratio results in an improvement of energy conservation in end products of fermentation utilizable by the host animal. However, there is uncertainty as to how VFA pathways compare regarding capture of fermentation energy in high-energy phosphate bonds, which are necessary for the production of microbial protein. The present analysis uses basic knowledge of biochemical pathways and thermodynamics to examine the utilization of free energy in the main VFA pathways, and identifies steps where research is needed for a more complete characterization of energetic efficiency. Theoretical lower and upper limits for moles of ATP generated per mole of hexose fermented could be 4.5 to 6 for acetate, 0.3 to 5 for propionate and 3.25 to 4.5 for butyrate. The ample variation in ATP generation in the propionate pathway is due to the partition between the randomizing and non-randomizing pathways, the utilization of ATP-equivalents in oxaloacetate (or malate) formation, and the stoichiometry of ATP generation by electron transport-linked phosphorylation during fumarate reduction. These limits may be narrower because ATP generation in different reactions within a pathway is likely interdependent. Changes in ATP generation in a pathway not only affect the availability of energy for microbial protein production but can shift the VFA profile by altering VFA equilibrium. Ultimately, the nature of thermodynamic control of the VFA profile determines that a decrease in ATP generation of a pathway should make it thermodynamically more favorable and shift more carbon in that direction until a new equilibrium is reached.

Key Words: Rumen, Fermentation, ATP

M252 Buffer pH and clarified ruminal liquid effects on stability of an exogenous fibrolytic enzyme. E. Meraz-Romero[1], S. S. González*[1], G. Mendoza-Martínez[2], O. Loera-Corral[3], M. Meneses-Mayo[1], M. Cobos-Peralta[1], and J. Avellaneda-Cevallos[4], [1]*Colegio de Postgraduados*, *Montecillo, Edo. de México, México*, [2]*UAM-Xochimilco*, *México D.F., México*, [3]*UAM-Iztapalapa*, *México D.F., México*, [4]*Universidad Técnica Estatal de Quevedo*, *Quevedo, Ecuador*.

The objective of this trial was to evaluate the activities of xylanase, cellulase and laccase (phenoloxidoreductase), from an exogenous fibrolytic enzyme (Fibrozyme, ALLTECH Inc.; enzyme), under a buffer or anaerobic culture with clarified ruminal liquid. Treatments were buffer pH 6.0, buffer pH 7.0, clarified ruminal liquid pH 6.5. The experimental design was completely randomized, data was analyzed using SAS and treatment means were compared utilizing Tukey; besides, a first order kinetic model was fitted to the data. The enzyme showed xylanase (292 ± 0.02 IU g^{-1}) and cellulase (36 ± 0.007 IU g^{-1}) activities, but laccase activity was not detected. For buffer pH 6.0, cellulase was more stable than xylanase and both showed activities during 46 h. Rate constants (k) for enzymatic inactivation were -0.054 and 0.008 h^{-1} for xylanase and cellulase, whereas half time values (t½) were 12.8 and 87.7 h, respectively. For buffer pH 7.0, cellulase activity was longer than xylanase which showed no activity at 32 h; k values were -0.07 and 0.009 h^{-1} and t½ were 9.99 and 77.0 h for xylanase and cellulase, respectively. Under anaerobic culture with clarified ruminal liquid, cellulase activity was longer than xylanase which showed activity during 4 h (k = -1.815 and 0.009 h^{-1}; t½ = 0.38 and 26.87 h, respectively). According to these results, both buffer pH and ruminal bacteria enzymes seem to affect stability of an exogenous fibrolytic enzyme.

Key Words: Exogenous fibrolytic enzyme, Enzymatic stability, Xylanase

M253 *In vitro* fermentative characteristics of tropical grasses supplemented with tree/shrub forage. E. González*[1,2], O. Cáceres[1], E. Albanell[2], G. Caja[2], and J. Arece[1], [1]*Estación Experimental de Pastos y Forrajes*, *Matanzas, Cuba*, [2]*Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*.

In vitro fermentation of current forage diets under tropical agroforestry systems were evaluated. Two common tropical grasses (*Panicum maximum* cv. likoni, PM; *Pennisetum purpureum* cv. CT-115, PP) were supplemented with four tree/shrub forage (*Leucaena leucocephala*, LL; *Gliricidia sepium*, GS; *Trichantera gigantea*, TG; *Morus alba*, MA). Representative forage samples were randomly selected in an agroforestry experimental field of Matanzas, Cuba (22°48′N, 81°2′W; 60 masl). The *in vitro* gas production (IVGP) technique of Theodorou *et al. (1994)* was used in two consecutive incubation series (96h), using rumen inoculum from two ruminally cannulated *Holstein Frisian* dairy cows, previously adapted. A factorial arrangement design (2×4) was used to evaluate combination of grasses (n = 2) and trees or shrubs forage (n = 4) as supplements (ratio 60:40 of grass:supplement). Treatments were: 1) PM-LL; 2) PM-GS; 3) PM-TG; 4) PM-MA; 5) PP-LL; 6) PP-GS; 7) PP-TG; 8) PP-MA. Fermentation profiles of grasses (PP; PM; without supplement) were considered as ″controls″. The IVGP, fermentative parameters (*a*; *b*; *c*; ″*lag time*″, *T*), and *in vitro* disappearance of dry matter (IVDDM) and neutral detergent fiber (IVDNDF) were determined. Gas production (GP) data were fitted to the France *et al.* (1993) equation. There were significant differences ($P< 0.05$) in fermentative patterns among diets. The IVGP (PP > PM), and IVDDM or IVDNDF, were higher and lower ($P< 0.05$), respectively, for sole grasses compared to their respective combined diets. Except diet PM-GS (highest IVGP values), IVGP was lower ($P< 0.05$) in supplemented diets when compared to control (PM) despite its *T* value (2.18), degradation rates (μ) or IVDMD (559.4 g kg^{-1}DM). Supplement TG resulted with the lowest fermentative values for both grasses.

Table 1. Adjusted parameters and in vitro disappearance of DM and NDF

Diet	A	b	c	T	μ48	IVDMD	IVNDFD
PM	200	0.019	0.09	2.18	0.377	559	481
PM+MA	176	0.020	0.20	1.89	0.754	664	483
PM+TG	150	0.050	-0.01	1.68	0.160	622	554
PM+LL	172	0.001	0.23	2.07	0.815	607	454
PM+GS	275	-0.005	0.23	1.99	0.777	599	464
PP	212	0.024	0.09	1.81	0.383	629	560
PP+MA	170	0.040	0.09	1.46	0.447	681	533
PP+TG	157	0.046	0.05	1.76	0.330	646	584
PP+LL	171	0.021	0.14	2.13	0.541	621	619
PP+GS	163	0.010	0.24	2.21	0.857	618	634

A:potential GP at 96h (ml/800mg DM); *b*, *c*: rate constants (h^{-1} and $h^{-1/2}$, respectively); T:*lag time*; μ: degradation rate (h^{-1}) at 48h

Key Words: Tropic forage, Grass, Tree fodder

M254 Microbial yield and fiber digestion from sucrose, starch, pectin and bermudagrass fiber fermentation. L. Holtshausen*[1] and M. B. Hall[2], [1]*Stellenbosch University*, *Stellenbosch, South Africa*, [2]*USDA-ARS*, *Madison, WI*.

Effect of nonfiber carbohydrates (NFC: sucrose, starch and pectin) fermented with isolated bermudagrass neutral detergent residue (iNDF) on microbial product yield and neutral detergent fiber (NDF) digestion was examined. iNDF with three concentrations of individual NFC (~40 to 120 hexose equivalents; HE) were fermented in six 24 h anaerobic batch culture fermentations with Goering & Van Soest medium and rumen inoculum in 50 ml tubes fitted with gas release valves. Fermentation tubes were destructively sampled every 4 hours and analyzed for microbial glycogen (GLY), organic acids, microbial crude protein (MCP), and residual NDF. Differences among NFC treatments at their maxima with NFC expressed on an HE basis were evaluated by heterogeneity of regression analysis. Significance was declared at $P < 0.05$. The linear increase in maximum GLY per NFC HE was similar for sucrose and pectin, but their intercept values were numerically different and that for sucrose dwarfed the calculated increase per HE. Yield of total volatile fatty acids (VFA) per NFC HE at 24 h was similar among individual NFC. As NFC HE increased, the proportion of residual NDF at 24 h differed among pectin (less digestion), starch (almost no difference) and sucrose (more digestion). The pattern of MCP yield with increasing NFC HE was quadratic and similar among NFC. The NFC differed in fermentation product yield and effects on NDF fermentation. It is not warranted to regard the various NFC as a uniform entity in ruminant nutrition.

Table 1. Regression values by NFC for maximum yield of product. x = HE

Max. GLY (mg)		VFA at 24 h (acetate + propionate + butyrate)	
Starch	-	Starch	$15.24 + 0.38x + 8.80E\text{-}04x^2$
Sucrose	$2.37 + 0.01x$	Sucrose	$25.83 - 0.05x + 2.09E\text{-}03x^2$
Pectin	$-0.19 + 0.03x$	Pectin	$17.57 + 0.22x + 8.25E\text{-}04x^2$
24 h NDF (% of original NDF)		Max. MCP (mg)	
Starch	$60.55 + 4.54E\text{-}03x$	Starch	$3.56 + 0.27x + 9.00E\text{-}04x^2$
Sucrose	$61.29 - 0.01x$	Sucrose	$3.97 + 0.21x + 7.10E\text{-}04x^2$
Pectin	$62.89 + 0.03x$	Pectin	$6.30 + 0.19x + 1.70E\text{-}04x^2$

Key Words: Nonfiber carbohydrates, Microbial product yield, Neutral detergent residue

M255 The relationship between feed acidogenic value and in vitro ruminal pH changes. B. Rustomo*, J. P. Cant, M. P. Fan, T. F. Duffield, N. E. Odongo, and B. W. McBride, *University of Guelph*, *Guelph, Ontario, Canada*.

The increasing use of ruminally fermentable carbohydrate in diets is considered the critical link between nutrition and sub-acute ruminal acidosis in dairy cows. However, starch or non fibre carbohydrate (NFC) content of the diet is not a satisfactory predictor of rumen pH changes due to the high variation in the rate and extent of starch or NFC fermentation in the rumen. A simple in vitro technique was used to assess acidogenic value (AV) of feedstuffs. This technique is based on the dissolution of Ca from $CaCO_3$ after 24 and 48 h incubation of feedstuffs in rumen liquor. A series of feeds, ranging from energy, fiber and protein sources were evaluated. Ruminal fluid pH changes in the incubation medium were also measured at the end of 24 and 48 h incubation. The relationship between AV and rumen fluid pH and AV and feed chemical composition was determined using regression analysis. Comparison between 24 and 48 h incubations were conducted using paired t-test. Non fiber carbohydrate-rich feedstuffs had the highest AV; forage sources had intermediate AV and high-protein feedstuffs had the lowest AV. There were no differences in apparent AV and rumen fluid pH changes between 24 and 48 h incubation, suggesting a rapid initial fermentation rate and little or no further

fermentation after 24 h. Thus, the 24 h AV measurements might be acceptable to qualitatively rank feedstuffs based on the estimated accumulated acid-load during fermentation. The rate of rumen fluid pH changes showed similar patterns to AV in ranking feedstuffs. Energy sources showed the highest rumen fluid pH decrease; fiber sources were intermediate and protein sources were lowest in rumen fluid pH change after 24 h of incubation suggesting that NFC-rich feedstuffs had the lowest rumen buffering capacity compared to fiber and protein rich feedstuffs. Rumen fluid pH changes after 24 h of incubation had a stronger relationships with AV for all feedstuffs ($R^2 = 0.74$) compared to starch ($R^2 = 0.35$) and NFC ($R^2 = 0.56$). The best predictors of feed AV were NFC and ADF ($R^2 = 0.81$). However, further studies are needed to examine the effect of feed AV on in vivo ruminal pH changes in dairy cows.

Key Words: Acidogenic value, In vitro, Ruminal pH

Swine Species

M256 Effects of conjugated linoleic acid (CLA) on sow and litter performance. R. Patterson*, M. L Connor, C. M. Nyachoti, and D. O. Krause, *University of Manitoba*, *Winnipeg, Canada*.

The potential for CLA supplementation to improve physiological benefits affecting sow and litter performance was evaluated using 14 Cotswold sows in a completely randomized design with a 2x2 factorial arrangement of treatments. Diet (0% or 2% CLA) and parity (IM=Immature or M=Mature) corresponded to the following: 1) 0%IM n = 3; 2) 0%M n=3; 3) 2%IM n=4; 4) 2%M n=4. Treatment diets were fed as gestation rations from d 85 through d 110 and as lactation rations from d 110 until weaning. On gestation d 85, 105, and 112 and lactation d 1, 3 and 17 plus 4 d post-weaning, sow BW, back fat depths and condition scores were taken. Piglets were weighed on d 1, 3 and 17. Parity effects ($P < 0.01$) were observed for sow BW at each period. However, parity only affected ($P < 0.05$) back fat depth at d 17 of lactation and 4 d post-weaning and condition scores on d 1 of lactation and 4 d post-weaning. Diet did not affect ($P > 0.05$) piglet weaning weights. In a follow-up experiment, 78 of these piglets were weaned at 17±1 d and randomly arranged in a 2x2 factorial based on lactation and weaning diets as follows: 1) 0:0 (0%CLA sow: 0%CLA piglet); 2) 0:2 (0%CLA sow: 2%CLA piglet); 3) 2:0 (2%CLA sow: 0%CLA piglet); 4) 2:2 (2%CLA sow: 2%CLA piglet). Piglets weaned from 2% sows had greater feed to gain ratios ($P < 0.035$) and tended ($P < 0.058$) to have higher ADFI compared to those weaned from 0% sows by d 28, but diet did not affect piglet performance by d 36. On d 28 piglets were given an oral *E.coli* K88+ challenge. Fecal scores were taken at 8, 24, 48 and 56 h post-challenge. Piglets weaned from 2% CLA sows had less severe scours ($P < 0.05$) at all sampling periods and a dietary interaction effect ($P < 0.05$) was observed at 56 hours. Weaning diets reduced ($P < 0.1$) scour incidence only at 48 hours. It is thus apparent that provision of CLA during gestation and lactation improves litter performance. Further work is intended to determine the immunological/physiological mechanisms underpinning these improvements.

Key Words: CLA, Sows, Piglets

M257 The effects of feeding grains naturally-contaminated with Fusarium mycotoxins to gestating and lactating sows on metabolism and reproduction and the efficacy of a polymeric glucomannan adsorbent in preventing those effects. G. Díaz-Llano* and T. K. Smith, *University of Guelph*, *Ontario, Canada*.

The feeding to swine of feedstuffs naturally-contaminated with *Fusarium* mycotoxins can reduce feed intake, and hepatic protein synthesis. An experiment was conducted to investigate the effects of feeding grains naturally-contaminated with *Fusarium* mycotoxins on reproductive performance, serum chemistry, ADFI and ADG of first parturition sows during late gestation and lactation, and to test the efficacy of a polymeric glucomannan mycotoxin adsorbent (GMA) in preventing these effects. A completely randomised block design, 36 sows, 12 sows per treatment was used in the experiment. Diets consisted of corn, wheat and soybean meal and were fed from 91 days of gestation up to the weaning on d 21 post farrowing. The diets were: (1) control (C), (2) contaminated grains (CG) (5.5 ppm DON + 0.5 ppm 15-acetyl DON + 0.3 ppm zearalenone), and (3) contaminated grains + GMA. Means were compared using Tukey's test and significance was declared at $P < 0.05$. During gestation, *Fusarium* mycotoxins did not reduce ADFI. The ADG was reduced in sows fed CG ($P = 0.03$) but not in sows fed CG + GMA. Growth to feed ratio was also reduced in sows fed CG compared to C ($P = 0.047$), but not in sows fed CG + GMA. Stillbirth rate was increased in piglets born from sows fed CG compared to piglets born from sows fed CG + GMA ($P = 0.03$). During lactation, ADFI of sows fed CG and CG + GMA was reduced compared to C ($P < 0.001$). Higher body weight losses were seen in sows fed CG compared to controls ($P = 0.007$). Total serum protein concentrations were lower for sows fed CG compared to sows fed CG + GMA ($P = 0.045$). Weaning to estrus interval tended to increase in sows fed CG and CG + GMA compared to controls ($P = 0.094$). It was concluded that the feeding of grains naturally-contaminated with *Fusarium* mycotoxins reduces the reproductive efficiency of gestating and lactating sows. The feeding of GMA can prevent much of this inefficiency.

Key Words: Sows, *Fusarium*, Growth

M258 Effects of exogenous porcine somatotropin and transportation on physiological parameters in weaned pigs. C. J. Kojima*, P. E. Roberson, M. P. Roberts, T. Sun, and H. G. Kattesh, *University of Tennessee*, *Knoxville*.

An experiment was performed to examine effects of exogenous porcine somatotropin (S) on physiological measures of health and well-being in weaned pigs with or without subsequent transport (T). We hypothesized that S may abrogate stress-related decreases in health and well-being in recently weaned and transported pigs. On d 17 of lactation pigs were were weighed and assigned to treatment groups (n=8/group): NS-NT (vehicle injection, no transport), S-NT (S injection, no transport), NS-T (vehicle injection, transport at weaning), and S-T (S injection, transport at weaning). Upon allocation, all pigs received daily intramuscular injections containing S (0.5 mg/kg) or vehicle for 5 d. On d 21, a blood sample was drawn immediately prior to injection (0800 h). At 1200 h on d 21, pigs were weighed and blood was collected. Pigs in the NT groups were then weaned into mixed nursery pens while pigs in the T groups were mixed and transported by truck for 3 h before being brought back to the nursery. All weaned pigs were fed a standard nursery diet. Blood samples and body weights were taken on d 22, 29 and 37. Data were analyzed by a mixed model procedure with a factorial design and repeated measures. Transport resulted in lower