

genetic decision-making deeper into the pork chain will call for extraordinary skill and experience. GMO will continue to be examined as an option while society debates the risks and benefits. Driving the revolution in healthy genetic improvement efforts are the following factors: consumers are likely to want from their food more health-enhancing qualities, safety, convenience and value; industry integration of linked sectors will call for genetic decision-makers to optimize weightings on many measures throughout the pork chain, from reproduction to food processing; confidence in the food supply will necessitate traceability at low cost; selection decisions will increasingly need to factor in any interactions between genotype and environments, intrinsic and extrinsic; technology will continue to refine functions in all sectors of the pork chain and offer more control; DNA testing costs per data point will decrease substantially; accrued knowledge about genes and their effects will increase geometrically; capabilities in information processing will continue to increase dramatically; breeding decisions will require close integration of input from several disciplines.

**Key Words:** Swine Industry, Healthy Genetic Improvement, Technology

#### 48 Evaluating the functional quality of pork. Eric Berg\*, *University of Missouri-Columbia*.

Pork quality can be characterized by level of freshness, wholesomeness, grade, color (appearance), eating satisfaction or processing attributes (functionality). Many factors influence pork quality characteristics: 1)

### Graduate Paper Competition CSAS Graduate Student Competition

#### 49 Variation in phytate content in Ontario soybean samples. S.D. Leech\* and C.F.M. de Lange, *University of Guelph, Guelph, Ontario*.

Characterization of phosphorus (P) content and phosphorus availability in feed ingredients is critical for addressing feeding costs and impacts of animal production on the environment. In feedstuffs for monogastric animals, phosphorus availability is inversely related to the proportion of phosphorus present in the phytate form (% phytate P). The objectives of this study were to identify variation in total P and phytate content among Ontario soybean samples cultivated under typical management conditions, and to explore rapid indicators of phytate content. A total of 108 samples were analyzed: 58 samples representing 13 varieties and 13 growing locations in 1999; 50 samples representing 12 varieties and 12 growing locations in 2000. Nine subsets of samples from varieties grown at various locations allowed an assessment of the effects of location, variety and year on total P and phytate content. Analysis for P and phytate contents were conducted according to AOAC procedures and checked for repeatability and accuracy using potassium phosphate and sodium phytate standards. Total P content (%) averaged 0.55 (SD 0.08) in 1999 and 0.61 (SD 0.09) in 2000; phytate content (%) averaged 1.07 (SD 0.20) in 1999 and 1.27 (SD 0.26) in 2000; % phytate P (%) averaged 54.7 (SD 4.6) in 1999 and 57.9 (SD 5.1) in 2000. Location and year effects were observed in the majority of sample subsets for total P and phytate content ( $P < 0.05$ ), but not for % phytate P. Variety effects on these three measures were absent ( $P > 0.05$ ) in most sample subsets. Location and variety effects explained a large proportion of the variation in total P ( $R^2 > 0.75$ ), phytate content ( $R^2 > 0.72$ ) and % phytate P ( $R^2 > 0.44$ ). A strong correlation existed between total P and phytate content ( $R^2 = 0.87$ ;  $SEE = 0.09$ ). Considerable variation in total P and phytate content was observed among Ontario soybean samples with differences largely attributable to location effects.

**Key Words:** Phosphorus availability, Phytate, Soybeans, Monogastric animals

#### 50 Effect of supplementing corn-soybean-based diet with microbial phytase and organic acid in young pigs. F. O. Omogbenigun\*, B. A. Slominski, and C. M. Nyachoti, *University of Manitoba, Winnipeg, MB*.

An in vitro assay and a 4-wk growth trial were conducted using 96 pigs weaned at 181 d to study the effect of microbial phytase (MP) and organic acid (OA) addition on nutrient digestion and growth performance. Four diets; positive control (formulated according to NRC, 1998; D1),

genetics; 2) nutrition; 3) growth promotants 4) pre-slaughter handling and transportation; 5) immobilization (stunning procedure); 6) dehairing; 7) post-slaughter handling; and 8) packaging and storage. Early postmortem measurement of pH and temperature are common measurements taken to identify potential meat quality problems, yet these easily obtained measures do not quantify the specific factors that affect pork functionality (use in further processed or value-added products) and (or) consumer acceptance (retail marketability). The CIE L\*, a\*, b\* scale was designed to represent the human perception of color and has been used to evaluate fresh pork color and incorporated into computerized vision analysis systems that identify and sort acceptable and unacceptable colored lean. Early fiber-optic probe (FOP) instruments developed to predict the functional component of pork (water holding capacity; WHC) were totally dependent on the marginal relationship between fresh pork color and WHC. More recently, FOP probes operating in the near infrared (NIR) region of the color spectra have been developed to quantify glycolytic potential or collagen content of fresh pork. Due to the large number of factors that can influence pork quality and the marginal predictive ability of the more commonly used predictors (pH and color), development or identification of electronic equipment used to measure pork quality must account for, or attempt to quantify, functional meat quality from basic meat biochemical, physiological, molecular, and (or) structural factors that ultimately influence the appeal of pork.

**Key Words:** pork, quality, electronic equipment

negative control (D1 without inorganic phosphorus [P]; D2), D2 + phytase (500U/kg; D3), and D3 + OA (D4) were used. In the in vitro assay, diet samples were incubated under simulated gut conditions to determine phytate hydrolysis. Addition of MP increased ( $P=0.003$ ) phytate hydrolysis by 54.5% over D1; this was further increased by 2.9% by adding OA. In the growth trial, each diet was randomly assigned to six replicate pens each with 4 pigs balanced for initial BW and sex. ADFI, ADG, and FCE were determined weekly. Six pigs per treatment were killed at the end of wk 4 to obtain ileal digesta, and the 3rd metatarsal bone from the hind right leg for nutrient digestibility and bone ash measurements, respectively. ADFI, ADG and FCE were similar among diets ( $P=0.79$ ), although ADG was 6.5% higher in pigs fed D4 compared to D1. Pigs fed D3 and D4 had a higher ( $P=0.003$ ) bone ash content than D1 fed pigs. Apparent ileal DM and CP digestibilities were similar ( $P > 0.10$ ) among diets and averaged 80.7 and 79.4%, respectively. Of all amino acids (AA), only apparent ileal digestibility of isoleucine, histidine and aspartic acid were increased ( $P < 0.05$ ) by MP and OA addition. Digestibilities of other AA were only numerically improved by MP and OA addition and that of essential AA averaged 79.4, 77.7, 80.1 and 81.6% for D1, D2, D3, and D4, respectively. Apparent ileal P digestibility was increased ( $P=0.0001$ ) and the amount of P excreted reduced ( $P=0.03$ ) by 19.9% due to MP + OA addition compared to D1. In conclusion, addition of MP and OA to pig starter diets improved P digestion and utilization and may also improve dietary AA utilization.

**Key Words:** Pigs, Microbial phytase, Organic acid

#### 51 Utilization of apparent ileal digestible threonine intake for body protein deposition in the pig appears related to endogenous gut protein losses and microbial fermentation in the gut. C.L. Zhu\*, Y. Yin, and C.F.M. de Lange, *University of Guelph, Guelph, ON, Canada*.

Previous studies showed that intake of soluble fiber (pectin) reduced utilization of apparent ileal digestible threonine (THR) intake for THR retention in body protein in pigs (from .87 to .79 at 0 and 120 g/kg diet pectin, respectively), while intake of insoluble fiber (cellulose) had little effect. The objective of this study was to relate THR utilization to aspects of digestion. Five barrows (16 to 46 kg BW), fitted with a simple T-cannula at the terminal ileum, were fed one of 5 experimental diets at 2.6 times maintenance energy requirements according to a 5 x 5 Latin square design. Pigs were adjusted to diets for 8 days prior to sampling feces and ileal digesta. Soybean and cornstarch-based diets were formulated with 0, 40, 80, 120 g/kg pectin or 80 g/kg cellulose, respectively, replacing cornstarch. At the distal ileum, flow (all in g/kg DM intake)

increased linearly ( $P < .01$ ) with increasing diet pectin level for DM (133 to 218, SE 8), total THR (1.21 to 1.75, SE .09), endogenous THR (.68 to 1.54, SE .1; determined using the homo-arginine technique), NDF plus pectin (30.7 to 134.7, SE 5.2) and diaminopimelic acid (DAPA) (.097 to .203, SE .023). Intake of fecal digestible NDF plus pectin (71.4 to 192.7, SE 0.3) and fecal DAPA flow (.063 to .112, SE .008) increased linearly ( $P < .01$ ) with diet pectin level. For the cellulose diet these values were: flows of ileal DM 212, total THR 1.30, endogenous THR 1.06, NDF plus pectin 75.35, DAPA .124; fecal digestible intake of NDF plus pectin 108.5, fecal DAPA flow .137. Across diets utilization of apparent ileal digestible THR was related most closely to ileal flow of endogenous THR ( $R^2 = .90$ ) and NDF plus pectin ( $R^2 = .95$ ), or to fecal digestible NDF plus pectin intake ( $R^2 = .90$ ). Utilization of apparent ileal digestible THR intake appears related to both endogenous THR losses and microbial fermentation in the gut.

**Key Words:** Pigs, Threonine, Digestion

**52 The optimal dietary level of vitamin B12 in gestating gilts.** F. Simard<sup>1</sup>, F. Guay<sup>1</sup>, J.P. Laforest<sup>1</sup>, A. Giguere<sup>2</sup>, C.L. Girard<sup>2</sup>, and J. J. Matte<sup>2</sup>, <sup>1</sup>Universite Laval, Quebec, Qc, Canada, <sup>2</sup>Agriculture and Agri-Food Canada, Lennoxville, Qc, Canada.

Thirty-eight nulliparous Large-White x Landrace sows were randomly assigned to 5 dietary levels of vitamin B12 (B12) at 0, 20, 100, 200, and 400 ppb to evaluate, during gestation, the optimal level of dietary B12 on some aspects of B12 and homocysteine (Hcy) metabolisms as well as on reproductive performance. Hcy is a detrimental intermediate metabolite of the B12-dependent remethylation pathway of methionine. Treatments were applied for 2 estrous cycles before mating and throughout gestation. For all sows, the lactation diet contained 25 ppb of B12. Blood samples were collected from each sow, 7 times from initiation of treatments up to parturition, and thereafter, 4 times up to weaning (21 d). Liver samples were collected after slaughter at weaning. During gestation, plasma B12 increased (dietary B12 quadratic,  $P < 0.01$ ) with the levels of dietary B12. Average values ( $\pm$  SE) (pg/mL) were  $71.8 \pm 3.7$ ,  $129.8 \pm 4.9$ ,  $171.4 \pm 6.3$ ,  $238.4 \pm 6.0$ , and  $228.5 \pm 8.5$  for 0, 20, 100, 200 and 400 ppb of dietary B12. The maximal plasma B12 was estimated to be reached with 298 ppb of dietary B12 ( $R^2 = 0.96$ ). These effects of gestation treatments persisted during lactation for plasma B12 (dietary B12 linear,  $P < 0.01$ ) as well as for liver B12 at weaning (dietary B12 quadratic,  $P < 0.04$ ). During gestation, plasma Hcy decreased (dietary B12 quadratic,  $P < 0.01$ ) with increasing levels of dietary B12. Litter size at parturition and weaning were influenced (dietary B12 quartic,  $P < 0.06$  and  $P < 0.02$ , respectively) by dietary B12 during gestation. Litter size at parturition was  $12.4 \pm 0.5$  for 100, 200 and 400 ppb vs  $11.1 \pm 0.8$  for 0 and 20 ppb; the corresponding values at weaning were  $10.9 \pm 0.2$  and  $9.5 \pm 0.7$ . Treatment effects on litter weight at parturition were similar (dietary B12 quartic,  $P < 0.03$ ) to those on litter size,  $17.4 \pm 0.6$  kg for 100, 200 and 400 ppb vs  $15.3 \pm 1.0$  kg for 0 and 20 ppb. In conclusion, the dietary level of B12 required to maximize B12 status and minimize Hcy appears much higher (close to 300 ppb) than the level recommended by NRC (1998) of 15 ppb. The relevance of such high levels of dietary B12 for reproductive performance needs to be confirmed with a larger number of animals.

**Key Words:** Vitamin B12, Gestation, Gilts

**53 Low protein diets can be fed to lactating sows with few adverse effects.** D. J. McMillan\*, S. Möhn, and R. O. Ball, *University of Alberta, Edmonton, Canada.*

The goal of feeding low protein amino acid (AA) supplemented diets is to reduce nitrogen excretion without reducing sow performance. We studied the effect of low protein AA supplemented diets on sow performance and nitrogen excretion for two consecutive parities. Eighty 2nd parity sows were fed either a conventional diet (HP) during lactation containing 19.3% CP or an isoenergetic diet containing 16.3% CP with added lysine and threonine (LP). Both diets met or exceeded all other nutrient requirements (NRC, 1998). Body weight of 2nd parity sows at farrowing was similar (206.8 kg, LP vs. 208.9 kg, HP). LP sows lost more weight from farrowing to weaning ( $p = 0.004$ ) at 21 d. Sows receiving the LP diet consumed 500 g less per day during lactation than sows fed HP. Number of piglets born (11.22, LP vs. 11.20, HP), and weaned (10.42, LP vs. 10.98, HP) were not significantly different. Average piglet weight at birth (1.37 kg, LP vs. 1.42 kg, HP) and weaning (6.22 kg, LP, vs. 6.38 kg, HP) were also not different. Wean to estrus

interval of 5.42 days (SEM 0.54) for LP sows was not different from HP sows (4.59 days, SEM 0.10). Third parity body weight of LP sows was slightly lower at farrowing (231.12 kg vs. 237.15 kg) but not significantly. Weight loss during the 3rd lactation was similar for both groups (4.94 kg, LP vs. 4.09 kg, HP). Feed intake for LP sows was 300 g per day lower than HP sows. Number of piglets born (12.18, LP vs. 12.32, HP), and average weight at birth and weaning were not different ( $p > 0.1$ ). Number of piglets weaned was slightly different, with LP sows weaning 0.75 piglets less per sow ( $p = 0.05$ ). Wean to estrus interval was not different (4.66 days, LP vs. 4.75 days, HP). Sow backfat measurements were not different at any stage. Calculated urinary nitrogen excretion was not different for 2 parities; LP sows excreted 30% less nitrogen during lactation than HP sows ( $p < 0.01$ ). These results show that low protein diets can support similar performance of sows during lactation while significantly reducing nitrogen excretion.

**Key Words:** Low Protein, Sow, Lactation

**54 Effects of sulphur amino acid (SAA) ratios and concentrations on the performance of weaned piglets.** R.D. Harte\*, A.K. Shoveller, R.F.P Bertolo, and R.O Ball, <sup>1</sup>University of Alberta.

Previously, we reported that the gut utilizes 35% of dietary methionine (MET). The objective of this study was to investigate the interaction between ratio and total sulphur amino acid (TSAA) intake on growth performance and intestinal function and development in early-weaned piglets. 42, 10-d old piglets (3.7 kg SD=0.37) were weaned from the sow and housed in pairs for d 1-3. On d 4, piglets that had re-gained their weaning weight (3.7 kg SD=0.39) were randomly allocated to 1 of 7 test diets: diet 1(25% of MET requirement:25 CYS), diet 2(25:50), diet 3(50:25), diet 4 (50:50), diet 5(50:100), diet 6(100:50) and diet 7(100:100). The piglets received test diet for 7 d and daily feed intake, urinary nitrogen and body weights were recorded. On d 11, piglets were sacrificed and tissues were collected. The intake of excess CYS relative to MET acted to decrease piglet performance, both when MET intake was below requirement and when it was adequate. The intake of excess TSAA also decreased piglet performance. Piglet maximal performance was achieved when 100% TSAA requirement was fed at a 1:1 ratio of MET: CYS. Preliminary data indicates that both TSAA ratio and intake may influence some intestinal parameters.

Ratio	25: 25	25: 50	50: 25	50: 50	50: 100	100: 50	100: 100	p		
%TSAA	50	75	75	100	150	150	200	diet	ratio	TSAA
ADG (g)	97	117	186	194	163	185	149	.001	.04	.002
ADFI (g)	140	127	191	197	174	184	181	.004	.02	.06
F: G	1.47	1.10	1.06	1.01	1.02	1.03	1.03	.0001	.85	.0001
NR(%)	70.2	65.5	77.7	84.5	84.1	83.6	78.8	.0001	.26	.0001

**Key Words:** Sulphur Amino Acids, Weaned Pigs, Growth

**55 Fecal excretion of major odor-causing and acidifying compounds in response to dietary supplementation of chicory inulin extract in pigs.** T. C. Rideout and M. Z. Fan, *University of Guelph, Ontario, Canada.*

Fecal excretion of major odor-causing and acidifying volatile compounds in response to dietary supplementation of chicory inulin extract was investigated with six Yorkshire barrows, average initial BW of 30 kg, according to a two-period cross-over design. Two diets, a control diet containing no inulin extract and a treatment diet with 5% inulin extract at the expense of cornstarch, were formulated to contain 16% CP from corn (51%) and soybean meal (29%). Each period lasted for 14 d with 10-d adaptation and 4-d collection of fecal samples. The fecal samples were analyzed for the following four major classes of odor-causing and acidifying compounds: 1) volatile fatty acids (VFA); 2) volatile sulfides measured as hydrogen sulfide (H<sub>2</sub>S) unit; 3) nitrogen-containing compounds including ammonia (NH<sub>3</sub>) and total nitrogen; and 4) phenols and indoles such as *p*-cresol, indole and skatole. Supplementation of chicory inulin at 5% had no effects ( $P > 0.05$ ) on the fecal excretion of VFA, volatile sulfides, NH<sub>3</sub>, *p*-cresol and indole. However, fecal excretion of total nitrogen was increased ( $P < 0.05$ ,  $6139.0 \pm 122.0$  vs  $5103.0 \pm 136.0$  mg/kg DMI) and fecal excretion of skatole was decreased ( $P < 0.05$ ,  $9.07 \pm 1.50$  vs  $18.93 \pm 3.37$  mg/kg DMI) in response to 5% chicory inulin supplementation. In conclusion, dietary supplementation

of 5% chicory inulin to corn and soybean meal diets is not optimal in reducing nitrogen-related odor and environmental pollution, but may be beneficial in minimizing the odorous emission associated with skatole.

**Key Words:** Odor-Causing Compounds, Chicory Inulin, Pigs

### 56 Thirteen polymorphic microsatellite markers for American mink. I.R. Vincent, A. Farid, and C.J. Otieno, *Nova Scotia Agricultural College*.

The objective of this study was to develop microsatellite markers for mink, a species for which fewer than 50 are reported. A mink genomic library was constructed by digesting DNA with Sau3AI and cloning 300 to 800 bp DNA fragments into the BamH I site of the dephosphorylated pGEM-3Z vector. The ligation product was used to transform competent *E. coli*, which were plated out on LB/ampicillin/IPTG/X-gal media and cultured overnight. Recombinant colonies (n=5660) were transferred onto LB/ampicillin media and were lifted onto Hybond-N+ nylon membranes after over-night growth. Colonies were fixed on membranes and were screened with an (AC)15 probe using a chemiluminescence DNA detection kit (ECL) following exposure to X-ray films. DNA inserts in the positively hybridized colonies were amplified by the polymerase chain reaction (PCR) using T7 and SP6 primers, and were bi-directionally sequenced. Thirteen microsatellite loci were detected and primers were designed to amplify the loci by PCR. Genotypes of 86 mink of different color types (black, brown, pastel) as well as wild mink were determined using an ABI 377 automated DNA sequencer. The number of alleles per locus were 4, 6, 7, 7, 8, 8, 8, 8, 9, 9, 9, 11 and 12, indicating that all the loci were highly polymorphic. Allele frequency distributions of the four mink types at the 13 loci were significantly different in 66 of the 78 pairwise comparisons.

**Key Words:** Mink, Microsatellite, Polymorphism

### 57 Persistence of transgenic DNA from Roundup Ready® canola during processing for feed and in vitro ruminal incubation. T.W. Alexander<sup>1,2</sup>, R. Sharma<sup>1</sup>, T.A. McAllister<sup>1</sup>, R.J. Forster<sup>1</sup>, Y. Wang<sup>1</sup>, and W.T. Dixon<sup>2</sup>, <sup>1</sup>*Agriculture and Agri-Food Canada, Lethbridge, AB*, <sup>2</sup>*University of Alberta, Edmonton*.

Glyphosate tolerance in Roundup Ready® canola (RRC) is conferred by the 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) coding region derived from *Agrobacterium tumefaciens* strain CP4. Persistence of this transgene in whole canola seed (WS), cracked seed (CS), meal (M), and diet prepared from the meal (D), and during in vitro ruminal incubation of these substrates, was studied to assess its potential for transfer to ruminal bacteria. The study included RRC and the parental line from which it was derived (PAR). Genomic DNA extracted from WCS exceeded 23 kb. Extracted DNA from M and D was highly fragmented, but did contain 23-kb genomic DNA. A portion of a gene of the Rubisco small subunit family served as a positive control for detection of plant DNA. This fragment (546 bp) was detected in WS, CS, M and D from PAR and RRC by PCR analysis. The complete 1363-bp EPSPS gene was detected in all RRC samples but not PAR. For batch culture, WS, CS, M and D (250 mg) were each incubated in 20 mL buffered ruminal fluid (39°C) for up to 48 h, and DNA was extracted from pellet (1000 × g) and supernatant. The Rubisco gene fragment was detected in all WS and CS pellets (RRC and PAR), but was not amplifiable beyond 8 h in pellets of M or D. Whole EPSPS gene was detected in RRC pellets from WS and CS (to 48 h), from M (at 0, 2, 4 and 8 h) and from D (0 and 2 h only). A 144-bp fragment of the EPSPS gene was detected similarly. All supernatants were negative for Rubisco and both amplicons of EPSPS gene. Bacterial DNA was detectable in all samples. Canola DNA is fragmented during processing for livestock diets, however, high molecular weight DNA and intact genes remain and are detectable in the diets. Lysis of plant cells during digestion exposes plant DNA to the ruminal environment and rapid degradation. Bacterial DNA was amplifiable for 48 h whereas endogenous and transgenic plant DNA were not, suggesting bacterial transformation by plant DNA is an extremely rare event.

**Key Words:** EPSP Synthase, Roundup Ready® Canola, Rumen

### 58 Elimination of *Escherichia coli* O157:H7 through the use of electrolyzed oxidizing (EO) water. S.M.L. Stevenson\*, S.R. Cook, S.J. Bach, and T.A. McAllister, *Agriculture and Agri-Food Canada, Lethbridge, AB*.

Research into identifying sources, prevalence and transmission of microbial pathogens such as *Escherichia coli* O157:H7 in and among feedlot cattle is increasing. Studies have identified multiple environmental sources, including water, in which *E. coli* O157:H7 can remain viable for long periods of time. New technologies and farm management practices continue to be developed and modified in attempts to control the prevalence of pathogenic agents. Electrolyzed oxidizing (EO) water is produced by exposing deionized water containing 0.1% (w/v) sodium chloride to an electrolyzing chamber containing an anode and a cathode separated by a diaphragm. Anode- (pH < 2.5) and cathode- (pH > 11.0) EO waters result. Anode-EO water has been shown to eliminate water-borne pathogens. This study investigated the use of electroactivated water (Biostel North America, Inc.) for specific inactivation of *E. coli* O157:H7. *Escherichia coli* O157:H7 (approximately 10<sup>2</sup> cells) was exposed for 30 s to 0, 0.5, 1.0, 2.0, 4.0, 8.0 or 16% (v/v) solutions of anode-, cathode- or 50/50 combined EO water in sterile, 2X-distilled water, then 100-μL aliquots of the bacterial suspensions were cultured overnight on MacConkey agar. The cathode-, anode- and combined EO water products had pH of 2.02, 11.11, and 6.93, respectively, and were stable for at least 48 h. Exposure to the combined EO water at 2.0% (v/v) or the anode-EO water at 0.5% killed the *E. coli* O157:H7 cells completely. Conversely, the cathode-EO water was ineffective at 16% (v/v). Growth of *E. coli* O157:H7 cells exposed to 0% EO was not inhibited. No correlations between pH and inactivation of bacterial cells were identified. These results suggest that point source inactivation of potential waterborne pathogens by minimal concentrations of EO water solutions may be possible. Further study is necessary to determine the value and feasibility of using this novel technology in a feedlot environment.

**Key Words:** *Escherichia coli* O157:H7, Electrolyzed Oxidizing Water, Water Microbiology

### 59 Relationship between feeding behavior and performance of feedlot steers. D.D. Hickman<sup>\*1,3</sup>, K.S. Schwartzkopf-Genswein<sup>2</sup>, R. Silasi<sup>2</sup>, D.H. Crews Jr.<sup>1</sup>, C.R. Krehbiel<sup>3</sup>, and T.A. McAllister<sup>1</sup>, <sup>1</sup>*Agriculture and Agri-Food Canada, Lethbridge, AB*, <sup>2</sup>*Alberta Agriculture, Food and Rural Development, Lethbridge, AB*, <sup>3</sup>*Oklahoma State University, Stillwater*.

The relationship between eating patterns and performance of feedlot cattle was evaluated using 74 Charolais cross steers (277 ± 111 kg) blocked by BW and assigned to two feedlot pens equipped with a radio frequency identification system (GrowSafe Systems). Each pen featured five feeding stalls that allowed single animal access to a feed tub suspended on load cells. The system recorded animal ID and time, duration and amount of feed consumed during each bunk visit. It allowed calculation of daily variation in intake (DVI) for each steer, as well as the absolute difference between feed consumed by a steer and the amount allotted per head that day in that pen (DDC). Barley silage/barley grain diets were delivered 2 or 3X/d to meet ad libitum intake over a 213-d trial comprising backgrounding (BKGD) and finishing (FNSH) phases. Steers were weighed every 14 d. To relate feeding behavior to performance, steers were grouped by their DM intake, ADG and FE and categorized as average (within pen mean ± SD), high (> mean plus SD) or low (< mean minus SD). In BKGD and FNSH, the high ADG steers exhibited greater (*P* < 0.001) DVI and DDC (2.66 and 2.07 kg, respectively) than those with average ADG (DVI = 2.53 kg; DDC = 1.92 kg) or low ADG (2.22 and 1.70 kg); their intake was also higher (*P* < 0.001) than for the average or low ADG steers. As a group, steers with the best FE also had higher (*P* < 0.001) DVI (2.54 kg) than average- (2.35) or poor (2.22) FE steers, during BKGD, FNSH, and overall. Compared to average or poor FE steers, DM intake by best FE steers was highest during BKGD and lowest during FNSH (*P* < 0.001). Their bunk visits (6.06/d) were more frequent (*P* < 0.001) but they spent the least (*P* < 0.001) time eating (86.6 min/d). In this study, steers with more variable eating patterns performed better, contrary to industry perception.

**Key Words:** Cattle, Performance, Feeding Behavior

**60 Observational study of factors associated with seasonal variation in milk urea nitrogen observed on intensively and extensively managed pastures, during the summer 2000 grazing season, in Prince Edward Island, Canada.** E Leger, I Dohoo, G Keefe, J Wichtel, P Arunvipas, and J VanLeeuwen, *Atlantic Veterinary College*.

The effects of pasture management and pasture supplementation on milk urea nitrogen (MUN) were explored to better understand protein and energy interactions during the grazing period. The overall objective of this observational study was to identify the significant factors associated with seasonal variation in milk urea nitrogen, in dairy cows grazing intensively or extensively managed pasture. Pasture management, stage of lactation, sample date and pasture supplementation on MUN levels, were examined during the summer 2000 grazing period. In total eighteen dairy herds were assessed. Ten of the herds were intensive grazing management (IGM) farms and 8 were extensive grazing management (EGM) producers. Each farm was visited within 48 hours after each Atlantic

Dairy Livestock Corporation (ADLIC) test. During each visit, pasture and stored forages were sampled and a detailed questionnaire relating to nutrition and management was completed. Collected ration information was evaluated using a computerized ration evaluator (Spartan). Multilevel modeling (2327 records) was used to compute the relationships between the energy-protein ratio (EPR), a ratio which represents the protein and energy requirements relative to protein and energy delivery, grazing management, presence of rye grass, stage of lactation, milk production and their interactions on milk urea nitrogen. Stage of lactation, grazing management, milk yield, presence of ryegrass, the EPR and the interaction between intensive grazing management practices and the presence of rye grass were found to be significant predictors of MUN. Predicted MUN values were 3.9 units higher on IGM herds where rye grass was present when compared to EGM herds where ryegrass was absent.

**Key Words:** Milk Urea Nitrogen, Pasture, Dairy Nutrition

## Graduate Paper Competition Dairy Foods

**61 Purification and characterization of two types of bile salt hydrolase from *Bifidobacterium* spp.** GB Kim\* and BH Lee, *Dept. of Food Sci. & Agri. Chemistry, McGill University*.

Previous research has indicated that bifidobacteria possess higher bile salt hydrolase (BSH) activity than other probiotics. To investigate the diversity of bile salt hydrolase activity and to understand the molecular organization, BSH activities from 30 strains (22 strains of human origin and 8 strains of animal origin) of bifidobacteria were screened using natural bile salts as well as a synthetic chromogenic substrate (a conjugate of cholic acid and 5-amino-2-nitro-benzoic acid). Among 30 strains tested, only two strains from honey bee hind gut (*Bifidobacterium aasteroides* ATCC 25910 and *B. coryneforme* ATCC 25911) did not show BSH activity. All positive strains contained constitutive intracellular BSH enzymes. From the profiles of native PAGE and BSH activity staining, two groups (group A and group C) of BSH enzyme were revealed. Most of bifidobacteria originated from ATCC was classified as group A, while many of commercial strains belong to group C. Group A and C showed different electrophoretic mobility and chromatographic profiles from anion exchange and hydrophobic interaction columns. This suggests that BSH enzymes from the same group have some similarities in their structure and amino acids composition. To investigate the biochemical characteristics of two enzymes, bile salt hydrolases were purified from *Bifidobacterium bifidum* ATCC 11863, *B. infantis* KL412, *B. longum* ATCC 15708, *B. longum* KL507, and *B. longum* KL515. The N-terminal amino acid sequences determined by Edman degradation were homologous to those of several lactobacilli as well as *Clostridium perfringens*. The native molecular weight of the enzyme in all five strains was estimated to be between 140 and 160 kDa and the subunit molecular weight determined as 35 kDa, indicating that the BSH enzyme is a tetramer. The isoelectric point (pI) determined by isoelectric focusing (IEF) was 4.4 and 4.6 for the BSH enzymes of group A and C, respectively. The relationship between the BSH types, bile tolerance and the molecular characteristics of group A and C enzymes is currently under investigation.

**Key Words:** Bile salt hydrolase, Bifidobacteria, Probiotics

**62 Exopolysaccharide production by *Lb. rhamnosus* RW-9595M.** D. Bergmaier\*<sup>1</sup>, C. Lacroix<sup>1</sup>, and C.P. Champagne<sup>2</sup>, <sup>1</sup>*Dairy Research Centre STELA*, <sup>2</sup>*Food Research and Development Centre, Agriculture and AgriFood Canada*.

Exopolysaccharides (EPS) synthesized by lactic acid bacteria (LAB) play an important role in the manufacturing of fermented dairy products. They contribute to the texture, mouthfeel, taste perception and stability of the final products. Furthermore, EPS could contribute to human health as prebiotics with positive effects on gut microflora. However the low production of EPS by LAB is a constraint for their commercial use as food additives. The immobilized cell technology (ICT) could be an attractive solution to enhance EPS production. The high biomass maintained in the reactor during repeated-batch or continuous culture could largely increase process productivity. In this study, bacterial growth and EPS production during batch and continuous cultures with *Lb. rhamnosus* RW-9595M, an efficient EPS producer, were

compared to repeated-batch cultures with cells immobilized on solid supports (ImmobaSil<sup>®</sup>). Cultures were conducted at pH 6 in whey permeate medium (5% or 8% (w/w) WP) supplemented with 1% (w/w) yeast extract, 0.5 g/L MgSO<sub>4</sub>·7H<sub>2</sub>O, 0.05 g/L MnSO<sub>4</sub>·H<sub>2</sub>O and 1 ml/L Tween-80. For free cell batch cultures in 8% WP medium, maximum cell counts (1.4·10<sup>10</sup> CFU/ml) and EPS production (2374 mg/L) were measured after 20 and 32 h, respectively. This is one of the highest EPS productions reported in the literature for lactobacilli. For continuous cultures in 8% WP, maximum EPS production (1808 mg/L) and volumetric productivity (542.6 mg/L·h) were obtained for a low dilution rate of 0.3 h<sup>-1</sup>. High immobilized biomass (2.6·10<sup>11</sup> CFU/ml support) and EPS concentrations (1800 mg/L) were measured during repeated immobilized cell cultures for incubation periods of 8 h in 5% WP. The high biomass in the system increased EPS volumetric productivity (225 mg/L·h) compared to free cell batch cultures, even though this fermentation was limited by the low carbon source concentration. Our study clearly shows the high potential of *Lb. rhamnosus* RW-9595M and ICT for production of EPS as functional and nutraceutical food ingredients.

**Key Words:** *Lactobacillus rhamnosus*, exopolysaccharides, immobilization

**63 The effect of lactic acid bacteria and bifidobacteria on interleukin-6 and interleukin-8 production by Caco-2 cells.** C. Wong\*<sup>1</sup>, J.J. Pestka<sup>1</sup>, and Z. Ustunol<sup>1</sup>, <sup>1</sup>*Department of Food Science and Human Nutrition, Michigan State University*.

Probiotics and the milk products produced using these microorganisms have been reported to stimulate both non-specific and specific immune responses. However, the number of studies using human cell lines has been limited in the past. The objective of this study was to examine the interleukin (IL)-6 and IL-8 production by Caco-2 cells stimulated with *Lactobacillus acidophilus* LA2, *Lactobacillus bulgaricus* NCK 231, *Lactobacillus casei* ATCC 39539, *Lactobacillus reuteri* ATCC 23272, *Streptococcus thermophilus* St 133, *Bifidobacterium* Bf-6 or *Bifidobacterium adolescentis* M101-4. Caco-2 cells resemble normal human intestinal epithelial cells, and thus were chosen for this study. Lactic acid bacteria or bifidobacteria were added to 10% non-fat dry milk (NFD) at concentrations of 10<sup>6</sup>, 10<sup>7</sup>, and 10<sup>8</sup> cfu/ml. Bacteria samples were either heat killed (95°C, 30 min) immediately after preparation or after fermentation (37°C, 4 hr). Cell numbers increased one log after fermentation. Bacterial samples were incubated with a monolayer of Caco-2 cells for 24 h. Uninoculated NFD was used as the control. Cytokine, IL-1β, was used as the positive control for both IL-6 and IL-8 stimulation by Caco-2 cells. Supernatants of all treatments were collected and frozen at -80°C until assayed for IL-6, and IL-8 using ELISA. The complex effects of NFD, probiotic cultures, probiotic dose, fermentation and their various interactions on the levels of IL-6 and IL-8 production will be presented. Since IL-6 and IL-8 are secreted by cells involved in inflammatory responses, their stimulation may or may not be desirable depending on the immune status of the individual.

**Key Words:** Lactic acid bacteria, Cytokine, Milk