through friends, retail stores, internet and media advertisements, but, unfortunately, this information may be incomplete or biased. The judicious use of pet supplements have provided veterinarians an emerging segment that helps address client demand and promote animal health and well being.

Key Words: pet supplements

208 Who are we, what do we do and how can we help? W. Bookout*, *National Animal Supplement Council*, *Valley Center, CA*.

The National Animal Supplement Council was founded in 2002 in response to the lack of a legal category for dietary supplements for companion animals and initiatives to remove them from the US marketplace. Over 100 companies now belong to NASC. In 1994, the Dietary Supplement Health and Education Act created a specific legal category for these products under the Federal Food, Drug and Cosmetic Act that allowed their marketing for human use. The agency responsible for the regulation of animal food and drugs is the FDA's Center for Veterinary Medicine. CVM works closely with the states through regulatory associations like AAFCO. In 1996, CVM published a notice explaining why DSHEA does not apply to animals. This ruling gives products marketed for animals that are similar to human dietary supplements only two possible legal categories under US law: animal feed or drugs. If a product on the market is not approved as an animal drug or contains unapproved feed ingredients, it may be deemed an adulterated drug or feed, and subject to regulatory action. NASC had three options to address this issue: 1) file legal action challenging the ruling that DSHEA does not apply to animals; 2) introduce new legislation; or 3) engage regulatory agencies at the state and federal levels to identify key metrics for responsible industry conduct, thereby allowing products to be marketed under regulatory discretion in the near term while establishing the foundation for a long-term solution. We clearly believe the last approach is in the best interest of all stakeholders. To support this goal, NASC implemented: a comprehensive adverse event reporting system (NAERS); labeling guidelines; scientific review for ingredient risk; an independent mandatory audit program for member companies; guidance for labeling claims; and other requirements suggested by CVM and AAFCO including proposed cGMP guidelines. We have a productive working relationship with US regulatory agencies and are currently working with organizations in other countries as they address similar issues in their markets.

Key Words: companion animals, regulatory, dietary supplements

Food Safety

209 *Clostridium difficile* in cattle and swine. R. Harvey*, *FFSRU, ARS, USDA*, *College Station, TX*.

There are some implications that human disease from *Clostridium difficile* (Cd) may originate from animals or meat. The objective of this study was to determine the prevalence of Cd among different age and production groups of swine in a vertically integrated swine operation in Texas in 2006, and to compare our isolates to those originating from humans, meat, and other animals. Cultivation of Cd was performed utilizing enrichment/concentration techniques and restrictive media. We recovered 131 Cd isolates from 1008 swine fecal samples with the majority (72%) of isolates occurring in nursing piglets. Decreased prevalence was observed in grower/finisher swine (11.5%) and pork trim (3.0%). Isolates were tested for resistance to 11 commonly used antibiotics. Molecular characterization demonstrated that 127/131 of the isolates were positive for toxins A and B genes, were positive for binary toxin, possessed a 39 bp gene deletion, and were of toxinotype V. These results compare favorably to our non-clinical human isolates (toxinotype V), but differ from clinical isolates of human hospitals in which most are the more virulent toxinotype III. Our swine isolates appear to be genetically similar to each other and have similar antibiotic resistance patterns to isolates from cattle which tend to be of toxinotype V. When sampling meat, we recovered 4 Cd isolates from pork trim, and 1 each from pork chorizo, ground turkey, and pork sausage, but not ground beef. All 7 were toxinotype V. This is in contrast to isolates from ground beef and veal in which the majority have been toxinotype III. Our isolates tended to be less resistant to antibiotics than human clinical isolates. In this study, Cd primarily originated from nursing piglets, but not in grower/finisher swine. If Cd were to be considered food related, then a relatively low prevalence in late production and the predominance of toxinotype V (a less virulent strain of Cd), suggest a low food safety risk. Our results do not appear to implicate Cd as food-vectored.

Key Words: *Clostridium difficile*, cattle, swine

210 Optimising fluorescence of feces as a real-time solution for the detection of fecal contamination on carcasses. M. R. F. Lee*[1], V. J. Theoblad[1], M. K. Theodorou[1], A. Veberg Dahl[2], F. Lundby[2], and J.-P. Wold[2], [1]*Aberystwyth University*, *Wales, UK*, [2]*Nofima Mat*, *Ås, Norway*.

In most abattoirs carcasses are checked by `eye' and washed with chemical sprays or dissected to remove areas contaminated with feces or digesta contents. Unfortunately small areas of contamination are seldom visible to the naked eye and may harbour millions of potentially pathogenic bacteria. The `VerifEYE ®' system uses ultra-violet imaging to detect chlorophyll and its fluorescent degradation products in feces. Not surprisingly animals offered fresh forage have a greater concentration of fluorescent compounds in their feces than animals offered conserved forages and concentrate based diets. Consequently the accuracy of the `VerifEYE ®' detection system can vary as it depends on the nature of the animal′s diet and this may explain the poor uptake of the technology by the industry. We have investigated the use of five different markers to be added to the diet in a pre-slaughter feed in an attempt to provide a stable level of fluorescence in the feces. Ten Cheviot sheep were offered a concentrate and barley straw diet and split into five treatment groups during a duplicate changeover 5 × 5 Latin square design where each period lasted 2 weeks. Four of the groups received a different marker at a rate of 1 g/d for the second week of each experimental period. The last group received no supplement and was used as the control. At the end of each period feces were collected and analysed for fluorescent compounds and intensity of the fluorescence. There were no differences in fecal concentration of the markers or their derivates 3.1 ± 0.15 and 7.2 ± 0.37 mg/g DM, respectively. Each of the markers significantly increased the fluorescence intensity of the feces over the control. The use of markers in pre-slaughter diets would thus improve the accuracy of fecal detection as a result of greater fluorescence and pin pointing the excitation wavelengths of the marker to help with visualisation. Further work is being continued to identify the most suitable marker and feeding regime.

Key Words: fecal contamination, fluorescence markers, pathogenic bacteria

211 Influence of serum prolactin concentrations on fecal shedding of *E. coli* O157:H7 in cattle. R. L. Farrow*, T. S. Edrington, K. M. MacKinnon, R. C. Anderson, and D. J. Nisbet, *USDA - ARS*, *College Station, TX*.

Previous research in our laboratory demonstrated hormones known to respond to changing day length can influence fecal shedding of *E. coli* O157:H7 in cattle. Continuing with this research, we examined the effect of serum prolactin concentrations on fecal shedding of *E. coli* O157:H7 and cellular immune response. 2–Bromo–α–ergocryptine methanesulfonate salt (BROMO) a dopamine agonist and sulpiride a D–2 dopamine receptor blocker were administered to decrease and increase prolactin levels, respectively. Fifteen Holstein steers experimentally infected with *E. coli* O157:H7 were randomly assigned to receive BROMO (0.05 mg/kg BW), sulpiride (0.05 mg/kg BW) or control (ethanol) via s.c. injection, twice daily. Fecal samples were collected daily and shedding of *E. coli* O157:H7 was determined via an immunomagnetic separation technique. Blood samples were collected via jugular venipuncture for analysis of serum prolactin concentrations and circulating neutrophils were isolated from peripheral blood on d 7 and 14 and degranulation and oxidative burst (OB) assays conducted. When examined over the 14-d experimental period, BROMO decreased ($P = 0.0001$) the percentage of cattle shedding *E. coli* O157:H7 (56% vs. 25.33% for control and BROMO treatments, respectively) while sulpiride had no effect ($P > 0.10$). BROMO decreased ($P < 0.0001$) serum prolactin concentrations, while sulpiride injections had no effect ($P > 0.10$). Oxidative burst by neutrophils for BROMO vs. control showed no significant difference on d 7, however, on d 14 OB by neutrophils tended to be higher for BROMO vs. controls ($P = 0.08$). Serum prolactin concentrations tended to be negatively correlated with OB ($P = 0.09$). No significant differences were observed for degranulation in BROMO vs. control on either d 7 or 14. These results support our hypothesis that hormones influenced by day length are responsible for the seasonality of *E. coli* O157:H7.

Key Words: *E. coli* O157:H7, beef cattle, seasonal shedding

212 Oral delivery systems for encapsulating bacteriophage targeted at *E. coli* O157:H7. K. Stanford*[1], T. P. Stephens[1], T. A. McAllister[2], D. Niu[1,3], and R. P. Johnson[4], [1]*Alberta Agriculture and Rural Development*, *Lethbridge, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [3]*Dalian University of Technology*, *Dalian, China*, [4]*Public Health Agency of Canada*, *Guelph, ON, Canada*.

Bacteriophages (PHAGE) are natural predators of *E. coli* O157:H7 in feedlot cattle and their environment. As PHAGE are inactivated at low pH, protection against gastric acidity may enhance efficacy of orally-administered PHAGE. *In vitro*, polymer encapsulation effectively protected 4 spray-dried PHAGE (wV8, rV5, wV7 and wV11) from acid digestion and a mean of 2.70 x 10^9 PFU was recovered across PHAGE types after 20 min exposure to pH 2.8. Twenty-four steers were administered 10^{10} CFU of naladixic acid-resistant *E. coli* O157:H7 (NalO157) on D0 and housed in 6 pens of 4 animals. Two pens served as CONTROL (NalO157 inoculation only) and remaining animals received 10^9 PFU of polymer-encapsulated PHAGE on d-1, 1, 3,6 and 8. Two pens received PHAGE orally in a gelatin capsule using a starch carrier (BOLUS) while the remaining 2 pens received PHAGE top-dressed on barley silage in the feed bunk (FEED). A daily 150g sample of FEED was retained to verify PHAGE titre using a standard plaque assay. Fecal shedding of *E. coli* O157:H7 was monitored for 10 wk by collection of fecal grab and hide swab samples from individual animals and via collection of fecal pats, feed and water in environment. Acceptable viability of mixed PHAGE was found in BOLUS and FEED treatments, averaging 1.82 and 1.50 x 10^9 PFU, respectively. However, treatment with PHAGE did not reduce numbers of animals shedding NalO157 compared to CONTROL, although duration of shedding was reduced by 14 d in BOLUS as compared to CONTROL animals. This study developed 2 successful delivery systems for PHAGE, but a better understanding of PHAGE-*E. coli* O157:H7 ecology is required to make PHAGE therapy a viable mitigation strategy in the feedlot.

Key Words: bacteriophage, *E. coli* O157:H7, cattle

213 Effects of Aviplus® on *E. coli* O157:H7 in pure culture and in mixed ruminal culture fermentations. T.R. Callaway*[1], E. Grilli[2], M. R. Messina[2], and A. Piva[2], [1]*Food and Feed Safety Research Unit, Agricultural Research Service, USDA*, *College Station, TX*, [2]*DIMORFIPA, University of Bologna*, *Bologna, Italy*.

Foodborne pathogenic bacteria can be harbored in the gut of food animals and transmitted to humans through the food supply, through water supplies or animal contact. Populations of the pathogenic bacteria E. coli O157:H7 can be affected by changes in the native flora of the intestinal tract. Organic acid products have been suggested for use as non-antibiotic modifiers of the gastrointestinal fermentation of animals. However, the impact of these acids on the overall microbial ecology of the intestinal tract remains unknown. Therefore, this study was designed to examine the effects of these acids on populations of the foodborne pathogen, Escherichia coli O157:H7. Pure cultures 3×10^5 CFU/ml of E. coli O157:H7 were added to tubes that contained Aviplus® added at 0, 0.1, 1, 2, 5, and 10% (w/v; n = 3). Aviplus® did not affect ($P > 0.1$) the growth rate or final populations of E. coli O157:H7 in pure culture, indicating that Aviplus® does not directly kill this pathogen at levels similar to those found in the intestinal tract. Ruminal fluid was collected from cows fed concentrate and placed in in vitro buffers. E. coli O157:H7 was added to in vitro ruminal fermentation, respectively, that contained Aviplus® at concentrations of 0, 1, 2, 5, and 10% (w/v; n = 2) and were incubated for 24 h. Aviplus addition did not affect ($P > 0.1$) populations of E. coli O157:H7 in the ruminal fluid. The ruminal A:P ratios were reduced ($P < 0.07$) by Aviplus® treatment. Organic acid products, such as Aviplus®, can alter the intestinal microbial ecology and impact animal productivity and health, however in vitro it does not appear that Aviplus® has an impact on populations of tested foodborne pathogenic bacteria inoculated at relatively high initial populations.

Key Words: Aviplus, food safety, fermentation

214 Control of *E. coli* O157:H7 in corn silage with inoculants under anaerobic and aerobic conditions. A. F. Pedroso[1,2], A. T. Adesogan[2], O. C. M. Queiroz*[2], and S. K. Williams[2], [1]*Brazilian Agricultural Research Corporation, Embrapa Cattle-Southeast*, *Sao Carlos, Sao Paulo, Brazil*, [2]*Department of Animal Sciences, Institute of Food and Agricultural Sciences, University of Florida*, *Gainesville*.

The aim was to determine if bacterial inoculants could eliminate *E. coli* O157:H7 (ECOL) in contaminated corn silages and if inoculants transferred antibacterial activity to silages. Chopped corn forage was ensiled in triplicate after treatment with:1) distilled water (control); 2) 5 x 105 cfu/g of ECOL (EC); 3) EC and 1 x 106 cfu/g of *Pediococcus pentosaceus* and *Propionibacterium freudenreichii* (EC+BII); 4) EC and 1 x 106 cfu/g of *Lactobacillus buchneri* (LB; EC+LB); 5) EC and 1 x 106 cfu/g of LB and *P. pentosaceus* (EC+B500). Silos were opened after 3, 7, 31, and 82 d and analyzed for pH and ECOL counts as well

as VFA, lactate, and aerobic stability on d 82. By d 3, all silages had pH was <4 (SE=0.33; p=1) and pH did not increase subsequently; therefore ECOL was not detected in any silage. The Kirby-Bauer disc diffusion test showed that all pure cultures of inoculants had pH-independent antibacterial activity against ECOL but inoculated silages did not, suggesting that ECOL elimination was mediated by pH reduction. Inoculation with LB resulted in less lactate (SE=0.31; p<0.05), more acetate (SE=0.35; p<0.05), and greater aerobic stability (SE=7.1; p<0.05) versus control. Day-82 silages were reinoculated with EC at silo opening (immediate) or after 144 h of exposure (delay) and ECOL were enumerated 24 h later. All immediately reinoculated silages had low pH values (<4) and no ECOL 24 h later. Control, EC, and EC+BII silages reinoculated after the delay had relatively high pH values (4.71, 5.67, and 6.03) (SE=0.74; p<0.05) and ECOL counts (2.87, 6.73, and 6.87 log cfu/g) (SE=1.4; p<0.05), whereas those treated with LB had low pH values (<4) and undetectable (EC+B500) or low ECOL counts (1.96, cfu/g; EC+LB). Inoculants did not enhance elimination of ECOL during ensiling, but *L. buchneri inoculants* increased stability and eliminated or inhibited ECOL in aerobically exposed silages.

Key Words: *E. coli* O157:H7, inoculant, silage

215 Characterization of antimicrobial-resistant *Escherichia coli* from samples collected throughout processing of feedlot cattle at a commercial abattoir. T. W. Alexander*[1], G. D. Inglis[1], L. J. Yanke[1], E. Topp[2], and T. A. McAllister[1], [1]*Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada*, [2]*Agriculture and Agri-Food Canada, London, Ontario, Canada*.

This study investigated antimicrobial-resistant *Escherichia coli* from samples throughout abattoir processing of feedlot cattle fed diets containing chlortetracycline plus sulfamethazine (AS700) or no antimicrobials (control). For each treatment, samples analyzed were: 1) feces collected at the feedlot (N=30); 2) hides after euthinization (N=15); 3) carcasses after evisceration and after 24 h in the chiller (N=15 for both); 4) ground beef stored for 1 and 8 d (N=15 for both); 5) digesta and mucosa from nine sections of the lower digestive tract (N=5 for each); 6) environmental abattoir samples (N=10); 7) air samples during slaughter (N=15). Generic, ampicillin (AREC)-, and tetracycline (TREC)-resistant *E. coli* were isolated on MacConkey agar or MacConkey agar containing ampicillin or tetracycline. All animals harboured AREC and TREC. Compared to control animals, the number of AREC (26.5% vs. 7.9%) and TREC (50.9% vs. 12.6%) were greater in feces from AS700 treated animals (P < 0.05) but were similar between hide, digesta and mucosa samples. Generic *E. coli*, AREC and TREC were detected from carcasses after evisceration and after 24 h in the chiller and d1- and d8-ground beef samples. Generic *E. coli* were isolated from all air samples. Resistant *E. coli* were isolated from the abattoir environment after slaughter of both groups of animals. Susceptibilities to 11 antimicrobials and pulsed field gel electrophoresis (PFGE) analyses were conducted on 362 AREC and TREC isolates across all samples. Twenty-five antibiogram profiles were detected. Most (28.2%) AREC were multi-resistant to ampicillin, streptomycin, and tetracycline while TREC (53.5%) were mainly resistant to tetracycline. From PFGE, 11 and 26 genotypes were detected amongst AREC and TREC respectively. Generally, isolates from meat and environmental samples had genetic backgrounds similar to isolates from animal tissue, digesta, or hide samples. These data indicate that antimicrobial-resistant *E. coli* from feedlot cattle can contaminate meat products at the slaughter plant and enter the food chain.

Key Words: antimicrobial resistance, abattoir, *Escherichia coli*

216 Screening of class IIa bacteriocin-producing lactic acid bacteria from Chinese traditional fermented food by PCR based method. H. Yi, L. Zhang*, Y. Tuo, X. Han, and M. Du, *Harbin Institute of Technology, Harbin, Heilongjiang, China*.

Class IIa bacteriocins of lactic acid bacteria are by far the most investigated and have been considered as one of the most interesting and potential groups of antimicrobial peptides for use in food preservation. There are abundant and various traditional fermented foods in China, which are likely to be valuable database containing class IIa bacteriocin-producing LAB. However, how to screen the desirable LAB rapidly from the complex fermented food ecosystem presents challenge. Therefore, development of rapid and reliable method for screening of microbes producing class IIa bacteriocins from potential organisms holds the key to the discovery of new and applicable class IIa bacteriocins. A method based on colony-PCR was developed and applied to screen class IIa bacteriocin-producing bacteria from 43 traditional fermented products (18 raw milk or yoghurt samples, 15 koumiss and 10 fermented vegetables samples) collected from specific ecological localities (Qinghai, Gansu, Sinkiang, Tibet) throughout the northwestern China. Results showed that 6 of 275 isolates gave rise to PCR fragments. Fragments of 3 kb can be detected with strain SB31 and Q5, while 3.4 kb with strain J20, J23 and 3.8 kb with strain M18 and X20 were obtained. The discrepancy of the amplicons size suggests that the size of peptide between bacterioncin and histidine kinase exists strain-specific. Amplicons of 332 bp (with strain M18 and X20), 412 bp (with strain SB31 and Q5), 428 bp (with strain J20 and J23) indicate the presence of pediocin, enterocin, plantaricin, respectively. This assay showed agreement with the conventional well-diffusion method. It offers several advantages over the existing methods in terms of rapidity, simplicity and accuracy, which make it a promising alternative to the conventional protocols. In addition, isolates of LAB from natural niches with the plateaus climate in the northwestern China could not only preserve the native microbes, but also eventually be an important resource for the development of novel starter cultures as well as food biopreservatives.

Key Words: class IIa bacteriocin, lactic acid bacteria, screen

217 *Salmonella* infection and immune response in finishing pigs. M. H. Rostagno*, S. D. Eicher, and D. C. Lay, *USDA, ARS, Livestock Behavior Research Unit*, *West Lafayette, IN*.

Finishing pigs infected with *Salmonella* pose food safety risks by carrying the pathogen into abattoirs. A study was conducted to determine the dynamic of *Salmonella* infection in finishing pigs, and immunological alterations that occur in *Salmonella*-carrier pigs, by longitudinally comparing infected to non-infected pigs. Pigs (n=24) were individually inoculated with *Salmonella* Typhimurium. Fecal and blood samples were collected from each pig, and 3 pigs were randomly selected and euthanized to collect additional samples (spleen, liver, mesenteric lymph node, ileum, and cecum) on days 1, 2, 7, 14, 21, 28, 35, and 42 post-inoculation (p.i.). A control group (n=15) of non-infected pigs was maintained for comparison by sampling at 1, 2, 7, 14, and 21 days. No inoculated animal showed any clinical sign of infection. Bacteriological data revealed that all inoculated pigs started shedding *Salmonella* within 24 h p.i., and persistently shed the bacteria up to the end of the study. Ileal and cecal content samples were all positive throughout the study. Mesenteric lymph nodes were also positive during the entire study and at the same level as intestinal content samples. All samples contained 3-4 logs (cfu/g) of *Salmonella* at 24 h p.i., and 4-5 logs (cfu/g) of *Salmonella* up to 4 wk p.i. Interestingly, levels of *Salmonella* dropped markedly (P<0.05) in all samples at 5 wk p.i., being detectable only by enrichment.

The number of peripheral blood monocytes tended to be less in infected pigs, with no difference between groups for other white blood cell measures. Tumor necrosis factor-Î± was greater (P<0.05) in infected pigs: 1) in the mesenteric lymph nodes by 48 h p.i.; 2) at 24 h and 3 wk p.i. in the ileum; and 3) in the cecum and spleen by 3 wk p.i. Interleukin-12, IL-1 and its antagonist, and a porcine specific antimicrobial peptide RNA expression in tissues changed over time, but were not different between groups. Immune data demonstrate that site specific immune changes occurred first, followed by more peripheral responses. These results will enable us to develop and plan the application of intervention strategies that will contribute to increase pork safety.

Key Words: swine, salmonella, food safety

Graduate Student Paper Competition-CSAS Oral Competition: CSAS Graduate Student Competition 2

218 The effect of animal location during transit on heart rate of pigs transported to slaughter using two vehicle types. J. A. Correa*[1], H. Gonyou[2], R. Bergeron[3], S. Torrey[4], T. Crowe[5], T. Widowski[3], J. P. Laforest[1], C. Dewey[3], N. Lewis[6], and L. Faucitano[4], [1]*Laval University*, *Quebec, QC, Canada*, [2]*Prairie Swine Centre*, *Saskatoon, SK, Canada*, [3]*University of Guelph*, *Guelp, ON, Canada*, [4]*Agriculture & Agri-Food Canada*, *Sherbrooke, QC, Canada*, [5]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [6]*University of Manitoba*, *Winnipeg, MB, Canada*.

The objective of this study was to assess the effect of the location in the vehicle on heart rate of pigs during transport. A total of 1,597 crossbred pigs (BW:124.2±7.9kg) were transported over 6 weeks (February-March 2008) from a commercial growing-finishing unit to a slaughter plant (2 h journey time) using two types of vehicles, a three-deck pot-belly trailer with internal ramps to upper and lower levels (PB; 181 pigs per week in 8 experimental compartments; 0.41 m2/pig) and a double-decker hydraulic truck without internal ramps (DD; 85 pigs per week in 4 compartments; 0.40 m2/pig). A sub-population of 252 pigs (PB: 28 pigs/week; DD: 14 pigs/week) was equipped with heart rate monitors (Polar Electro Canada) and randomly distributed through the selected compartments in both vehicles. Heart rate was recorded at 5 sec intervals and averaged over the following events: loading (L), wait before departure from the farm (W), transport (T) and unloading (U). Heart rate data were analyzed using the mixed model procedure in SAS, with the pig as the experimental unit. In the DD truck, independently of the deck position, a higher (P<0.05) heart rate was recorded during T in pigs located in the rear compartments (127.4±2.9 beats/min) of the vehicle compared to those loaded in the front ones (118.9±2.9 beats/min). No difference in heart rate was found between these locations in the PB trailer. In the PB trailer, pigs located on the upper deck showed higher (P<0.05) heart rate during W (165.8±3.2 beats/min) compared to those loaded in the middle (158.6±3.5 beats/min) and lower (157.3±4.0 beats/min) decks. During U, pigs from the upper (172.1±4.3 beats/min) and lower (171.1±4.9 beats/min) decks showed higher (P< 0.01) heart rates than pigs from the middle deck (163.6±4.3 beats/min). Overall, the heart rate of pigs during transport can be affected by their position in the vehicle.

Key Words: pigs, transport, heart rate

219 Utilization of electrolytes to encourage early feed and water consumption in weanlings. A. K. Gigiel*, N. J. Lewis, and M. L. Connor, *University of Manitoba*, *Winnipeg, MB, Canada*.

Three trials were conducted to determine the best management strategy for providing electrolytes to weanlings. Each trial used 90 piglets (19±1d) in a repeated measures design with a 2×5 factorial arrangement of treatments. Piglets were weaned for 12 or 0h and transported (<1h) to an offsite research facility. Trials 1 and 2 were done to determine the effects of providing electrolytes for different durations (T1) and at different concentrations (T2) on feed intake (FI) and growth rate. In T1, electrolytes (Vetoquinol, QC, Canada) were provided at the label dose of 60ml/940ml of water for 0, 6, 12, 18 or 24h on d1–d3. In T2, electrolytes were given *ad lib* at 100, 75, 25, 50 or 12.5% of the label dose on d1–d3. Trial 3 (T3) was done to determine the optimum number of days that electrolytes should be made available in order to maintain piglet weight and encourage FI. Electrolytes, at the label dose, or water (control) were given *ad lib* on d1, d1 and d2, d1–d3, or d1 and d3. All piglets had water *ad lib* from d4–d14. Piglets were weighed daily on d0–d7 and on d14, and FI was recorded daily to d4. ADG was calculated using d7 and d14 weights. Data was analyzed using PROC Mixed. In T1, on d7 percent weight change from d0 (%Wt) was significantly higher in the groups that received electrolytes for 12h and 18h than in the 24h group (9.2±1.65, 10.0±1.59 vs. 6.2±1.56%; P=0.04), but FI on d4 was higher in the 12h group than in the 18h and 24h groups (300.1±29.49 vs. 184.2±29.26, 209.8±27.47g/d; P=0.07). In T2, on d14%Wt was significantly higher in the 25% concentration group than in the 75% group (56.4±5.53 vs. 39.0±5.53%; P<0.05), and ADG was higher in the 25% group than in the 50, 75 and 100% groups (0.4±0.05 vs. 0.3±0.05, 0.3±0.05, 0.3±0.05g/d; P<0.10). In T3, there were no differences after d3 in %WT, FI or ADG. The data suggests that weanlings benefit from electrolytes at lower concentrations (<100%) for a shorter time period (<24h/d) than currently recommended. A subsequent experiment will focus on verifying the best combination of electrolyte concentration and total duration of treatment.

Key Words: piglet, electrolyte treatment, performance

220 Identification of single nucleotide polymorphisms influencing feed efficiency and performance in multi-breed beef cattle using a candidate gene approach. M. K. Abo-Ismail*[1], M. J. Kelly[1], E. J. Squires[1], K. C. Swanson[1], J. D. Nkrumah[2], and S. P. Miller[1], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*Igenity Livestock Production Business Unit, Merial Ltd.*, *Duluth, GA*.

Mutations in genes involved in biological processes associated with economically important traits are candidates which can be targeted for QTL detection to facilitate marker assisted selection. Therefore, the objectives of this study were to identify new SNPs in nine genes involved in digestive function and metabolic processes associated with feed efficiency and to examine the discovered SNPs for associations with feed efficiency and performance. An in silico study was conducted to discover SNPs in the candidate genes. Briefly, expressed sequence tags (ESTs) were acquired from the gene bank NCBI, and then ESTs were aligned using DNA sequence assembly software Sequencher. Single nucleotide polymorphisms, change in the sequence of amino acids, and the position of each SNP were detected. Animals (993) were genotyped for selected SNP (43) with 23 SNP identified as real (not fixed).