**M79 Cull cow and calf marketing methods employed by Idaho dairies.** M. Chahine and J. B. Glaze, Jr.*, *University of Idaho*, *Twin Falls*.

To assess the awareness, knowledge, understanding, and implementation of beef quality assurance (BQA) principles on Idaho dairies, a survey of dairy farmers in Idaho was conducted. Each of the 736 known dairies operating in Idaho received copies of the survey. Two-hundred, thirty six dairies returned the survey for an overall response rate of 37%. One section of the survey inquired about the cull cow and calf marketing methods employed by Idaho dairies. The marketing questions offered auction market, order buyer, forward contract, and private treaty, as marketing options for cull cows and calves. An additional marketing option listed for cull cows was direct market to the packer. To determine which marketing methods were most used by dairies, survey participants were asked to select any or all of the marketing options used by their dairy. The selections were compiled and used to assign use percentages. As dairies market their cull cows, they use auction markets most often (64%), followed by order buyers (17%), direct to the packer (17%), private treaty sales (16%), and forward contract (1%). The most used calf marketing method was private treaty sales (52%), followed by auction markets (42%), order buyers (14%), and forward contracts (1%). When the selections were compiled based on dairy size, results indicated that large dairies (more than 1000 cows) used auction markets most often (62%) to market their cull cows, followed by order buyers (33%), private treaty sales (23%), and direct to the packer (23%). Medium-sized dairies (200-1000 cows) favored auction markets (61%) over direct to the packer (17%), private treaty sales (15%), and order buyers (14%) when marketing cull cows. Small dairies (less than 200 cows) chose auction markets (66%) to market their cull cows more often than direct to the packer (15%), private treaty sales (14%), and order buyers (13%). Regardless of size, dairies chose private treaty sales over auction markets, order buyers, and forward contracts to market their calves.

**Key Words:** Marketing, Cull Cow, Calves

**M80 Financial performance of dairies in Florida and Georgia in 2005.** L. O. Ely*[1], R. Giesy[2], B. Broaddus[2], C. Vann[2], A. Bell[2], and A. deVries[2], [1]*University of Georgia*, *Athens*, [2]*University of Florida*, *Gainesville*.

The Dairy Business Analysis Project (DBAP) includes an annual survey of the financial performance of dairies primarily located in Florida and Georgia. Its objective is to document the dairies' financial success using standardized, accrual accounting methods in order to calculate benchmarks and provide feedback on the dairies financial strengths and weaknesses. Twenty-six dairies submitted financial data in 2005. Twenty-one dairies were included in the summary results. Of these, 15 were located in Florida, and 6 in Georgia. The average herd size was 1,045 cows and 538 heifers with 18322 lbs. milk sold per cow. The average culling rate was 36%. There was an average of 19 FTE workers per farm and 0.93 million lbs milk sold per FTE worker. Total revenue per cwt. was $20.73 / cwt with $18.24 / cwt milk income. The average total expense was $20.20 / cwt. The largest expense items were purchased feed ($7.22 / cwt), labor ($3.50 / cwt), livestock ($2.01 / cwt) and milk marketing ($1.22 / cwt). Net farm income from operations was $0.53 / cwt and net farm income was $0.07 / cwt. The debt to asset ratio was 0.39, the rate of return on assets was 0.04, the rate of return on equity was 0.02, the operating profit margin ratio was 0.02. Total expenses decreased and returns increased with herd size in 2005. Herds >670 cows had the middle total revenue ($20.44 / cwt) and the lowest expenses ($17.65 / cwt) resulting in the highest net farm income ($2.79 / cwt). The herds with the highest milk production (>19,500 lbs / cow / year) had the middle total revenue ($20.29 / cwt) and the lowest expenses ($18.98 / cwt) resulting in the highest net farm income ($1.19 / cwt).

**Key Words:** Dairy, Financial, Management

## Food Safety - Livestock and Poultry

**M81 Preventing *Salmonella* colonization in cement using Bio Deep Seal.** K. S. Macklin*, J. B. Hess, and D. E. Conner, *Auburn University*, *Auburn, AL*.

*Salmonella* is an important foodborne pathogen that is often associated with poultry. Unfortunately, the ability to properly clean and disinfect an area to remove this pathogen and/or other bacteria can be difficult. This is especially true in a constantly wet environment, such as that typically found in a poultry processing plant. In this study a commercial product (Acon Bio Deep Seal) that claimed to kill, encapsulate or displace bacteria was tested. This product was tested on cement blocks that had been impregnated with *Salmonella typhimurin*. To test the product an experiment was designed to include four treatments that were tested in five blocks each. The four treatments were an unchallenged group (CON), a challenged untreated group (CHAL), a challenged/pre-challenged treated group (PRE), and a challenged/post-challenge group (POST). The PRE group was treated with the product according to the manufacturer specifications. After 1 h, the PRE, CHAL, and POST blocks were placed in a broth that contained approximately 5 x $10^9$ cfu/mL of a *S. typhimurin*. After 24 h, the blocks were removed and the POST group was treated. After 6 h from removal from the broth, swabs were taken of the surface from each block. After the external swabs were taken, internal swabs were also obtained. Swabs were taken in duplicate with one swab being placed in TTB Hajna and the other being used for direct plating onto XLT4. After 24 and 48 h of incubation, the XLT4 plates were examined for presence of *Salmonella*. The TTB blocks were incubated for 48 h before being streaked onto XLT4. *Salmonella* counts (cfu/$cm^2$) for the XLT4 plates were transformed using log10. The data were analyzed using the GLM procedures of SAS with $P < 0.05$ and the means were separated using Tukey's HSD. *Salmonella* was detected on the block's exterior from treatments CHAL and PRE, but not from the CON and POST treatments. *Salmonella* was detected on the interior of the blocks only from the CHAL group. The results showed that Bio Deep Seal is an effective cement treatment to eliminate *Salmonella* when it is applied either before or after the cement was exposed to the pathogen.

**Key Words:** *Salmonella*, Disinfection, Cement

**M82 Effects of transport stress on subclinical infection in an *Escherichia coli-Listeria monocytogenes* challenge model.** G. R. Huff*[1], W. E. Huff[1], V. Dutta[2], R. Nannapaneni[3], and M. G. Johnson[3],

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We hypothesized that stress-induced subclinical infection of turkeys with *Listeria monocytogenes* (Lm) may be a source of contamination in processing plants and we have shown that concurrent *Escherichia coli* challenge can increase Lm colonization. The objective of this study was to determine effects of transport stress on isolation of Lm in an *E. coli*-Lm challenge model. Thirteen-wk-old male turkeys housed in floor pens were challenged by exposure to *E. coli* and Lm Scott A using coarse spray and feed inclusion. Positive controls were given an immunosuppressive dose of dexamethasone (Dex) during challenge. At 15 wk, a sample of birds was subjected to 12 h transport stress and all birds were bled and necropsied the following morning. Leukocyte numbers and percentages and hematological indices were determined. Knee and hip joints were sampled using transport swabs and cultured using pre-enrichment in University of Vermont medium and Fraser broth, and isolation of Lm on Listeria selective agar plates. Challenged birds, challenged-transported birds, and challenged-Dex or Dex treated birds had lower ($P < 0.05$)BW than the controls. Isolation of Lm was achieved from the knee or hip joints of 71% of challenged-Dex treated birds, 44% of challenged birds, and 23% of challenged-transported birds. Peripheral blood leukocyte count and percentage of heterophils (H) increased ($P < 0.05$) by Dex and by Transport. Dex decreased ($P < 0.05$) percentage of lymphocytes (L). The H/L ratio increased ($P < 0.05$) by Dex. Total erythrocyte counts, hematocrit, and hemoglobin decreased by Dex ($P < 0.05$) and by Transport ($P < 0.09$). The data suggested that subclinical infection with Lm can result from environmental exposure and Dex treatment could increase incidence of Lm colonization. Transport stress also tend to decrease Lm isolation from hip joints relative to unstressed challenged birds and this effect may be related to an increase in heterophil numbers.

**Key Words:** Turkeys, *Listeria monocytogenes*, Transport

**M83 A dual system based on the use of electronic identification and molecular markers to ensure lamb traceability.** G. Caja*, J. J. Ghirardi, M. Hernández-Jover, and A. Sánchez, *Universitat Autònoma de Barcelona*, *Bellaterra, Spain*.

As a part of a European Union project (FAIR5 QLk1-2001-02229: EID+DNA Tracing) the efficiency of a dual traceability system based on animal electronic identification (e-ID), by radiofrequency boluses (Rumitag, Barcelona, Spain) containing low-frequency (LF, 134.2 kHz) transponders of 32 mm, and genetic fingerprinting (DNA) by analyzing specific sets of ovine microsatellites (n = 12) in biopsies, was evaluated. A high-frequency (HF, 13.56 MHz; Tiris, Almelo, Holland) read-write inlay transponder (45 × 76 mm) was used for transferring e-ID code to the carcass. All animals also had visual ear tags (VE). Lambs (n = 1,908) on seven farms (Badajoz and Barcelona, Spain) were e-ID during suckling by using two LF mini-boluses (B1 [9 g; 10 × 39 mm; n = 1,091] and B2 [20 g; 11 × 56 mm; n = 817]). At bolus administration, biopsying ear tags (BE) were also attached (n = 980; Biopsytec, Rheinbach, Germany). Lambs were slaughtered before 3 mo of age in two commercial abattoirs. Mini-boluses were automatically read just before evisceration by a LF transceiver interfaced with a HF recorder. Bolus LF code was transferred to HF labels which were attached on the shank of the carcass after recording. Carcass samples (n = 868) were taken by using sampling tubes (Biopsytec). Ear and carcass samples were frozen until DNA analysis. On-farm traceability was lower for VE (96.8%) than for BE (99.7%), B1 (98.4%) and B2 (100%). Semi-automatic data transfer to carcasses was 98.9% successful. Abattoir traceability as well as total traceability differed between B1 (97.7 and 96.1%) and B2 (99.9 and 99.9%), respectively. When tracing back of carcasses to lambs in 50 random samples, one pair did not match (2.0%), showing 98.0% lamb traceability. In conclusion, the dual e-ID and DNA tracing system showed high traceability efficiencies (98%) under practical conditions, although improvement in label design and reading equipment is needed.

**Key Words:** Traceability, Transponder, Fingerprinting

**M84 Reduction of cecal *Campylobacter* spp. in broiler chickens by egg powder, mannobiose, or their combination.** Y. Han, G. I. Page*, and J. J. Brennan, *Maple Leaf Foods Agresearch*, *Guelph, Ontario, Canada*.

Fresh chicken is the main risk factor for human Campylobacteriosis. Two trials were conducted to study effects of dietary addition of egg powder (EP) or mannobiose (MB) on number of *Campylobacter* spp. in broiler chickens. In Exp. 1, 240 birds were fed the same medicated diet until d 34. From d 35 to 42, four different diets were fed to six pens (replications) per treatment (10 birds/pen). The following test material was added into the medicated (55 ppm bacitracin) control diet: 5% EP, 130 ppm MB, or 13 ppm MB. On d 29, 37, 39, and 42, two birds per pen were sacrificed for cecal *Campylobacter* counts. In Exp. 2, five experimental diets were fed to six pens (replications) per treatment (15 birds/pen) of 450 d-old chicks for 2 wk, followed by a common feed until d 41. The following product was added into a medicated control diet, 5% EP, 130 ppm MB, 5% EP + 130 ppm MB, or 2.5% EP + 65 ppm MB. On d 14, 21, 28, and 41, two birds per pen were analyzed for cecal *Campylobacter* counts and cecal total IgA. In both experiments, the test materials did not affect ($P > 0.05$) growth performance or mortality of the birds. In Exp. 1, all birds were positive for *Campylobacter* by d 29. No differences ($P > 0.05$) in cecal *Campylobacter* counts were found on d 37 or 39. However, on d 42, birds fed the 5% EP had lower ($P < 0.05$) *Campylobacter* counts than those fed the Control or the 13 ppm MB diet (0.94 vs 2.50 or 2.69 log cfu/g), but not different ($P > 0.05$) from those fed the 130 ppm MB diet (2.09 log cfu/g). In Exp. 2, the test materials did not prevent the newly placed birds from being colonized by *Campylobacter* by day 14. By d 41, the cecal *Campylobacter* counts in the control birds were numerically higher ($P > 0.05$) than those in the birds fed the 5% EP, the 130 ppm MB, the combination of both, or the 2.5% EP + 65 ppm MB diets (2.61, .98, 1.03, 1.27, or 1.20 log cfu/g, respectively; $P = 0.09$). Cecal total IgA concentrations on d 41 were higher ($P < 0.05$) in the birds fed the EP, the MB, or the combination diets than in those fed the control diet. It was concluded that egg powder and mannobiose could be used to reduce *Campylobacter* colonization in broiler chickens.

**Key Words:** *Campylobacter* spp., Egg Powder, Mannobiose

**M85 Development of a polymerase chain reaction-based method to identify poultry, ruminants, and equine components in fish meal.** A. Heravi Moussavi*[1], M. Nassiri[1], G. Pourseifi[1], M. Soltani[1], A. Javadmanesh[1], and R. Noorbakhsh[2], [1]*Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavy, Iran*, [2]*Standards*

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Fish meal is a widely used feedstuff for poultry and ruminants. The objective of this study was to develop a polymerase chain reaction (PCR)-based method to identify poultry, ruminants, and equine components in fish meal. In this experiment, 10 different available commercial fish meals were used. The nitrogen contents were measured using the Kejeldal method to investigate the correlation between nitrogen contents and the possible non-fish species components. Mitochondrial DNA extraction was carried out using a commercial kit based on phenol-chloroform method. Specific primers for every species were designed and calibrated to generate exclusively a PCR product with a specific size when DNA for each species was present in the sample. Blood samples of hen, cow, sheep, and horse were run as the positive controls. The results demonstrated that only two products were not contaminated and the others were contaminated with at least one of the species. The correlation between nitrogen content and possible non-fish species components was not significant ($P = 0.57$; $r = 0.2$). The results demonstrated that evaluation of fish meal by measuring its CP content is not accurate and it should be evaluated by other methods such as PCR-based methods. It is recommended that PCR methods to be considered for feedstuff standards as tools to assure quality.

**Key Words:** Fish Meal, PCR, Adulteration

**M86 Detection of *Escherichia coli* O157:H7 using Au nanoparticles mediator on an electrochemical amperometric immunobiosensor.** S.-H. Chen*[1], Y.-H. Lin[1,2], Y.-C. Chuang[1], Y.-R. Lin[1], C. A. Chang[1], T. Y. Shen[2], and C.-S. Lin[1], [1]*National Chiao Tung University*, *Hsinchu, Taiwan, R.O.C*, [2]*Apex Biotechnology Corporation*, *Hsinchu, Taiwan, R.O.C*.

A screen-printed carbon electrode (SPCE) immunobiosensor, based on 13-nm Au nanoparticles (AuNPs) as mediator for amplifying electronic conduction and detection signal, was used for real-time detection of *Escherichia coli* O157:H7. We investigated the impact of electronic conduction using horseradish peroxidase (HRP) reacted to hydrogen peroxide ($H_2O_2$) through an AuNPs-modified SPCE surface. The AuNPs were used to increase electron conductivity and surface area of SPCE for amplifying detection current in developing immunobiosensing system. In the assembling process of SPCE, the AuNPs-mediator was first addressed onto the SPCE surface and immobilized the first specific antibody against *E. coli* O157:H7. The modified SPCE was then used to detect the samples containing *E. coli* O157:H7. After the procedures of detection and washing, the SPCE was treated with the second *E. coli* O157:H7 specific antibody conjugated with HRP, and reacted to $H_2O_2$, the free electron generated could be detected by an electrochemical amperometric biosensor. The detection results demonstrated that the 13-nm AuNPs, as in an immunobiosensor mediator, could enhance the current around 60 folds compared with those without AuNPs-modified electrodes. The AuNPs-modified SPCE developed in this study enabled the detection of *E. coli* O157:H7 at a low concentration of $10^2$ cfu/strip within 1 h and the reproducibility reaches 85%, which shows that this technique is more efficient than traditional culture plate methods. The SPCE immunobiosensing system has potential for further applications and lays the groundwork for incorporating the method into an integrated system for rapid pathogen detection.

**Key Words:** *Escherichia coli* O157:H7, Screen-printed Carbon Electrode, Immunobiosensor

**M87 Effect of heat treatments on stability of β-lactams in milk.** M. Roca[1], M. A. Zorraquino[2], C. Igualada[3], R. L. Althaus[4], and M. P. Molina*[1], [1]*Universidad Politecnica de Valencia*, *Valencia, Spain*, [2]*Universidad Publica de Navarra*, *Pamplona, Spain*, [3]*Generalitat Valenciana*, *Valencia, Spain*, [4]*Universidad Nacional del Litoral*, *Esperanza, Republica Argentina*.

The presence in milk of residues of antimicrobial substances may have serious toxicological and technical consequences. Studies referring to the influence of heat treatments on antimicrobial residues in milk are very scarce. The objective of the study was to analyze, using HPLC assays, the effect of different heat treatments (60, 70, 80, 90, and 100°C at six different times) on milk samples fortified with 5,000 μg/kg of penicillin, amoxycillin, ampicillin, cloxacillin, cephalexin, cephalonium, cefquinome, cefoperazone, cephapirin, and cephuroxime. The half-life (losses of 50% of the initial concentration) calculated for β-lactams showed that penicillins are more stable molecules than cephalosporins. Using the obtained prediction equations, the thermal loss percentages in concentration for the frequent heat treatments carried out in the control laboratories and dairy industry, are calculated. The results showed that the sample homogenization (40°C for 10 min) caused no inactivation in most of the β-lactams, whereas heating to 83°C for 10 min to inactivate the natural milk inhibitors, caused a small reduction in penicillin concentrations, around 6%, but a higher one in cephalosporins (15 to 53%). The LTLT pasteurization (60°C for 30 min) caused less degradation (3 to 6%), somewhat higher in the cephalosporins (16 to 43%). The HTST pasteurization (72°C for 15 s) produced very small losses in all β-lactams (< 1%). In contrast, sterilization (120°C for 20 min) produced a marked heat degradation ranging between 47% (amoxicillin) and 93% (ampicillin) for the penicillins and greater than 90% for most cephalosporins. In turn, the inactivation percentages of the treatment at 140°C for 10 s (UHT) are low for nearly all β-lactams, being situated between 1 and 8%, and moderate for cephuroxime (19%) and cefoperazone (37%). In conclusion, only sterilization produced a high inactivation level of β-lactams in milk. The other treatments were no guarantee that these molecules would lose their antimicrobial activity.

**Key Words:** Antibiotics, Milk, Thermostability

**M88 Effects of feed withdrawal times prior to slaughter on cecal fermentation and *Salmonella* shedding at the abattoir.** S. Martín-Peláez[1], E. Creus[1], B. Peralta[2], J. F. Pérez*[1], E. Mateu[2], and S. M. Martín–Orúe[1], [1]*Animal Nutrition, Management and Welfare Research Group, Universitat Autònoma de Barcelona*, *Spain*, [2]*Departament de Sanitat i Anatomia Animals, Universitat Autònoma de Barcelona*, *Spain*.

The objective of this study was to determine whether different times of feed withdrawal in pigs prior to slaughter have any effect on cecal fermentation and *Salmonella* shedding. One commercial farm subclinically infected with *Salmonella* (prevalence of carriers = 13%) was studied. Two groups of pigs (45 each) were either deprived of feed for 15 or 30 h before slaughter. Fecal samples were collected the day before slaughter at the farm. The weight of the gastrointestinal tract (GIT) was recorded and fecal samples from the rectum were collected for *Salmonella* detection. Cecal samples were also collected to evaluate possible changes in pH, concentrations of short chain fatty acids (SCFA) and $NH_3$, and numbers of lactobacilli and enterobacteria by means of qPCR. The GIT weight decreased ($P < 0.05$) with increasing feed withdrawal time (6.76 vs 6.39 kg) whereas cecal pH (5.9 vs 6.4)

increased ($P < 0.05$). Concentration of total SCFA (89.5 vs 77.8 mM) decreased ($P < 0.05$) with increasing feed withdrawal time but the percentage of branched SCFA (1.9 vs 3.1%) increased ($P < 0.05$). The $NH_3$ concentration (366.6 vs 769.3 mg/L also increased ($P < 0.05$) with increasing feed withdrawal time. The numbers of enterobacteria (8.7 vs 9.1 log 16 S rDNA copies/g FM) increased ($P = 0.08$) with increasing feed withdrawl time whereas the numbers of lactobacilli (9.6 vs 9.0 log 16 S rDNA copies/g FM) decreased ($P < 0.05$). The percentage of pigs with *Salmonella* in the rectal contents was higher ($P < 0.05$) in the group that was fasted for 30 h (18 vs 33%). The results suggested feed withdrawl for a short period of time (e.g., 15 h) to have the potential to decrease presence of *Salmonella* in the GIT of pigs arriving at the abattoir.

**Key Words:** Swine, *Salmonella*, Feed withdrawal

**M89 Efficacy of a micro-encapsulated or non-encapsulated blend of lactic and formic acid to reduce the prevalence of *Salmonella* in finishing pigs.** J. dos Santos[1], E. Creus[1], J. F. Pérez*[1], E. Mateu[2], and S. M. Martín–Orúe[1], [1]*Animal Nutrition, Management and Welfare Research Group, Universitat Autònoma de Barcelona*, *Spain*, [2]*Departament de Sanitat i Anatomia Animals, Universitat Autònoma de Barcelona*, *Spain*.

Micro-encapsulated acids in the feed have been proposed to increase acid concentrations in the posterior sections of the gut. The objective was to examine if an economically affordable dose of protected acid could improve efficacy of a non-protected blend in reducing *Salmonella* in finishing pigs. One commercial farm subclinically infected was selected. A total of 261 pigs were allocated to three dietary groups that included a control (CTR), the CTR with a blend of lactic and formic acids added at 0.4% each (NPB), and the CTR diet with a lipid microencapsulated blend of each acid (0.14% each) added (PB). The pigs had ad libitum access to the diets for 5 wk. Blood samples for ELISA were taken before starting the diets (d-0) and immediately after slaughter (d-36), and fecal samples were collected on d-0 and d-36 for microbiology tseting. Cecal contents were also collected for measuring pH, short chain fatty acids (SCFA), and both formic and lactic acids. No change was detected in cecal pH but increased concentrations ($P < 0.05$) of formic and lactic acids were detected with feeding the NPB diet (3.2 and 12.9 mM, respectively) and the PB diet (4.0 and 11.6 mM, respectively) compared with feeding the CTR diet (2.0 and 4.8 mM, respectively). Concentrations of SCFA were higher ($P < 0.05$) with feeding the PB diet (233 mM) than with feeding the CTR (177) or the NPB (173) diets. Five weeks of feeding the NPB diet decreased ($P < 0.05$) seroprevalence (from 59.4 to 8.8%) but not the rest of diets. No change in *Salmonella* shedding was detected from d-0 to d-35. However increases ($P < 0.05$) were found after transport to the abattoir with feeding the CTR (12.5 vs 77.4%) and the PB (0 vs 17.4%) diets, but not with the NPB diet (0 vs 3.3%). The results suggested that inclusion of a non-protected blend of formic and lactic acids in finishing diets could decrease *Salmonella* seroprevalence in swine. The microencapsulated blend, however, did not decrease *Salmonella* prevalence.

**Key Words:** Swine , *Salmonella*, Acidifiers

**M90 Effects of feed withdrawal and lairage time prior to slaughter on the gut environment and cecal *Enterobacteriaceae* in finishing pigs.** S. Martín–Peláez[1], S. M. Martín–Orúe[1], J. F. Pérez*[1], A. Dalmau[2], E. Fàbrega[2], A. Velarde[2], J. Tibau[2], and J. Gasa[1], [1]*Animal Nutrition, Management and Welfare Research Group, Universitat Autònoma de Barcelona*, *Spain*, [2]*IRTA*, *Monells, Girona, Spain*.

The objective of this study was to determine effects of different feed withdrawal and lairage times prior to slaughter on the gut environment of pigs and also on growth of *Enterobacteriaceae* as a possible marker of *Salmonella* shedding. Two groups of finishing pigs (36 each) were deprived of feed for 2 or 12 h before their lairage at the slaughterhouse. Each group was divided into three subgroups and held in different holding pens for 0, 5, or 10 h before slaughter. The weight of the gastrointestinal tract (GIT) was determined and samples of cecal contents were collected to measure pH, short chain fatty acids (SCFA), and the numbers of lactobacilli and enterobacteria by means of qPCR. The GIT weight decreased ($P < 0.05$) with feed withdrawal (6.8 vs 5.7 kg) but not with increasing lairage time. Similarly cecal pH increased ($P < 0.05$) only with feed withdrawal (6.14 vs 6.55). Cecal concentration of total SCFA decreased ($P < 0.05$) with feed withdrawal (165 vs 125 mM) and increasing lairage time (182, 147, and 105 mM for 0, 5, and 10 h, respectively). Lactobacilli population decreased ($P < 0.05$) with increasing lairage time (10.0, 9.3, and 8.6 log 16 S rDNA copies/g FM for 0, 5, and 10 h, respectively) whereas *Enterobacteriaceae* increased ($P < 0.05$) with feed withdrawal (9.0 vs 9.5 log 16 S rDNA copies/g FM) and increasing lairage time (8.9, 9.4, and 9.6 log 16 S rDNA copies/g FM for 0, 5, and 10 h, respectively). The results showed that antemortem feed depriviation time can have a significant impact on intestinal environment and potential growth of pathogens of the *Enterobacteriaceae* family.

**Key Words:** Swine, Pathogens, Feed Withdrawl

**M91 The relationship between *Salmonella* detection from milk filters and bulk milk and fecal shedding of *Salmonella* in a dairy herd.** J. S. Van Kessel*[1], J. S. Karns[1], D. R. Wolfgang[2], E. Hovingh[2], and Y. Schukken[3], [1]*USDA-ARS-EMSL*, *Beltsville, MD*, [2]*The Pennsylvania State University*, *University Park*, [3]*Cornell University*, *Ithaca, NY*.

Although dairy cattle are known reservoirs for *Salmonella*, cattle that are shedding this pathogen are often asymptomatic and difficult to identify. A dairy herd experiencing an outbreak of *Salmonella enterica* subsp. *enterica* Cerro was monitored for 2 yr. Fecal samples from lactating cows were collected every 6 to 8 wk and were tested for presence of *Salmonella* using traditional culture methods. Fecal shedding of *Salmonella* fluctuated throughout the test period and the prevalence ranged from 8 to 88%. During this period, bulk milk and milk filters were also tested for *Salmonella* on a weekly basis. *Salmonella* was detected in 15% of milk samples (n = 109) and in 78% (n = 107) of milk filters. Results of weekly bulk milk quality testing (i.e. bulk tank somatic cell score, standard plate count, and preliminary incubation count) were typically well within acceptable ranges. The recovery of *Salmonella* from milk filters and to a lesser extent from bulk milk, closely matched that from the feces. Analysis of in-line milk filters has been used previously as a useful method to detect presence of zoonotic bacteria entering bulk tanks. It is concluded that milk filter analysis could be used as a convenient method for monitoring *Salmonella* shedding in dairy herds.

**Key Words:** *Salmonella*, Dairy Cattle, Pathogens

**M92 Validation of peracetic acid as an antimicrobial for poultry chillers.** S. R. McKee*, L. J. Bauermeister, and J. W. Bowers, *Auburn University*, *Auburn, AL*.

Spectrum™ (peracetic acid; PAA) has been approved as an antimicrobial for use in poultry chillers. To validate its effectiveness, laboratory and commercial trials were conducted. In the laboratory trials, 200 poultry carcasses were inoculated with *Salmonella* ($10^6$ cfu) and were randomly allocated into chill water containing chlorine (30 ppm) or PPA (25, 100, or 200 ppm). The results illustrated that PPA concentrations of 100 or 200 ppm to effective in reducing *Salmonella* when compared with the chlorine treatment. A sensory study was also conducted with another set of 200 carcasses (not inoculated) treated with water, chlorine (30 ppm), or PPA (100, 150, or 200 ppm). Sensory panels and microbial data were collected weekly on randomly sampled carcasses that were stored at 4°C for 21 d. The PAA-treated carcasses at 150 and 200 ppm had an extended shelf life that ranged from 3 to 4 d beyond those treated with water or chlorine. On d 15, the only treatments that could be served to sensory panelists were the carcasses treated with 150 or 200 ppm PAA. The carcasses treated with water, chlorine, or 100 ppm PPA had off-colors, off-odors, and high microbial counts. In another trial, 65 ppm PPA was compared with the 30 ppm chlorine treatment in a commercial setting. In this trial, 100 carcasses were sampled for *Salmonella* prior to the chiller and 100 were sampled after chilling. In all, 400 carcasses were sampled using 65 ppm PPA in the chiller and 400 carcasses were sampled using the chlorine treatment. *Salmonella* was reduced by 90% using the 65 ppm PPA treatment and it was reduced by 55% using the chlorine treatment. Peracetic acid appears to be an effective antimicrobial in poultry chillers. It also appears to have the potential to extend the shelf-life of poultry when used at concentrations of 150 or 200 ppm.

**Key Words:** *Salmonella*, Poutlry Chilling, Peracetic Acid

**M93 Evaluation of rep-PCR and denatured gradient gel electrophoresis (DGGE) in identifying *Salmonella* serotypes isolated from processed turkeys.** P. N. Anderson*[1], M. E. Hume[1,2], J. A. Byrd[1,2], and D. J. Caldwell[1], [1]*Texas A & M University*, *College Station*, [2]*USDA-ARS, FFSRU*, *College Station, Texas*.

*Salmonella* has been reported as the leading foodborne pathogen in the U.S. Researchers are continually evaluating different molecular typing methods to identify the most suitable technique that is able to discriminate among *Salmonella* serotypes. A study was conducted to compare the use of automated repetitive extragenic palindromic (rep-PCR) and denaturing gradient gel electrophoresis (DGGE) as diagnostic tools for identifying *Salmonella* serotypes. The interspersed conserved repetitive sequence of the bacterial genome and the 16-23S rDNA intergenic spacer region were amplified for rep-PCR and DGGE, respectively. Fifty-three *Salmonella* isolates from two turkey processing plants (A and B) were used for this comparison: Brandenburg, Derby, Hadar, and Typhimurium with n = 6, 21, 12, and 15, respectively. The rep-PCR was fully automated, while DGGE was run on an acrylamide gel and the image was captured digitally and the dendrograms were created using the unweighted pair group method with arithmetic average. There were more variations in percentage similarity in DGGE when compared with rep-PCR. The banding patterns were more distinct and uniform in the rep-PCR group than with DGGE group. The results from the rep-PCR were generated within an hour, while the DGGE required nearly a day to run. The data suggested that DGGE and rep-PCR are useful tools for identifying *Salmonella* serotypes. In addition, rep-PCR is more rapid, may have a higher discriminatory power, but may be less cost effective than DGGE.

**Key Words:** *Salmonella*, Detection, Molecular Methods

**M94 Association between on-farm milk and wash water temperature variations and bulk milk coliform counts.** J. C. F. Pantoja, C. Hulland, G. J. M. Rosa, D. J. Reinemann, and P. L. Ruegg*, *University of Wisconsin*, *Madison*.

The objective was to determine the impact of temperature variations during milk storage and wash procedures on bulk milk coliform counts. Data were collected from two dairy farms between July and December, 2006. Farm A had 1,110 lactating cows that produced 42,184 kg milk/d with a log somatic cell counts (SCC) of 5.01. Farm B had 400 lactating cows that produced 13,607 kg milk/d with a log SCC of 5.04. Cows in both farms were housed in freestalls and were milked in parallel parlors. Both farms cooled milk using plate coolers, loaded milk directly into tankers, and had temperature recording charts for monitoring milk and wash water temperatures with sensors located in the milk line between the chiller and the tanker entry. The farms were visited monthly and daily somatic cell, standard plate, coliform, and laboratory pasteurized counts were downloaded from the processor website. Temperature charts were examined to detect minor temperature failures (temperature recorded between 7.2 and 10.0°C), major temperature failures (>10°C) and failure to reach 60°C during wash cycles (wash failures). The association between the occurrence of failures and coliform spikes (values above 100 cfu/mL) was analyzed using SAS. The distribution of failures, was minor (n = 101), major (n = 49), and wash failure (n = 11). Coliform counts varied between 0 and 1,500 cfu/mL and there were 32 occurrences of spikes. The occurrence of temperature failures was associated with occurrence of coliform spikes (P = 0.001) and the risk of a coliform spike was 3.58 higher when > 1 temperature errors occurred within a 2-d interval. Coliform spikes and temperature errors decreased from summer to winter. For the two farms investigated, there was an association between coliform count spikes and temperature variations. The results contribute to increasing the understanding of the complex factors impacting microbial ecology of raw milk.

**Key Words:** Milk Quality, Milking, Bcteria

**M95 Meat quality and microbial shelf life of chicken breast fillets from air or immersion chilled processing systems and packaged under modified atmospheres.** D. Monsalve*[1], H. Thippareddi[1], and S. Russell[2], [1]*University of Nebraska*, *Lincoln*, [2]*University of Georgia*, *Athens*.

The effects of modified atmosphere packaging (MAP) on microbial shelf life, lipid oxidation, and color stability of chicken breast fillets were determined during refrigerated storage. Chicken breast fillets were obtained from an air-chill and an immersion-chill establishment. Fillets were packaged aerobically (tray-pack) or under vacuum or flushed with nitrogen. Breast fillets for each packaging system were stored at 1 or 5°C. Changes in color, TBARS (2-thibarbituric acid-reactive substances), and microbiota were determined at 1, 7, 14, and 21 d of storage. Storage of breast fillets at 1°C and under a modified atmosphere (vacuum and nitrogen flush) extended the shelf life of the breast fillets, with lower microbial populations throughout the storage period. Vacuum and nitrogen flush packaged samples had

lower ($P < 0.001$) TBARS values (2,688 and 3,319 µg MDA/kg) than the aerobically-packaged samples (4,752 µg MDA/kg). Color values for lightness (L*), redness (a*), and yellowness (b*) were lower ($P < 0.001$) in air-chilled samples than in the immersion-chilled samples. The results indicated that modified atmosphere packaging of breast fillets can improve lipid stability and may extend shelf life.

**Key Words:** Storage, Modified Atmosphere, Shelf Life

**M96 Characterization and potential human health risks of Shiga toxin-producing *Escherichia coli* isolated from California dairy cattle over one year.** L. M. Bollinger*[1], H. S. Hussein[1], M. R. Hall[1], and E. R. Atwill[2], [1]*University of Nevada*, *Reno*, [2]*University of California*, *Davis*.

Worldwide awareness of Shiga toxin-producing *Escherichia coli* (STEC) increased in recent years due to tracing many human illness outbreaks to consumption of foods contaminated with cattle feces. Pathogenic STEC strains produce toxins responsible for causing (Shiga toxin 1 and/or Shiga toxin 2) or increasing (α-hemolysin and/or enterohemorrhagic *E. coli* [EHEC]-hemolysin) the severity of illnesses. These toxins are encoded by $stx_1$, $stx_2$, *hlyA*, and EHEC-*hlyA* genes, respectively. Because dairy cattle are STEC reservoirs, they can impose significant health risks to humans. The objective was to examine STEC prevalence in four dairy farms (averaging 712 cows) in California and to assess potential pathogenicity of the isolates. Analysis of 1,268 fecal samples from heifers (n = 261) and cows (n = 1,007) over one year resulted in detection of 33 isolates that belonged to 16 STEC serotypes (O15:$H^-$ [nonmotile], O116:$H^-$, O125:H20, O127:H19, O128:H20, O136:H10, O136:H12, O136:H19, O136:HUT [untypeable H antigen], O157:H7, O157:$H^-$, O166:H6, OX13 [new provisional O antigen]:H19, OX13:H20, OUT [untypeable O antigen]:H7, and OUT:$H^-$) and were lethal to Vero (African green monkey kidney) cells. Of these isolates, 17, 4, and 12 had $stx_1$, $stx_2$, or both genes, respectively. Except for one (belonging to the O128:H20 serotype, having both genes, and expressing only $stx_2$), all isolates expressed these genes. Only one isolate (belonging to the O166:H6 serotype) had and expressed the *hlyA* gene whereas 18 isolates had the EHEC-*hlyA* gene but only five expressed it. Of the 16 serotypes, three (O157:H7, O157:$H^-$, and OUT:$H^-$) cause hemolytic uremic syndrome, two (O15:$H^-$ and OUT:H7) cause other human illnesses, and eight (O125:H20, O127:H19, O128:H20, O136:H10, O136:H19, O166:H6, OX13:H19, and OX13:H20) have not been reported previously in cattle. Because our STEC isolates produced one (n = 18), two (n = 13), or three (n = 2) virulence factors, their pathogenic potential to humans should not be ignored. Our results demonstrate the potential health risks of O157 and non-O157 STEC isolates from dairy cattle origin.

**Key Words:** Shiga Toxins, *Escherichia coli*, Dairy Cattle

**M97 Characterization and potential human health risks of Shiga toxin-producing *Escherichia coli* isolated from feedlot cattle.** H. S. Hussein*[1], L. M. Bollinger[1], M. R. Hall[1], S. F. Khaiboullina[1], and E. R Atwill[2], [1]*University of Nevada*, *Reno*, [2]*University of California*, *Davis*.

Since tracing two outbreaks of human illnesses to consumption of beef contaminated with Shiga toxin-producing *Escherichia coli* (STEC) in 1982, the concerns with beef safety have been on the rise. The illnesses included bloody diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome (HUS). The ability of STEC to cause (Shiga toxin 1 and/or Shiga toxin 2) or increase (α-hemolysin and/or enterohemorrhagic *E. coli* [EHEC]-hemolysin) the severity of these illnesses is directly related to production of virulence factors. The genes coding for these factors are $stx_1$, $stx_2$, *hlyA*, and EHEC-*hlyA*, respectively. Because beef cattle are STEC reservoirs, they continue to impose significant health risks to humans. The objective was to examine STEC prevalence in four feedlots (ranging from 13,000 to 46,000 Holstein steers) in California and to assess potential pathogenicity of their isolates. To achieve this, 642 fecal samples (approximately 40 samples per feedlot per season) were collected from 321 growing and 321 finishing steers over one year. A total of 21 isolates belonging to 14 STEC serotypes (O86:H19, O114:H2, O125:H19, O127:H19, O136:H12, O136:$H^-$ [nonmotile], O153:$H^-$, O157:H7, O165:H7, OUT [untypeable O antigen]:H5, OUT:H12, OUT:H20, OUT:$H^-$, and OUT:HUT [untypeable H antigen]) were detected and were toxic to Vero (African green monkey kidney) cells. Of these isolates, 12, 5, and 4 had $stx_1$, $stx_2$, or both genes, respectively. Except for two (belonging to the O157:H7 and O165:H7 serotypes, having both genes, and expressing only $stx_2$), all isolates expressed these genes. None of the recovered isolates had the *hlyA* gene whereas 14 isolates had the EHEC-*hlyA* gene but only five expressed it. Of the recovered serotypes, two (O157:H7 and OUT:$H^-$) cause HUS, two (OUT:H12 and OUT:HUT) cause other human illnesses, and seven (O86:H19, O114:H2, O125:H19, O127:H19, O165:H7, OUT:H12, and OUT:H20) have not been reported previously in cattle. The results showed these beef cattle isolates to produce one (n = 14) or two (n = 7) virulence factors and demonstrated the potential health risks of O157 and non-O157 STEC isolates.

**Key Words:** Beef Cattle, Shiga Toxins, *Escherichia coli*

**M98 Prevalence and pre-harvest control factors affecting Shiga toxin-producing *Escherichia coli* in cattle grazing rangeland forages.** L. M. Bollinger*[1], H. S. Hussein[1], and E. R. Atwill[2], [1]*University of Nevada*, *Reno*, [2]*University of California*, *Davis*.

Shiga toxin-producing *Escherichia coli* (STEC) caused numerous outbreaks of human illnesses ranging from mild diarrhea to hemolytic uremic syndrome (HUS). Beef cattle are STEC reservoirs and impose health risks to humans through fecal contamination of beef. To minimize this risk, it is essential to identify and implement pre-harvest control measures that decrease fecal shedding of STEC. The objective was to determine effects of pre-harvest factors on STEC prevalence in California cattle grazing rangeland forages. In six cow/calf operations (ranging from 65 to 225 cows), 774 fecal samples (approximately 32 samples per operation per season) were collected from 463 cows, 40 heifers, and 271 calves (16 to 121-d-old) over one year. Prevalence of STEC was higher ($P < 0.05$) for calves and heifer (8.1 and 15%) than for cows (3.7%) and in the winter than in the other seasons (13.6 vs an average of 3.0%). The STEC isolates belonged to 38 serotypes (O1:H2, O5:$H^-$ [nonmotile], O26:H11, O39:$H^-$, O84:H1, O84:H2, O84:$H^-$, O86:H2, O96:H19, O111:H16, O111:$H^-$, O116:H2, O116:H36, O125:H2, O125:H16, O125:H19, O125:H27, O125:H28, O125:$H^-$, O127:H2, O127:H19, O127:H28, O128:H2, O128:H16, O128:H20, O146:H21, O157:H7, O157:H19, O157:$H^-$, O158:H16, O158:H19, O158:H28, O166:H2, O166:H6, O166:H20, OUT [untypeable O antigen]:H2, OUT:H19, and OUT:$H^-$). Of these, 10 (O5:$H^-$, O26:H11, O84:$H^-$, O111:$H^-$, O125:$H^-$, O128:H2, O157:H7, O157:$H^-$, OUT:H2, and OUT:$H^-$) cause HUS, three (O1:H2, O84:H2, and

OUT:H19) cause other illnesses, and 19 have not been reported previously in cattle. Lower ($P < 0.05$) STEC prevalence was associated with animal factors such as decreasing stock density (≤ 1.0 cow/acre), early separation of calves (≤ 6 mo), increasing the size of calving pasture (> 120 acres), and absence of diarrhetic calves 2 to 4 mo prior to fecal sampling. Of the dietary factors tested (e.g., supplementation of pregnant cows with alfalfa, molasses, or selenium), only molasses decreased ($P < 0.05$) STEC prevalence from 6.7 to 0%. Thus, decreasing fecal shedding of STEC by range cattle appears possible by altering management practices.

**Key Words:** Shiga Toxins, *Escherichia coli*, Beef Cattle

## Forages and Pastures - Livestock and Poultry: Forage Quality and Nutritive Value

**M99 Mineral concentrations of tropical forages in the regions of San Vicente de Caguan, Colombia.** R. Vargas, L. R. McDowell*, R. Van Alstyne, and N. S. Wilkinson, *University of Florida*, *Gainesville*.

In the San Vicente Zone of Colombia, South America, south of Llanos Orientales, beef cattle have been dying of a disease linked to nutrient deficiencies. Botulism is the major disease linked to the bovine mortality with 4000 deaths from 1995 to 2003. Animals were observed with abnormal appetite (pica) consuming old bones and bones from decaying carcasses. Mineral deficiencies, particularly P, are the suspected reason for the large consumption of bone. An experiment was designed to determine the mineral status of forages in relation to cattle requirements from eight ranches in the region of San Vicente de Caguan, Colombia. Forage samples (64) were collected equally between the rainy (September–December, 2002) and dry (January–March, 2003) seasons. The major forage was Brachiaria decumbens, with other important grasses including Axonopus pursuii, Tachypogan vestitus and Leersia hexandra. Samples were collected, dried, ground and analyzed by standardized procedures for 12 minerals. Significant ($P<0.05$) forage concentrations were found among farms and there were season differences ($P<0.05$) for K, Co and Zn. Potassium and Co were higher in the rainy season and Zn higher in the dry season. Forage macromineral concentrations (%) for rainy and dry seasons were as follows: Ca (0.18, 0.15); P (0.07, 0.07); Na (0.04, 0.04); K (5.5, 1.3); Mg (0.22, 0.14) and for trace minerals (ppm); Cu (6.7, 8.3); Co (0.09, 0.34); Se (0.07, 0.08); Zn (15, 34); Fe (108, 136); Mn (173, 238); Mo (0.08, 0.08). In relation to beef cattle requirements almost all samples were severely deficient in P, Na and Ca. Cobalt was deficient only in the rainy season. Potassium, Mg, Fe and Mn were not deficient and Mo was not in excess. The minerals most deficient and most likely causing death and botulism are P, Na, Ca, Se, Cu and Zn.

**Key Words:** Cattle, Botulism, Minerals

**M100 Effect of selenium fertilizer on forage selenium content.** S. J. Filley*, A. Peters, and C. Bouska, *Oregon State University*, *Corvallis*.

The objective of this experiment was to determine the effect of source and rate of Se applied as fertilizer on forage Se content. Low-Se pasture plots (three per treatment) containing perennial ryegrass (*Lolium perenne*) and subterranean clover (*Trifolium subterranean*) were assigned randomly to treatments of 0.0 (control), 0.6, 1.1, and 2.2 kg/ha sodium selenite, and 0.6 kg/ha sodium selenate. Plots were protected from grazing by use of electric fence, and total forage DM production and Se concentrations were measured after the spring growing season in year one. Pastures were grazed by sheep over the fall growing season, but then protected from spring grazing to enable sampling of residual forage Se concentrations during year two. Differences among treatments within year were analyzed with a Kruskal-Wallis non-parametric test. Welch's t-tests were conducted for each two-way comparison between the four active treatments and the control. The significance level was adjusted using a Bonferroni correction. Fertilization with 0.6 kg/ha selenate provided the highest ($P<0.01$) average forage Se content in year one (8.44±0.08 mg/kg). Plots treated with 0.6 and 2.2 kg/ha selenite contained greater ($P<0.01$) forage Se content (1.17±0.05 and 4.24±0.35 mg/kg, respectively) than control (0.09±0.06 mg/kg), whereas the 1.1 kg/ha selenite treatment only tended ($P=0.06$) to increase forage Se content (3.11±0.79 mg/kg). The second year after treatment, forage Se concentrations for the 0.6 kg/ha selenate and 2.2 kg/ha selenite application (0.43±0.04 mg/kg and 0.51±0.06 mg/kg, respectively) were greater ($P=0.04$ and $P=0.01$, respectively) than control (0.06±0.03 mg/kg). Fertilization with Se had no effect ($P=0.37$) on forage yield during year one. These data suggest that selenite and selenate fertilization increases forage Se concentrations for up to two years, and is a cost-effective method of supplying Se for grazing livestock.

**Key Words:** Selenium, Fertilization, Forage

**M101 Effect of organic and chemical nitrogen fertilization on mulberry (*Morus alba*) fodder production.** J. A. Elizondo Salazar* and C. Boschini Figueroa, *Estación Experimental Alfredo Volio Mata. Facultad de Ciencias Agroalimentarias*, *Universidad de Costa Rica, Costa Rica.*

Feeding woody plants as a supplement in dairy and beef systems has been widely used in Costa Rica and many other areas of the world. However, high fodder yields and adequate crude protein levels require application of large doses of chemical N, increasing production costs and pollution risk. To reduce cost, producers are utilizing organic fertilizers from manure without knowing the impact on production. For this reason, a study was conducted to evaluate the application of 150 kg/ha per yr of N from 2 organic fertilizers: vermicompost and compost; and from 1 chemical fertilizer: ammonium nitrate (33.5% N) on fodder production. A 12-yr-old mulberry plantation planted at spacings 0.9 × 0.40 m (27,777 plants/ha) was utilized in a randomized block design with 4 treatments: 2 organic fertilizers, ammonium nitrate, and a control (no fertilizer). All plots were uniformly pruned at 0.6 m from the ground at the beginning of the trial. Fertilizers were applied in 2 doses during the rainy season. For a 365-d period, plants were pruned consecutively every 90 d. Leaves and stems were separated and analyzed for dry matter and crude protein content. Dry matter production was 23% higher for the chemical fertilizer. Crude protein content was also significantly higher for the chemical nitrogen, while dry matter content was lower. The amount of N in the soil was sufficiently high for the control treatment to yield fodder and crude protein levels similar to those of organic fertilizers.