

states but regionally and nationally. However, much less common are regional or multi-state programs where individuals are identified to provide direct support to commodity-based clientele in states other than their own. Utah State University has experience with this type of programming through MOUs developed to provide dairy extension expertise for Montana, Wyoming, and Nevada, which lack dairy specialists but were getting requests from clientele for support. The MOU for each state specified the amount of time spent within the state as well as other activities to be made available. In return, specialist time was bought by the participating state. Our experience provides evidence that these programs can be successful, providing that there is appropriate support from administrators, specialists from the host state, and local county agents. County agent support is critical for achieving the greatest success. Alternatively, there may be opportunities for agreements between states on a county-basis, rather than a state-basis because of proximity of a specialist to localized clientele. Our experience suggests that it works best if money is paid by the state receiving the support to the state that is providing the expertise; it is much cheaper than hiring a new specialist. If a state wants to provide support but doesn't want to provide in-state visits, training workshops via electronic media are an easy option. With the advent of internet audio and video capabilities, extension programming can also be accomplished faster and more economically than physically traveling to that site. Sharing extension expertise across state borders makes sense in many situations, allowing for support of underserved clientele; however, the development of agreements and sharing of a specialist's time requires administrators who are willing to work under a different extension model.

Key Words: extension, multi-state, programs

0595 Extension faculty navigating the tenure and promotion process. N. E. Cockett*, *Utah State University, Logan.*

Decisions of tenure and promotion are a critical mechanism by which a university shapes its future. In addition, each tenure and promotion decision directly affects a faculty member's future in academia. It is imperative that there is clarity in expectations for a faculty position as well as the availability of "best practices" so that a faculty member can be successful in achieving those expectations. Utah State University has developed documents that articulate expectations for Extension faculty (the role statement) and a framework for success (the roadmap). These documents are used not only by faculty members and their direct supervisors to set goals and review performance but also by others, such as the university's central tenure and promotion committee, who are not familiar with the Extension specialist role. The major areas of expectation for Extension faculty include programming and scholarship. Expectations for programming include the identification of needs and issues that lead to the

development of programs that disseminate information and address the issues. Extension specialists should emphasize long-term programs with measurable outcomes and impacts and strong working relationships with Extension county agents. The value of Extension programs can be assessed by the number of participants or contacts and the resulting impacts, such as change in behavior, dollars saved, or dollars generated. At Utah State University, specialists demonstrate scholarship through the dissemination of materials, such as journal articles, fact sheets, web sites, curriculum materials, and presentations and abstracts at professional meetings. All materials should be peer reviewed. The value of scholarship can be determined using standard measurements, such as journal impact factors, citations, invitations for presentations or participation on working groups, and recognition through awards. However, the value of Extension scholarship can also be measured by the uptake or adoption by Extension peers. At USU, Extension specialists are tenured within the academic college, whereas Extension county agents are tenured within USU Extension. While the USU Vice President for Extension does not have direct authority over the decisions of tenure and promotion for Extension specialists, there are annual performance review meetings that include the Extension administration, the department head, and the academic dean. This review provides the academic administration with insight on the performance of the specialists in his or her Extension assignment. A single letter is returned to the faculty member so as to avoid mixed messages on performance.

Key Words: extension, faculty, tenure, promotion, expectations

FOOD SAFETY

0596 Monitoring of pesticide residues in animal feeds from the republic of Korea. H. Park*, H. J. Kim, M. S. Jeong, C. R. Kim, E. S. Choe, Y. S. Youn, J. K. Kim, and J. H. Lee, *Experiment and Research Institute, National Agricultural Products Quality Management Service (NAQS), Ministry of Agriculture, Food, and Rural Affairs (MAFRA), Kimcheon, South Korea.*

Animal feeds can be contaminated with pesticides due to the large number of different ingredients from diverse origins. Safe animal feed is important for both animal health and the safety of foods of animal origin. To ensure the safety of animal feeds, the Ministry of Agriculture, Food, and Rural Affairs (MAFRA) regulates the amount of each pesticide that

may remain in and on animal feeds. To strictly control the pesticide residues in animal feeds, the MAFRA expanded the number of the maximum residue limits (MRLs) in a wide variety of animal feeds from 27 pesticides to 121 pesticides in 2015. Therefore, the aim of this study was to investigate the amount of pesticide residues in various complete feeds and feed ingredients (corn, barley, wheat, oat, and roughage) from the Republic of Korea as a part of an official control. A total of 126 samples were collected in 2015 and monitored for 105 pesticides from diversified chemical classes, including organochlorines, organophosphates, carbamates, triazoles, pyrethroids, and others using a validated multi-residue pesticide analysis method. According to the pesticides monitoring results, no residue was found in 84.1% of the samples, whereas 15.9% of samples contained pesticide residues below the MRLs. Pirimiphos-methyl and cyproconazole were the two most frequently found pesticides. The results revealed that all commercial animal feeds monitored in 2015 were safe and below the Korean MRLs. The low levels of residues of pesticides found in animal feeds were not considered to be serious threats to human or animal health. However, continuous monitoring with tighter regulation for pesticide residues in animal feeds is recommended.

Key Words: pesticide residues, monitoring, animal feeds, MRLs, official control

0597 *Bacillus amyloliquefaciens* from UHT organic milk produces biofilm and demonstrates virulence potential. J. L. McKillip*, A. Grutsch, E. R. Wagner, and C. Klug, *Ball State University, Muncie, IN.*

This investigation identified an isolate of biofilm-producing *Bacillus* spp. present in ultra-high temperature (UHT) pasteurized organic whole milk. The overall goal of this project was to genotypically and phenotypically characterize thermophilic *Bacillus* bacteria for virulence potential from a

UHT dairy environment. Virulence determinants present in this species were detected, and virulence gene expression over time was quantified in a model food (UHT milk) system compared to *B. cereus* ATCC 14579, a known type strain containing the virulence genes of interest. Pure cultures of UHT organic dairy milk were obtained following nonselective enrichment, were biochemically identified to the species level using the Microgen *Bacillus* ID system (Hardy Diagnostics), and were validated further using fatty acid profiling and 16S rDNA sequencing (MIDI Labs Inc.) as *Bacillus amyloliquefaciens*. To confirm the presence of the virulence and regulator genes, DNA was extracted from TSB-grown pure cultures and used in real-time (SYBR Green-based) PCR with primers specific for each of the target genes. PlcR is a pleiotrophic extracellular virulence factor regulator, CodY is a flagellar repressor, NheA and HblC are well-characterized enterotoxins, and 16S served as the housekeeping gene standard. Results revealed that all gene targets were present in the UHT *B. amyloliquefaciens*. Biofilm production was quantified and determined to be produced in amounts that exceeded levels from the *B. cereus* ATCC type strain control. For virulence gene expression measurements, *B. amyloliquefaciens* was inoculated (10^2 CFU/mL) into sterilized organic milk and incubated at ambient temperature (23°C) for 72 h. Every 2 h, samples were removed for standard plate count (SPC)-based density determination and RNA extractions. mRNA for each gene target noted above were amplified with real-time NASBA and transcript-specific primers, revealing relative levels of expression of hblC, nheA, and plcR to be tightly correlated with density during late-log-to-stationary phase growth in the milk system. Dot-blot assays with anti-PlcR will be used to confirm the presence of this regulator protein in the *B. amyloliquefaciens* during incubation at the same time points used for RNA extractions. These data indicate that *Bacillus* spp. present in UHT milk harbor and express the same virulence determinants that are familiar to microbiologists in their psychrotrophic *Bacillus* counterparts, including biofilm potential. These results necessitate that the guidelines on proper storage and shipment of UHT

Table 0596.

Table 1. Summary of the Animal Feed Samples Analyzed for Pesticides

| Pesticide | Use | Total# of Samples | Quantifiable Samples | Feeds | Range (ppm) | Median (ppm) | MRL (ppm) |
|---------------------|-----------------------|-------------------|----------------------|---------------|-------------|--------------|-----------|
| Azoxystrobin | Fungicide | | 2 | Oat, Roughage | 0.66-1.05 | 0.86 | 15 |
| Chlorpyrifos-methyl | Insecticide | | 2 | Barley, Oat | 0.41-0.84 | 0.68 | 6 |
| Cyproconazole | Fungicide | | 5 | Corn | 0.58-0.95 | 0.65 | 2 |
| Piperonyl butoxide | Insecticide synergist | 126 | 1 | Complete feed | 0.30 | 0.30 | 24 |
| Pirimiphos-methyl | Insecticide | | 5 | Complete feed | 0.12-0.30 | 0.14 | 5 |
| Propiconazole | Fungicide | | 3 | Roughage | 0.10-1.48 | 0.12 | 2 |
| Tricyclazole | Fungicide | | 2 | Roughage | 0.11-0.32 | 0.22 | 5 |

milk products be revisited to ensure product safety.

Key Words: UHT milk, *Bacillus amyloliquefaciens*, biofilm, enterotoxins

0598 Occurrence of aflatoxin M1 in UHT, pasteurized, and powdered milk marketed in Hubei province (central China). J. L. Xiong¹, H. L. Zhou², L. Y. Wu^{*1}, and F. T. Meng¹, ¹Hubei Key Laboratory of Animal Nutrition and Feed Science, Wuhan Polytechnic University, Wuhan, China, ²Xiangyang Engineering Research Center of Animal Medicine, Xiangyang Vocational and Technical College, Xiangyang, China.

Aflatoxin M1 (AFM1), a strong carcinogenic derivate of aflatoxin B1 (AFB1), occurs in milk from dairy cows fed an AFB1-contaminated diet and subsequently contaminates dairy products. This survey was conducted to evaluate the occurrence of AFM1 in UHT, pasteurized, and powdered milk available in Hubei province (central China) and to compare these milk AFM1 levels with the maximum AFM1 limits of 50 and 500 ng/L set by the European Commission (EU) and China's Ministry of Health, respectively. A total of 271 samples, composed of UHT milk (120 samples), pasteurized milk (121), and powdered student formula (30) from two major dairy brands available in Hubei province were collected from November 2014 to February 2015 (winter season). Milk AFM1 was detected by using a commercial ELISA method (RIDASCREEN® Aflatoxin M1 test kit; R-Biopharm AG, Darmstadt, Germany) with the detection limit of 5 ng/L. Differences in the concentration of milk AFM1 were statistically analyzed by Mann–Whitney comparisons using SPSS version 19.0 software. The results showed that the mean of AFM1 concentration in positive samples of pasteurized milk was significantly higher ($P < 0.05$) than that in UHT milk (133.4 vs. 20.5 ng/L), and there were significant differences ($P < 0.05$) in AFM1 concentration in milk samples among two dairy brands. In addition, AFM1 was detected in 61 samples of UHT milk (50.8%) with concentrations of 5.5–62.3 ng/L and in 115 samples of pasteurized milk (95.0%) with concentrations between 5.2 and 346.2 ng/L. Moreover, 2 samples of UHT milk (3.4%) and 77 samples of pasteurized milk (63.6%) were found to contain AFM1 above the European tolerance limit, but all samples were below China's legal limit. All samples of powdered student formula were negative at the AFM1 detection limit. The findings of the study are as follows: 1) the content of AFM1 in all milk samples was below China's national legal limit though the incidence of AFM1 in UHT and pasteurized milk was high, 2) powdered student formula was free from AFM1 contamination and thus can be considered the safest milk product tested, and 3) the incidence and concentration of AFM1 in pasteurized milk was higher compared to other dairy products. To maintain milk

safety, strict monitoring systems are recommended.

Key Words: aflatoxin M1, milk, Hubei province

0599 An aptamer-based biosensor for detection of aflatoxin M1. X. Guo^{1,2,3,4}, F. Wen^{1,3}, N. Zheng^{1,2,3}, S. Li^{1,5}, M. L. Fauconnier⁴, and J. Wang^{*1,2,5}, ¹Ministry of Agriculture-Milk and Dairy Product Inspection Center (Beijing), Beijing, China, ²State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, ³Ministry of Agriculture-Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, ⁴Chimie générale et organique, Gembloux Agro-Bio Tech, Université de Liège, Gembloux, Belgium, ⁵Ministry of Agriculture Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.

Aflatoxin M₁ (AFM₁), one of the most toxic mycotoxins, imposes serious health hazards. AFM₁ had previously been classified as a group 2B carcinogen and has been classified as a group 1 carcinogen by the International Agency for Research on Cancer (IARC) of the World Health Organization (WHO). Determination of AFM₁ thus plays an important role for quality control of food safety. In this work, a sensitive and reliable aptasensor was developed for the detection of AFM₁. The immobilization of aptamer through a strong interaction with biotin-streptavidin was used as a molecular recognition element, and its complementary ssDNA was employed as the template for real-time quantitative polymerase chain reaction (RT-qPCR) amplification. Under optimized assay conditions, a linear relationship (ranging from 1.0×10^{-4} to $1.0 \mu\text{g L}^{-1}$) was achieved with a limit of detection (LOD) down to 0.03 ng L⁻¹. In addition, the aptasensor developed here exhibits high selectivity for AFM₁ over other mycotoxins and small effects from cross-reaction with structural analogs. The method proposed here has been successfully applied to quantitative determination of AFM₁ in infant rice cereal and infant milk powder samples. Results demonstrated that the current approach is potentially useful for food safety analysis, and it could be extended to a large number of targets.

Key Words: aflatoxin M₁, aptamer, RT-qPCR.

0600 Individual and combined cytotoxicity assessment of zearalenone and ochratoxin A/ α -zearalenol by full factorial design.

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The co-occurrence of zearalenone (ZEA) and ochratoxin A (OTA) is commonly found in cereals. These mycotoxins can be metabolized after livestock feeding and can then co-occur in later food products in the form of ZEA, α -zearalenol (α -ZOL), and OTA. However, toxicological data concerning the combined effects among these mycotoxins by full factorial analysis design are sparse. In the present study, the combined cytotoxic effects and oxidative damage of ZEA and OTA/ α -ZOL on a human hepatoma cell line (Hep G2) were evaluated by 3×3 full factorial analysis design and the estimated marginal means plot. Nine groups were adopted to investigate the combined effects of three levels of ZEA (0 μ M, 30 μ M, and 60 μ M), three levels of OTA (0 μ M, 6 μ M, and 12 μ M), and three levels of α -ZOL (0 μ M, 15 μ M, and 30 μ M) after 48 h of exposure. Statistical analysis of the data was performed using the SAS 9.2 statistical software package. For the individual mycotoxin, our results demonstrated that Hep G2 cells were more sensitive to OTA than α -ZOL, and α -ZOL was more cytotoxic than ZEA. For the combined mycotoxins, the cytotoxicity, intracellular superoxide dismutase (SOD), and glutathione peroxidase (GSH-Px) activities as well as malonaldehyde (MDA) and glutathione (GSH) contents showed antagonism in combination of ZEA + OTA, whereas the combination of ZEA + α -ZOL behaved from antagonism to synergism as the concentration of ZEA was increased on the overall interaction. There is a significant correlation between cytotoxicity and oxidative damage in the combinations of ZEA + OTA/ α -ZOL ($P < 0.05$), indicating that oxidative damage plays an important role in inducing cytotoxicity.

Key Words: mycotoxins, zearalenone, ochratoxin A, α -zearalenol, combined effect, full factorial design

0601 Distribution and genetic characterization of the top clinically-relevant Shiga toxin-producing *Escherichia coli* in feedlot cattle.

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Shiga toxin-producing *Escherichia coli* (STEC) are causative bacterial agents for severe gastrointestinal illness in humans that include the potentially fatal hemolytic uremic syndrome. Cattle shed STEC in their feces, and collectively, seven serogroups of STEC, including O26, O45, O103, O111, O121, O145, and O157, have been implicated as the main serogroups associated with human disease from contaminated beef. Consequently, screening and characterization of these top serogroups is important for mitigating STEC in the human food chain. The objectives of the current study were to characterize the distribution and genetic diversity of clinically-relevant STEC in feedlot cattle. Isolates that were PCR-confirmed as belonging to serogroups O26 ($n = 116$), O103 ($n = 74$), and O111 ($n = 20$) were obtained from the feces of cattle originating in five regions (southwest Alberta, southeast Alberta, central Alberta, Saskatchewan, and British Columbia) in western Canada over a 2-yr period. Isolates were subtyped by pulsed-field gel electrophoresis (PFGE) and compared to human strains from Alberta ($n = 47$) to assess the distribution of potential clinically relevant strains. O26 isolates from cattle were generally diverse, but isolates from southwest Alberta or British Columbia were more closely related ($P < 0.05$) than isolates from other locations and were most uniform in spring and summer seasons ($P < 0.05$). Isolates of O103 ($n = 74$) from southwest or central Alberta were genetically similar ($P < 0.05$) and more closely related in spring ($P < 0.05$). O111 was not frequently isolated from feces but had location-specific and season-specific PFGE profiles ($P < 0.05$), although isolates from southwest Alberta or those collected in spring were diverse. Human isolates within each serogroup were closely related ($P < 0.05$), but cattle isolates of six O26 strains and ten O111 strains from different seasons and locations were $> 90\%$ similar to human isolates of their respective serogroups. The results from this study showed that serogroups O26 and O103 were highly diverse in cattle, but certain strains persisted in geographic regions, with the least genetic diversity among O26 and O103 strains during the spring season. Some O26 and O111 cattle strains had $> 90\%$ similarity with human isolates, suggesting human pathogens are present in cattle. However, the diverse nature of the cattle isolates implies

that STEC are readily evolving and that only a fraction of cattle isolates are closely related to those causing human disease.

Key Words: Shiga toxin-producing *Escherichia coli*, non-O157, pulsed-field gel electrophoresis

0602 Isolation and characterization of listeriophages for control of growth of *Listeria monocytogenes* in dairy foods. S. H. Lee¹, H. S. Lee¹, S. Heo¹,

C. R. Lee^{1,2}, and G. B. Kim^{*1}, ¹*Department of Animal Science and Technology, Chung-Ang University, Anseong, South Korea*, ²*Feed Industry Research Institute, Korea Feed Association, Seoul, South Korea*.

In this study, two lytic bacteriophages (LMP1 and LMP7) targeting *L. monocytogenes* were isolated from the intestinal content of healthy chickens to identify those with the greatest potential in reducing *L. monocytogenes* in dairy foods. The host specificity of these bacteriophages was determined with different serotypes of *L. monocytogenes* strains by the formation of lytic zones and plaques on host lawns. Genomic and morphological analyses of these phages were also performed to investigate their potential as a means of biocontrol of *L. monocytogenes* in the dairy industry. Lytic activity of *Listeria* bacteriophages was assessed in tryptic soy broth inoculated with *L. monocytogenes* ATCC 7644 or ATCC 19114 and incubated at 30°C for 24 h. Phage lytic activity was also evaluated at 10°C for 5 d in the same composition. LMP1 and LMP7 were able to inhibit the growth of *L. monocytogenes* ATCC 7644 and ATCC 19114 compared with the untreated control both at 30°C and 10°C. LMP1 was more effective than LMP7 against *L. monocytogenes* ATCC 19114; contrary to this, LMP7 was more effective than LMP1 against *L. monocytogenes* ATCC 7644. Morphological characterization from electron microscopy reveals that both LMP1 and LMP7 belong to the *Siphoviridae* family. Bacteriophage genome sequences were determined by next-generation sequencing, and they contain about 40 kb and 47 kb with 69 and 67 coding sequence genes, respectively. Comparative genome analyses could provide some evidence of their different host specificity. The effectiveness of phage cocktail (LMP1 and LMP7) on the growth of *L. monocytogenes* in milk samples was investigated at 30°C and 10°C. The growth of *L. monocytogenes* in milk was effectively inhibited by using the phage cocktail. In conclusion, two listeriophages (LMP1 and LMP7) exhibiting different host specificity were isolated and further characterized; a phage cocktail with these phages could serve as a tool of biocontrol of *L. monocytogenes* in dairy foods.

Key Words: *Listeria monocytogenes*, phages, biocontrol, dairy foods

0603 Effects of feeding NaturSafe on foodborne pathogens in finishing beef heifers. K. M. Feye¹, K. L. Anderson¹, M. F. Scott^{*2}, K. L. Dorton², D. L. Henry², C. R. Belknap², B. E. Depenbusch³, and S. A. Carlson¹, ¹*Department of Biomedical Sciences, Iowa State University, Ames*, ²*Diamond V, Cedar Rapids, IA*, ³*Innovative Livestock Services, Inc., Great Bend, KS*.

With more judicious use of antibiotics in the future, the beef industry will need new science-based strategies to mitigate foodborne pathogens, especially as standard industry technologies are removed from the diet. In this study, cross-bred heifers ($N = 1495$; 359 ± 3.4 kg) were utilized in a randomized complete block design at a commercial feedlot to determine the effects of a *Saccharomyces cerevisiae* fermentation product (NaturSafe; Diamond V, Cedar Rapids, IA) on foodborne pathogens when monensin, tylosin, and direct fed microbials (DFM) were not included in the diet. Upon arrival, heifers were allowed ad libitum access to water and long-stemmed hay. During processing, they received a feedlot tag and growth implant and were vaccinated and treated for parasites. Heifers were then blocked by arrival BW and randomly assigned to one of 2 treatments (10 pens/treatment, approximately 75 heifers/pen). Treatments consisted of a diet containing 1) monensin, tylosin, and Bovamine Defend (positive control, PC), or 2) NaturSafe at 18 g/head/d without monensin, tylosin, and the DFM. Diets were fed twice daily with heifers receiving half of the daily dose of treatment in the TMR at each feeding. Cattle were harvested on d 125 and 146 (5 pens per treatment per day). At the abattoir, fecal swabs and subiliac lymph nodes were obtained from 400 animals (200/treatment, 20/pen). Fecal samples were subjected to selective culture for *Salmonella* and *E. coli* O157:H7 enumeration. Only *Salmonella* were enumerated from the lymph nodes. *Salmonella* isolates from feces and lymph nodes were analyzed for virulence (in vitro assay) and antibiotic (ceftiofur, enrofloxacin, and florfenicol) susceptibility. Statistical analyses were performed using ANOVA with Tukey's test for multiple comparisons. Compared to PC, cattle fed NaturSafe had a lower ($P < 0.05$) concentration of *Salmonella* in the feces (74%) and lymph nodes (86%). The fecal concentration of *E. coli* O157:H7 was decreased ($P < 0.05$) by 58%. *Salmonella* isolates from feces and lymph nodes were less ($P < 0.05$) virulent (68% and 66%, respectively) and associated with a decreased expression of *hilA*, a genetic regulator of *Salmonella* invasion into eukaryotic cells. *Salmonella* resistance to select antibiotics was decreased by 17 to 100% (fecal isolates) and 42 to 75% (lymph node isolates). Results from this study indicate that NaturSafe can be used as a pre-harvest food safety intervention in beef cattle when standard industry technologies like monensin, tylosin, and DFM are removed from conventional production diets.

Key Words: *Saccharomyces cerevisiae* fermentation product, cattle, pathogens

0604 Moxidectin residues in tissues of lambs submitted to three programs of gastrointestinal endoparasite control.

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Moxidectin (MOX) has been reported to induce parasite resistance promoted by frequent drug utilization. To determine dynamic concentrations of drug residues in different sheep tissues according to a gastrointestinal endoparasite control program, two experiments were performed. The first one aimed to determine the time it takes for the MOX concentration to reach the maximum residue limit (MRL) in lamb leg muscles (near the site of drug application (50 µg/kg)) and fat (500 µg/kg). For that, twenty-two lambs were slaughtered on 2, 4, 7, 14, 28, and 42 d after treatment (DAT) with a single dose of MOX (0.2 mg kg⁻¹/body weight). The second experiment aimed to quantify MOX residue in serum, muscle (near and far to the application site), fat, liver, and kidneys of suckling lambs subjected to three programs of endoparasite control: (T1) preventive treatment every 28 d, (T2) treatment when egg count per gram feces (EPG) was equal or higher than 700, and (T3) selective treatment by FAMACHA method (FMC). The experiment was performed in a completely randomized design. The lambs were slaughtered when they reached an average of 30 kg body weight, respecting the time of minimum withdraw period of 28 d. Before slaughtering, blood was collected. Two grams of each tissue was sampled. MOX extraction was based on QuEChERS method. MOX residue was determined using HPLC with mass spectrometry (LC-MS/MS). The depletion curve of MOX for muscle showed a high drug concentration at 2 DAT (1854.2 µg/kg ± 495.0) followed by rapid absorption of the drug at the site of administration, reaching a concentration below MRL at 5 DAT. Longer persistence of MOX was noted at the high concentration, reaching values below the MRL at 17 DAT. Only one sample of fat from the selective treatment group (FAMACHA) showed a concentration of MOX (586.3 mL·kg⁻¹) above the MRL. No sample of serum showed MOX residue levels. Significant correlation was observed between MOX residue in fat and omental fat weight ($P < 0.05$; $r = 0.5310$), suggesting that animals with higher fat deposition may have increased residue persistence in their body. The production of suckling lambs with control of gastrointestinal endoparasites by selective (OPG and FAMACHA) or preventive methods (application every 28 d), considering the 28 d withdraw period, presents a

low risk of incidence (less than 1%) of high concentration of MOX in muscle, fat, kidney, and liver.

Key Words: FAMACHA, EPG, sheep

0605 Shiga toxin-producing *Escherichia coli* on cattle hides and bacterial transfer from hides to carcasses in Midwestern commercial beef slaughter operations.

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Shiga toxin-producing *Escherichia coli* (STEC) are foodborne pathogens that carry Shiga toxin genes (*stx1* or *stx2*) and can cause serious illnesses in humans. These bacteria, which are mainly shed in the feces of cattle, can contaminate beef carcasses during the hide removal and evisceration processes at harvest. Coliforms, including *E. coli*, are utilized as indicator organisms of fecal contamination of beef carcasses during in-plant processing. The objectives of this study were to determine the frequency of the major seven STEC O serogroups and their associated virulence genes on hide-on beef carcass samples and to determine the distributions of *E. coli* and coliform concentrations from cattle hides and carcasses in commercial slaughter operations. Samples were collected from four large commercial processing plants (two in the northern region and two in the southern region of the Midwestern U.S.), which were visited three times each during summer and fall of 2015. Twenty surface swabs were collected at each sampling station (hide-on, pre-wash, pre-evisceration, post-evisceration, and final product) during each plant visit. Hide-on samples were enriched in *E. coli* broth, subjected to immunomagnetic separation, plated on STEC selective media, and confirmed by PCR. Dilutions from hide-on and carcass samples were plated on *E. coli*/coliform 3M Petrifilm plates. The proportion of positive hide-on samples during summer months was 1.3% for STEC O26, 2.1% for STEC O103, 0.4% for STEC O145, and 21.7% for STEC O157, and no positive samples for STEC serogroups O45, O111, and O121. The proportion of positive fall hide-on samples was 0.8% for STEC O26, 0.8% for STEC O45, 0.4% for STEC O103, 0.8% for STEC O145, and 5.0% for STEC O157, and no positive samples for STEC serogroups O111 and O121. There was a greater number of hide-on samples with higher *E. coli* and coliform concentrations compared to pre-wash samples, demonstrating potential transfer of fecal-origin contamination to the carcasses during hide removal. For pre-evisceration and post-evisceration samples, the number of enumerable samples and the distributions of *E. coli* and coliform concentrations varied by region; the role of evisceration in carcass contamination is unclear and possibly due to plant-to-plant variation. There were few enumerable samples for the final product (before split carcasses enter the cooler), which indicates successful application of

interventions by the processing plants. These data will be inputted into a quantitative microbial risk analysis to model the risk of human illnesses due to STEC along the beef chain.

Key Words: STEC

**FOOD SAFETY SYMPOSIUM:
THE SPECTRUM OF FOOD SAFETY
IMPROVEMENT IN FOODS OF
ANIMAL ORIGIN**

0606 Have we improved food safety in live cattle?

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A number of technologies for reducing food-borne pathogens have been evaluated in live cattle, such as direct-fed microbials, vaccines, bacteriophages, and bactericidal feed ingredients. Many of these have been targeted to *E. coli* O157:H7, but efficacy in some cases has been variable, while regulatory approval of others has been less than forthcoming. As strategies to control *Salmonella* in live cattle have been even less successful, different approaches may be needed. For *E. coli*, Shiga-toxins are primary causative factors for human disease and are carried on prophages integrated into the bacterial genome. As transfer of these Shiga-toxin phages can convert previously nonpathogenic *E. coli* to pathogens and as these phages can be carried by other bacterial species, such as *Citrobacter freundii*, should we direct more future live animal food safety efforts to better controlling these endogenous phages? Fight phages with phages? Having a phage already integrated in the bacterial genome has been shown to block lysogeny by *stx*-carrying phages of the same species. Alternatively, as *E. coli* are commensal organisms in the bovine gastrointestinal tract and *E. coli* compete within the microflora for access to nutrients and valuable real estate, would it be possible to utilize the strategies of highly-competitive *E. coli* to suppress the growth of other *E. coli* with Shiga toxins? Could the safety of a direct-fed microbial containing a non-pathogenic but highly competitive strain of *E. coli* ever be assured? The CRISPR system evolved to protect prokaryote DNA from integration of viruses and plasmids. Could CRISPR-cas be used to block possible integration sites for Shiga-toxin phages in a highly-competitive nonpathogenic strain of *E. coli*? Should CRISPR-cas be used in this way? As contamination of hides is the primary route leading to contamination of meat; more emphasis on the control of pathogens on hides is warranted. A bacteriophage-based hide wash for control of *E. coli* O157:H7 has been approved by the USDA, but research data have been limited. However, a recent study by our laboratory demonstrated that non-O157 *E. coli* outweigh the pathogenic potential of O157 in feces of slaughter cattle, as serogroups such as O103 and O45 were relatively ubiquitous year-round and 55 to 65% of isolates of these serogroups

carried Shiga toxins. New pre-harvest approaches that will more successfully control the gamut of current and potential bacterial pathogens in live cattle are warranted.

Key Words: Shiga toxins, *E. coli*, cattle

0607 Improving food safety in live swine.

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Swine can be colonized by a variety of foodborne pathogens that can be harmful to humans who consume contaminated pork products or who are exposed to waste from swine facilities. The most common foodborne pathogenic bacteria that are associated with swine and pork are *Salmonella* and *Campylobacter*. Illnesses in humans attributed to pork products have declined in recent years due to a tremendous effort put forth by the industry; however, the record is still not perfect. While illnesses still occur, steps such as implementing on-farm biosecurity procedures, reducing exposure to pathogens during transport, and lairage have reduced the horizontal spread of these important pathogens in live swine. The economic and public health significance of intervening to reduce pathogen incidence and transmission will be discussed along with methods under development and future research avenues. Actual and theoretical interventions, such as segregated early weaning, group housing, social stresses, reducing transport stress, limiting lairage exposure, bacteriophage, colicins, and sodium chlorate applications will be described. While challenges indeed remain, work to reduce pathogen carriage in live swine holds promise to reduce human pathogen exposures and resultant illnesses.

Key Words: human pathogen exposure, foodborne pathogens, health

0608 Characterization of zoonotic bacteria from dairy cattle in the era of genomics. J. A. S. Van Kessel*, S. W. Kim, J. S. Karns, and B. J. Haley, *USDA-ARS, Beltsville, MD.*

Dairy farms are well-documented reservoirs for zoonotic pathogens. *Salmonella* spp., *Listeria monocytogenes*, Shiga-toxigenic *Escherichia coli*, and *Campylobacter* spp. are often excreted in the feces of cows, and it is common for infected cows to show no signs of illness and not be recognized as sources of human health risks. Historically, comparisons of bacterial isolates from animals and humans were made using molecular genotyping tools, such as pulsed-field gel electrophoresis and rep-PCR, or targeted sequencing techniques, like multilocus sequence typing. The discriminatory power of these tools has been exploited for strain differentiation and epidemiology tracing, the most widespread example being PulseNet. Decreased costs have made whole genome sequencing (WGS) a viable means of comparing the genomes of large numbers of bacterial isolates. Here, we describe several examples where we have used comparative genomics and