

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.

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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

FORAGES AND PASTURE II

0609 Influence of forage diversity on feeding behavior and diet digestibility in lambs. S. Lagrange^{*1,2}, and J. J. Villalba², ¹INTA EEA, Bordenave, Argentina, ²Utah State University, Logan.

metagenomics to describe relationships between dairy-associated isolates and isolates from other sources and elucidate the ecology of pathogens in dairy farm environments. Genome analysis of 118 *Salmonella enterica* serotype Kentucky (*S. Kentucky*) isolates from dairy, poultry, and humans identified some of the poultry and bovine isolates as sequence type (ST) 152, but there was a phylogenetic distinction between the poultry and bovine isolates. The human isolates were primarily distantly related ST198 strains. Three of the dairy isolates were ST198, suggesting that dairy animals are a potential reservoir of this human pathogen. We further compared the fecal microbial communities of *S. Kentucky*-shedding and non-shedding cows to search for potential shifts in community composition associated with *S. Kentucky* carriage. No significant differences between the two groups were observed, suggesting that *S. Kentucky* is a transient commensal gut inhabitant. For *L. monocytogenes*, we sequenced the genomes of 128 isolates from dairy cows and bulk tank milk and compared them to human-associated *L. monocytogenes* isolates. Phylogenetic inference revealed a high level of diversity among the isolated strains. Multiple sequence and virulence types were identified, including at least four virulence types known to be responsible for large outbreaks. Based on a whole genome phylogenetic analysis, several isolates were closely related to human clinical isolates, such as the strain isolated in the 2011 cantaloupe outbreak that was responsible for multiple deaths. Decreased cost and increased access to WGS is radically changing the understanding of the ecology of bacterial populations. With WGS data, much more subtle changes are readily accessible compared with historic methods of distinguishing strains.

Key Words: *Salmonella*, *Listeria*, dairy

Diverse combinations of forages with different nutrient profiles and classes of plant secondary compounds (PSC; tannins, saponins) may improve intake and nutrient utilization by herbivores. We tested the effects of increasingly diverse combinations of PSC-containing legumes on intake and diet digestibility in lambs. Freshly-cut birdsfoot trefoil (TRE), sainfoin (SAN), and alfalfa (ALF) at the early flowering stage were offered in ad libitum amounts to forty-two lambs in individual pens assigned to 7 treatments ($n = 6$): single species, a choice of all possible 2-way combinations, or a 3-way choice of the legumes. Compositated forage and fecal samples and acid detergent lignin were used to determine in vivo DMD. The change in concentration of BUN from the beginning to the end of the study (24 d) (Δ BUN) was also assessed. Dry matter intake (DMI) and digestible DMI (DDMI) were analyzed as repeated measures designs with lambs (random effect) nested within treatments. A complete random design was used for the remaining variables with treatment as a fixed factor. Lambs preferred ALF > SAN > TRE in 70:30 and 50:35:15 ratios for 2- and 3-way combinations, respectively ($P < 0.05$). Average DMI and DDMI were 10% greater for 2- and 3-way choices than for single species (Table 1). Digestibility values of tannin-containing legumes (SAN and TRE) and their combination were greater than those recorded for the saponin-containing legume (ALF) or ALF/TRE (Table 1). Feeding SAN in a single diet or in combination had lower Δ BUN and greater fecal N/N consumed ratio (Table 1) than ALF, TRE, or ALF/TRE, suggesting a shift in the site of N excretion from urine

Table 0609.
Table 1.

Items	Treatments							SEM	CHOICE vs Single Diets P-Value
	ALF	SAN	TRE	ALF/ SAN	ALF/ TRE	SAN/ TRE	ALF/ SAN/ TRE		
DM,%	19.7 ^a	18.2 ^{ab}	16.6 ^b					0.67	
CP,%	16.5 ^b	13.4 ^c	19.3 ^a					0.42	
ADF,%	31.1 ^b	39.3 ^a	31.6 ^b					1.13	
DMI, gr/Kg BW/d	35.9 ^{ab}	32.4 ^b	27.4 ^c	37.8 ^a	34.3 ^{ab}	33.5 ^{ab}	36.0 ^{ab}	1.88	0.0217
DMD,%	59.3 ^d	68.1 ^a	65.7 ^b	64.2 ^b	61.6 ^c	68.4 ^a	64.6 ^b	0.67	0.5450
DDMI, gr/Kg BW/d	21.3 ^b	22.1 ^{ab}	18.0 ^c	24.3 ^a	21.0 ^b	22.9 ^{ab}	23.2 ^{ab}	1.12	0.0087
Fecal N/N consumed	0.33 ^{cb}	0.38 ^a	0.28 ^d	0.35 ^b	0.32 ^c	0.35 ^b	0.34 ^{cb}	0.01	0.3390
Δ BUN, mg/dL	-1.0 ^{bc}	-4.2 ^d	2.3 ^a	-1.7 ^{dc}	1.7 ^{ab}	-0.3 ^{abc}	0.0 ^{abc}	1.18	0.3457

Means in a row with different superscripts differ ($P < 0.1$).