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3:30pm
DBI Room 102

Presence of pathogenic *Escherichia coli* is correlated with bacterial community diversity and composition on pre-harvest cattle hides
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ABSTRACT:

Background: Since 1982, specific serotypes of Shiga toxin-producing *Escherichia coli* (STEC) have been recognized as significant foodborne pathogens acquired from contaminated beef, and more recently, other food products. Cattle are the major reservoir hosts of these organisms, and while there have been advancements in food safety practices and industry standards, STEC still remains prevalent within beef cattle operations with cattle hides implicated as major sources of carcass contamination. To investigate whether the composition of hide-specific microbial communities are associated with STEC prevalence, 16S rRNA bacterial community profiles were obtained from hide and fecal samples collected from a large commercial feedlot over a three-month period. These community data were examined amidst an extensive collection of prevalence data on a subgroup of STEC that cause illness in humans, referred to as enterohemorrhagic *E. coli* (EHEC). Fecal 16S rRNA gene OTUs (operational taxonomic units) were subtracted from the OTUs found within each hide 16S rRNA amplicon library to identify hide-specific bacterial populations.

Results: Comparative analysis of alpha diversity revealed a significant correlation between low bacterial diversity and samples positive for the presence of *E. coli* O157:H7 and/or the non-O157 groups: O26, O111, O103, O121, O45, and O145. This trend occurred regardless of diversity metric or fecal OTU presence. The number of EHEC serogroups present in the samples had a compounding effect on the inverse relationship between pathogen presence and bacterial diversity. Beta diversity data showed differences in bacterial community composition between samples containing O157 and non-O157 populations, with certain OTUs demonstrating significant changes in relative abundance.

Conclusions: The cumulative prevalence of the targeted EHEC serogroups was correlated with low bacterial community diversity on pre-harvest cattle hides. Understanding the relationship between indigenous hide bacterial communities and populations may provide strategies to limit EHEC in cattle and provide biomarkers for EHEC risk assessment.