THE MICROBIOME OF A NEWLY CONSTRUCTED MEAT PROCESSING FACILITY DIFFERS BASED ON ROOM FUNCTION AND TIME

A. D. Belk[1*], N. Frazier[1], L. Fuerniss[1], I. Geornaras[1], B. Borlee[2], R. Delmore[1], J. Martin[1], and J. L. Metcalf[1],

[1]*Animal Science, Colorado State University, Fort Collins, CO, USA*,

[2]*Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, CO, USA*,

*aeriel.belk@colostate.edu

I. OBJECTIVES

Significant progress has been made towards reducing the occurrence of foodborne illness in the United States; however, foodborne pathogens still present a public health risk. These organisms, especially *Listeria*, find unique niches in meat processing facilities where they can then persistently contaminate food products. This phenomenon is well-described, but there is a knowledge gap in where these organisms originate and how they colonize these spaces. Recently, a new meat processing facility was constructed at Colorado State University providing a unique opportunity to study the succession of microbiota and the potential establishment of *Listeria* in a new built environment. The objectives of this study were to determine the patterns of microbial community composition within a new meat processing facility and how they associate to both *Listeria* presence as well as facility function.

II. MATERIALS AND METHODS

To investigate this, a longitudinal experiment was designed to characterize microbial communities and detect *Listeria* throughout the processing facility at 10 time points, beginning immediately after postconstruction cleaning and continuing monthly after the start of production. At each time point, surface samples were collected from the internal surfaces of all drains and select door handles in all production rooms, coolers, storage rooms, and human corridors. *Listeria* samples were collected using a premoistened, buffered sponge and quantified using real-time polymerase chain reaction. The microbial communities were collected via sterile swabs, then DNA was extracted using a commercial kit, and 16S ribosomal RNA gene amplicons were sequenced. These data were analyzed using the QIIME2 platform and R software. Statistics used an alpha level of 0.05.

III. RESULTS

During the first year of processing at the newly constructed facility, no resident population of *Listeria* was observed in any production room, though transient populations were identified in several locations. Principal coordinates analysis revealed that microbial communities identified in the facility associated more closely with the function of the room (i.e., harvest, fabrication) than the sampling time point, indicating that the microbes present in a room were influenced by the room activity. This trend was confirmed by permutational analysis of variance analysis ($P < 0.05$). Within a room, there were changes in the microbial communities over time, though it did not appear that a consistent community was established within the first year of sampling. However, samples taken at later time points appear more similar to each other than samples collected in the months after opening, suggesting that a resident community will form as production continues. Moreover, an

analysis of the composition of microbiomes demonstrated that there are several key taxa that are significantly different across facility spaces and time ($W = 161$). Clostridiales were more closely associated with live animal and harvest spaces, Pseudomonadales were associated with processing and fabrication spaces and became more persistent at later time points, and Bacteriodales were common in processing spaces.

IV. CONCLUSION

The microbial community of the meat processing facility differs among rooms and may be associated with specific functions of the room. Furthermore, results suggest that, with daily cleaning and sanitation practices, a resident *Listeria* community does not form in the first year of facility production.

Keywords: 16S, facility microbiome, *Listeria* spp., microbiome, processing environment