RESEARCH IN PROCESS

Identifying optimal methods of recovering bacteria from food processing plants for downstream microbiome analyses

SUMMARY

Microbiome studies have provided important insights into how microorganisms impact human and public health. While a large number identify microbial communities in the gastrointestinal tract of humans and animals, there is increasing interest in understanding diversity in the built environment such as food processing facilities. An accurate map of a building's microbiome requires the use of robust methods capable of recovering a representative collection of all microorganisms found on food-contact and non-contact surfaces. The current approach starts by swabbing surfaces with a pre-wetted swab or sponge, followed by DNA extraction. Given the importance of this step, it is surprising that potential sources of sampling bias are not rigorously tested in most microbiome surveys of food processing plants. In this proof-of-principle study, we will test four sampling-related assumptions made in many microbiome studies.

OBJECTIVES

This project will provide insights into several assumptions made in published microbiome studies:

1. That microbial communities are similar at proximal sites;
2. That microbial communities recovered using different sampling devises will not change;
3. That similar communities are recoverable from porous vs. non-porous surfaces; and
4. That microbial communities recovered are not affected by swabbing time.

METHODS

Sampling and data analysis from an apple packing facility

Ongoing studies in the lab of Co-PI LaBorde identified an apple packing facility in Pennsylvania that is routinely positive for *Listeria monocytogenes*. For Objectives 1 and 2, a 36" × 30"" area was selected (Fig. 1), and ten sections measuring 6" × 5"" were each swabbed with polyurethane, polypropylene, and cellulose sponges. For Objective 3, ten pieces of stainless steel and concrete bricks of similar size (Fig. 2) were inoculated with a liquid sample (Fig. 3) from the packing facility, and swabbing was done using only the polyurethane sponge. Objective 4 was carried out similarly, however the swabbing times were varied between 5 and 30 seconds. DNA from organisms captured in the sponges will be extracted, and microorganisms present will be identified by 16S rRNA sequencing. The software tool mothur will be used for data analysis.

RESULTS TO DATE

Collection of samples is complete

To date, we have collected all 90 samples for the four objectives. During Summer 2018, DNA from these samples will be extracted. The 16S rRNA amplification and analysis will be performed during the Fall 2018 semester.

BENEFITS TO THE INDUSTRY

This research will provide invaluable prerequisite information for future work in an important area of investigation. The immediate beneficiaries of this research are scientists working on projects that use microbiome analysis to understand the microbial diversity within food processing plants. There is a great deal of interest in applying these techniques, but we have little understanding of whether the sampling methods used are the most appropriate. Our work will provide scientific data needed to realize the full impact of this field in food safety, including the safety of fresh produce, making this industry the long-term beneficiary.

Figure 1.

Figure 2.

Figure 3.

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