When the *E. coli* hits the fan! Evaluating the risks of dust-associated produce cross-contamination

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Summary

Dust represents an understudied vehicle for microbial dispersal and produce contamination by pathogens. This study proposes the following: 1) To evaluate the role of dust in transferring foodborne pathogens to produce surfaces grown in eastern and western US regions, 2) To determine the role of humidity in the deposition of dust on produce and the survival of pathogens in dust, and 3) To test dust particulates from animal operations in both regions for the presence of biomarkers indicative of fecal contamination and the potential presence of pathogens. This study will enhance our understanding of pathogen transport from feces into and through produce fields and will quantify the risk associated with contamination from dust under varying environmental and atmospheric conditions.

Objectives

1. Evaluate the role of dust in transferring foodborne pathogens to the surfaces of produce commodities specific to the eastern and western agricultural regions of the United States.
2. Understand the role of humidity in the deposition of dust on produce and the survival of foodborne pathogens in dust particulates.
3. Test dust particulates from animal operations for the presence of biomarkers indicative of fecal contamination and the presence of enteric bacterial pathogens.

Methods

The transfer rates of *E. coli* O157:H7 and *Salmonella* species per gram of dust to the surfaces of conventional and organic romaine lettuce and spinach (Arizona), tomatoes and bell peppers (Georgia) will be determined in experiments (**Figure 1**) conducted in biosafety level 2 (BSL-2) environmental chambers, simulating the growing conditions in the region of interest. These data will be compared to cross-contamination by simulated water splashing and soil contact.

The role of humidity, agricultural practice (organic vs. conventional), and soil characteristics (clay vs. sandy soil) on cross-contamination will be evaluated. Persistence of bacteria on dust-contaminated produce will be monitored until harvest.

Dust particulates located at various distances away (e.g., 400 feet, 1,200 feet, and 1 km) from poultry and beef facilities will be collected over two years.

Results to Date

BSL-2 environmental growth chambers were set up in both Arizona and Georgia and fresh produce was planted (**Figure 2**).

Soil from conventional and organic farms were collected and assessed for background levels of bacteria, moisture content, and organic content. Moisture content, organic content, and background bacteria were found to be higher in soil from organic farms.

Because of the high background levels of bacteria in the soil to be used in the laboratory experiments, various *E. coli* O157:H7 and *Salmonella* Newport strains were constructed (**Table 1**) that contain antibiotic resistance genes found either on a plasmid (P) or on the chromosome (C) as well as the gene for green fluorescent protein (on a plasmid).

Benefits to the Industry

This project will enhance our understanding of pathogen transport from feces into and through produce fields, and quantify the risk associated with contamination from dust. Contamination of produce grown in two different regions of the US (Arizona and Georgia), with varying environmental and atmospheric conditions, is being investigated. We will develop exposure models using a QMRA framework to estimate risks from dust transporting microbial contamination onto produce and to determine the importance of dust particulate type, produce type, and proximity to animal operations. Information on the occurrence and survival of pathogens on fresh produce and the level of contamination under different conditions will be utilized for the implementation of this model. This research will help to improve the safety of fresh produce.

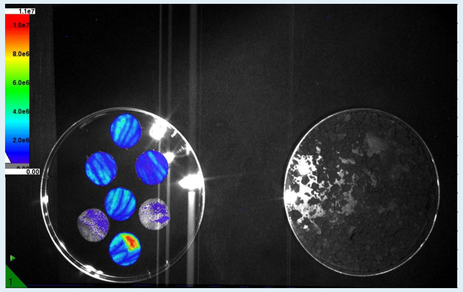

Figure 1. Biophotonic imaging of transfer of *Salmonella* Newport from conventional soil to iceberg lettuce discs after 30 minutes.

Figure 2. Constructed biosafety level 2 (BSL-2) environmental growth chamber.

Bacterial Strain	Primer Specificity	Primer Sequence (5'-3')	Amplicon Size (bp)	Doubling Time (min)
E. coli O157:H7 H1730 (non resistant)	5.90 ± 0.16	1.92 ± 0.06	2.22 ± 0.13	66.0
E. coli O157:H7 H1730 AMP P	6.08 ± 0.32	1.78 ± 0.03	2.38 ± 0.18	64. 2
E. coli O157:H7 H1730 AMP P Strep C	8.73 ± 0.10	2.44 ± 0.02	2.32 ± 0.20	98.4
E. coli O157:H7 H1730 Strep C	7.92 ± 0.08	2.19 ± 0.02	2.12 ± 0.09	97.1
E. coli O157:H7 H1730 AMP C	6.37 ± 0.12	2.47 ± 0.02	2.09 ± 0.08	66.5
E. coli O157:H7 H1730 AMP C Strep C	5.73 ± 0.18	1.77 ± 0.04	2.24 ± 0.10	80.4
Salmonella Newport (non resistant)	7.52 ± 0.92	0.92 ± 0.14	2.04 ± 0.30	52.2
Salmonella Newport AMP P	8.22 ± 0.50	0.98 ± 0.04	2.02 ± 0.13	56.4
Salmonella Newport AMP P Strep C	11.00 ± 0.71	0.84 ± 0.10	2.27 ± 0.09	79.8

Table 1. Analysis of growth rates of *E. coli* and *Salmonella* strains.