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Title:

Why We Peel Melons: A Peek into the Prevalence of Foodborne Pathogens Among Field-Grown Melons in Arizona

Introduction:

Foodborne outbreaks involving contaminated melons have occurred multiple times in the United States over the past decade.

Purpose:

Understanding the prevalence of indicator microorganisms and foodborne pathogens in Arizona grown commercial melons and their environmental samples will assist in a risk assessment of the melon production environments.

Methods:

In 2018 and 2019, 564 cantaloupes, 27 soil, 27 rhizosphere, 27 air, and 15 water samples were collected from nine different fields in Arizona. Each melon rind sample included a composite of rinds from three cantaloupes harvested from the same field. All samples were enriched in double strength Universal Pre-Enrichment Broth. Selective enrichment and plating were used to analyze the presence/absence of *Listeria* and *Salmonella* species and enumerate the indicator microorganisms.

Results:

The indicator microorganism population range for 2018 were 2.79 – 4.57, 1.53 – 4.04, <1 – 4.86, <1 – 2.11, and <1 – 2.72 and for 2019 were 2.3 – 4.1, 0.9 – 3.4, 2.3 – 4.6, <1 – 3.0, and 1.6 – 3.8 Log CFU/g for melon rind, soil, rhizosphere, air, and water samples, respectively. Overall, melon rind composites and rhizosphere samples had higher indicator microbial populations than the other environmental samples. The lowest indicator microbial population was observed in the air samples. None of the melon composites or environmental samples were positive for *Listeria* or *Salmonella* species. Three melon composite samples were positive for *Escherichia coli* on ECC-CHROMagar™, while none of the environmental samples were positive for *E. coli*. Further testing will be performed to determine if the *E. coli* colonies are O157:H7.

Significance:

These results will help us understand the level of risk during melon production due to the prevalence of *Listeria* and *Salmonella* species in Arizona growing conditions. The data can be used to correlate the potential of fecal contamination due to high levels of indicator bacteria with the prevalence of *E. coli* in a science-based risk assessment.