

Tracing foodborne pathogens on the farm

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Esther Fortes, a member of the Cornell Produce Sampling Team, collects a water sample from a stream located adjacent to one of the produce fields used in the study. Credit: Laura Strawn

(Phys.org)—In 2011, an outbreak of Listeria monocytogenes in cantaloupe led to almost 150 illnesses and 30 deaths. With a spate of recent outbreaks of such foodborne pathogens as Salmonella, Shiga toxinproducing E. coli and L. monocytogenes, the ability to predict where and how these deadly microbes enter the food supply chain could save lives and prevent disease.

Cornell researchers have created a method that uses geospatial algorithms, foodborne pathogen ecology and Geographic Information



System (GIS) tools to predict hot spots where these pathogens may be present and spread on farms prior to harvest. Many of the recent outbreaks of <u>foodborne pathogens</u> have been linked to contamination on the farm.

The method, which can be applied to any farm, uses classification tree tools with remotely sensed data, such as topography, <u>soil type</u>, <u>weather</u> <u>trends</u>, proximity to various sources (water, forests) and more, to predict areas where pathogens are likely to be present.

"We wanted to see if we could identify factors that gave us a higher or lower prevalence of finding these pathogens," said Laura Strawn, a graduate student in the field of food science and lead author of a study published online Nov. 9 in the journal <u>Applied and Environmental</u> <u>Microbiology</u>. "We can look at a farm and use this data analysis tool to tell the farmer where these hotspots may be for foodborne pathogens," she said.

"These tools are likely to provide a completely new science-based approach for guidance on how to reduce the likelihood of contamination with these bacteria," said co-author Martin Wiedmann, a food science professor and study co-author.

By knowing where the hot spots are, farmers may then implement such preventive practices as draining standing water, adjusting where livestock graze, or planting crops that should be consumed cooked rather than raw, for example, Strawn added.

The researchers collected 588 samples soil, water, feces and drag swabs (gauze attached to a string and dragged over a field) from four produce fields on five farms each. Samples were collected four times a year, during each season, from 2009 to 2011. The prevalence of L. monocytogenes, Salmonella and E. coli were 15.0, 4.6 and 2.7 percent



respectively across all the samples. L. monocytogenes and Salmonella were detected more frequently in water samples from irrigation sources or nearby streams, while E. coli was found in equal distributions across all the sample types.

L. monocytogenes and Salmonella were found in higher frequencies in areas with moist soils. For Salmonella, "if you had more precipitation before a sample was collected, you were more likely to find that pathogen," said Strawn. Also, well-drained fields had lower Salmonella prevalence. Knowledge of such factors would help predict whether an area of a farm may be at higher risk.

For Listeria, proximity to water, pastures, livestock and grazing cattle, wildlife habitation and nearby impervious surfaces, roads and ditches all predicted a higher prevalence of the pathogen.

Once such factors have been identified, the GIS platform may be used to filter out specific areas based upon those factors (such as filtering areas that have moist soils and close proximity to water) to create a color-coded map of any farm area with predicted prevalence for a pathogen.

"This work advances our understanding of the environmental microbiology of foodborne <u>pathogens</u> and permits tailored solutions to predict contamination of produce commodities during cultivation," said Peter Bergholz, a research associate in <u>food science</u> and the study's corresponding author.

Provided by Cornell University

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