RESEARCH IN PROCESS

Remotely-Sensed and Field-Collected Hydrological, Landscape and Weather Data Can Predict the Quality of Surface Water Used for Produce Production

SUMMARY

There is a clear need for improved, science-based tools to reduce the introduction of microbial produce safety risks into preharvest environments through surface water use. The purpose of this project is to use publically available data to (i) prioritize spatial and temporal risk factors for microbial contamination of surface water, and (ii) develop spatiotemporal models to predict surface water microbial quality, which will be assessed by quantifying generic *Escherichia coli,* and testing for key pathogens (e.g., *Salmonella, Listeria monocytogenes*) and indicator organisms (e.g., coliforms, *L. innocua*). Spatiotemporal variation in water quality will be assessed by repeatedly testing multiple water sources in Arizona and New York over two years. The data and models generated will allow growers to identify times and locations where surface water sources are more likely to be microbially contaminated. This will enable growers to better time water use, testing, and treatment to minimize produce safety risks.

OBJECTIVES

Objective 1: Perform sampling on 4 New York and 4 Arizona waterways throughout one growing season to examine changes in generic *E. coli* levels as well as pathogen presence at a fine temporal scale.

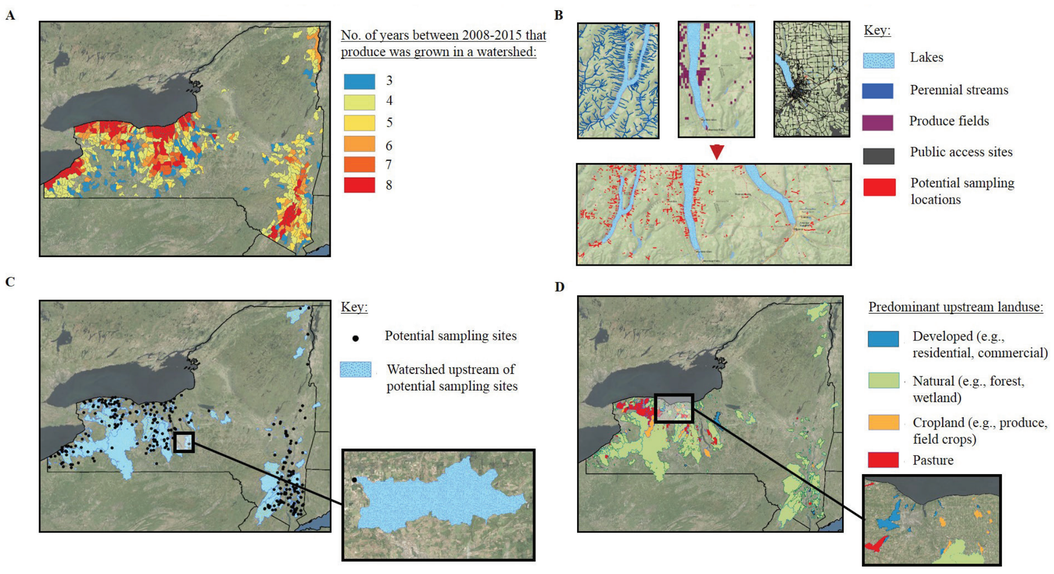
Objective 2: Perform sampling on 60 New York and 60 Arizona waterways throughout one growing season to allow us to assess spatiotemporal variation in generic *E. coli* levels, and pathogen presence.

Objective 3: Identify and prioritize consistent and region-specific factors that are associated with generic *E. coli* levels as well as pathogen presence in surface water, and to use these data to develop a series of spatiotemporal models to predict surface water quality in New York and Arizona.

METHODS

During the 2017 growing season, four streams (NY) and 4 canals (AZ) will be sampled to assess variation in surface water quality throughout (i) a growing season, (ii) a week, and (iii) a day (Figure 1). During the 2018 growing season, 60 streams (NY) and 60 canals (AZ) will be sampled five times to assess spatial variation in water quality. Relevant metadata (e.g., upstream landuse) will be obtained for each site and sample collection. At each sampling, a 24-h Moore swab (MS) and three 10-L grab samples (GS) will be collected. *E. coli* concentration and pathogen (e.g., *L. monocytogenes, Salmonella*) presence in the MS and GS will be determined. The collected data will be used to (i) assess the correlation between *E. coli* levels in matched MS and GS, (ii) quantify the association between *E. coli* levels and pathogen presence in surface water used for produce production, and (iii) develop a series of spatiotemporal models to predict surface water quality.

Figure 2. New York streams were enrolled in the study using the following steps. Watersheds where produce was grown for <2 of the last 8 years were identified (A). Within these watersheeds publicly accessible sites ≤50m from a perennial stream and ≤400m from a produce field were identified (B). Points were then randomly generated within the areas delineated in (B), and the upstream watershed for each point was calculated (C). The predominant upstream landuse for each watershed was then determined (D). Fifteen watersheds per landuse were enrolled in the study.



RESULTS TO DATE

As of April 2017, we have identified all waterways to be sampled in 2017, and all NY streams to be sampled in 2018 (Figure 2). We began sampling in AZ in February 2017. As of April 2017, sampling has been performed at two sites; one site was sampled over the course of a week ("weekly" sampling), and both sites were sampled over the course of a day ("daily" sampling; Figure 1). We collected17 grab samples (GS) and 6 24-h MS during these sampling trips. The average concentration of generic *E. coli* in the GS and MS was 7.4 MPN/100 mL [Standard Deviation (SD) = 8.0] and 669.4 MPN per MS (SD = 943.9), respectively. PCR screens for *Salmonella* and Shiga toxin–producing *E. coli* were positive for 9% of samples (2/6 MS and 0/17 GS) and 43% of samples (3/6 MS and 7/17 GS), respectively (Table 1).

BENEFITS TO THE INDUSTRY

The goal of this project is to provide data and tools that will help growers (i) minimize pathogen introduction into preharvest production environments, and (ii) manage surface water sources to comply with FSMA mandated standards for generic *E. coli* levels in irrigation water. Broadly speaking, the produce industry will benefit from the project as the findings will provide for more effective, scientifically justified preharvest risk management strategies that allow for improved management of agricultural water. The project will provide (i) risk factors associated with elevated *E. coli* levels and an increased likelihood of pathogen contamination in surface water, and (ii) spatiotemporal models that can be used to assess specific surface water sources. The spatiotemporal models will provide a framework for the development of improved GIS-based tools as more data become available. The proposed project will also provide information on the utility of remotely-sensed data and geospatial analyses to inform risk management efforts.

Figure 1. For Objective 1, sampling will be performed to assess variation throughout a (i) growing season, (ii) different days of the week ("weekly sampling"), and (iii) different times of the day ("daily sampling"). For weekly sampling, 7 grab samples and 6 Moore swabs will be collected over the course of one week (A). For daily sampling, 6 grab samples and 1 Moore swab will be collected over the course of one day (B).

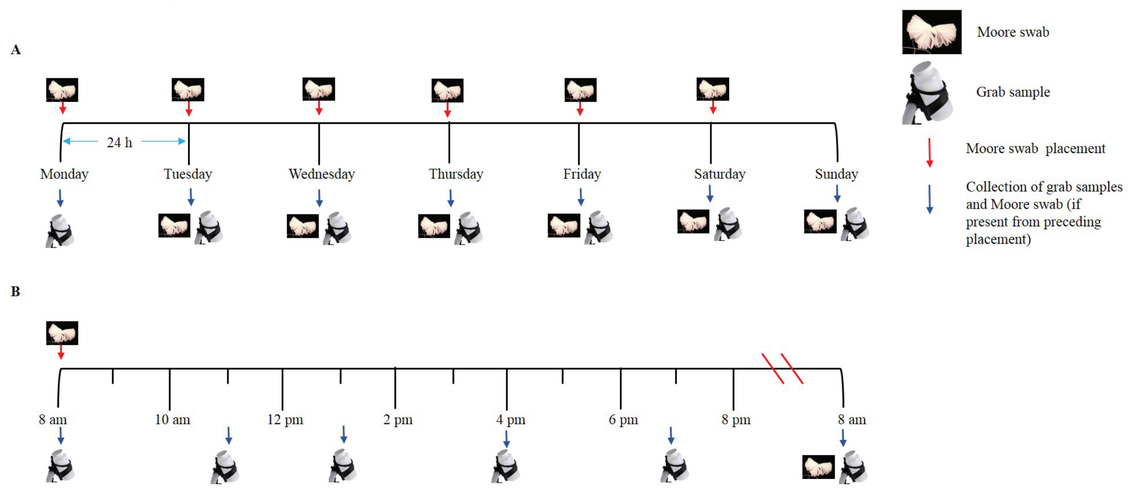


Table 1. Concentration of *E. coli* and total coliforms, and frequency of key foodborne pathogens in water obtained from Arizona canals in February and March 2017.

Sample Type	No. of Samples	Concentration [a] (Standard Deviation)		No. of samples positive by PCR for			
		Total coliforms	*Escherichia coli*	*Listeria monocytogenes*	*Salmonella*	Shiga-toxin producing *E. coli*	Enteropathogenic *E. coli* [b]
Grab sample	17	590.3 (358.3)	7.4 (8.0)	0 (0%)	0 (0%)	7 (41%)	5 (50%)
Moore swab	6	>2419.6 [d]	669.4 (943.9)	0 (0%)	2 (33%)	3 (50%)	2 (67%)

[a] Total coliform and *E. coli* concentration was determined using IDEXX Colilert-18 Quanti-tray assays. For grab samples the concentration is reported as MPN/100 mL, and for Moore swabs the concentration units is reported as MPN per Moore swab.

[b] Due to the assay used for detecting pathogenic *E. coli*, enteropathogenic *E. coli* (EPEC) can only be detected in samples that are negative for Shiga-toxin producing *E. coli* (STEC). As such, the prevalence of EPEC reported in the table is the number of samples positive for EPEC divided by the number samples negative for STEC.

[c] The total coliform concentration was above the detection limit (2419.6 MPN) of the IDEXX Colilert-18 Quanti-tray assay in all Moore swabs.

CONTACT

Martin Wiedmann
Department of Food Science
Cornell University
347 Stocking Hall
Ithaca, NY 14853
Phone: 607-254-2838 Fax: 607-254-4868
mw16@cornell.edu

AUTHORS

Daniel Weller, Natalie Brassill, Channah Rock (Co-PI), Martin Wiedmann (PI)

ACKNOWLEDGEMENTS

Sherry Roof, James Dalton, Amber Roberts, Stevi Zozaya, Jess Dery, Raul Betancourt

LENGTH OF FUNDING

January 1, 2017 – December 31, 2018

CPS CENTER for PRODUCE SAFETY