Agent-based models can predict appropriate risk-based set-back distances for flooded fields

Summary

Flooding of produce fields presents a food safety risk by introducing and dispersing bacterial hazards. Standard one-size-fits-all set-back distances cannot adequately manage risk because each flooding event is unique with regard to soil type, weather, and pathogen levels. To help growers implement situation-appropriate set-back distances, we are (i) developing an agent-based model (ABM) that predicts pathogen survival and dispersal after flooding and (ii) compiling experimental data on growth, die-off, and transfer of key bacterial hazards (*Salmonella*, enterohemorrhagic *E. coli*, *Listeria*). The model integrates soil, weather, and pathogen dynamics; parameters are being refined through a literature review, mesocosm studies across three soil types. A simulated flooding event in a commercial-scale field has been performed to generate data for validation.

Benefits to the Industry

This project will deliver (i) an open agent-based model, with user guidance, that predicts situation-appropriate set-back distances for flooded produce fields, and (ii) a peer-reviewed dataset of pathogen growth, die-off, and dispersal parameters that others can use to independently assess risk. These tools will help industry replace one-size-fits-all set-backs and wait-periods with location- and situation-specific risk management informed by soil type, weather, and pathogen. Growers making post-flood planning or harvest decisions, and groups that develop guidance on flood-related food safety risk (e.g., LGMA, state departments of agriculture), will be direct beneficiaries. By capturing differences across soil types and pathogens, the model supports more defensible, risk-based decisions than current prescriptive approaches.

Objectives

1. Develop an agent-based model (ABM) to model the dispersal and population dynamics of bacterial pathogens and to predict appropriate risk-based set-back distances.
2. Perform mesocosm studies using different soil types and moisture levels to collect dispersion rates from flooded soil to unflooded soil for the ABM developed in Obj. 1.
3. Validate the ABM predictions through a simulated flooding event in a commercial-scale field as well as published and unpublished data collected from natural and simulated flooding events.

Methods

The ABM is implemented in Python using the Mesa package and simulates water movement between soil blocks alongside microbial population dynamics for *Salmonella*, enterohemorrhagic *E. coli*, and *Listeria*. Soil parameters (for silt loam, sandy loam, clay loam) and daily weather (rainfall, solar radiation, soil temperature) are ingested dynamically. Mesocosm experiments using three soil types will quantify water and pathogen dispersal under controlled conditions. A field-scale simulated flooding event, using inoculation with non-pathogenic surrogates of the three target pathogens, generated data for both parameterization and validation. In parallel, a systematic literature review (1,385 records screened; 197 full-text reviewed) combined with an AI-assisted extraction pipeline is compiling equations and parameter estimates to inform the model.

Results to Date

The ABM supports multiple soil types and site-specific daily weather, simulating *Salmonella*, EHEC, and *Listeria* dynamics during and after flooding. Simulated *Salmonella* contamination in both the flooded and adjacent areas fell below detection (~0.81 log10CFU/g) by day 46 (**Figure 1**) as compared to 56 and 73 days for EHEC and *Listeria*. At 0-10 ft beyond the flooding edge, *Salmonella*, EHEC, and *Listeria* were predicted to decline below detection the detection limit within 16, 26, and 31 days, respectively. Literature extraction yielded 123 usable papers (58 with equations, 89 with datasets). Mesocosm methods and sampling were finalized and initial trials have been completed (**Figure 2**). Field-trial showed linear die-off for all three surrogates (*E. coli*: -0.011; *Salmonella*: -0.012; *Listeria*: -0.042 log10 CFU/day) (**Figure 3**).

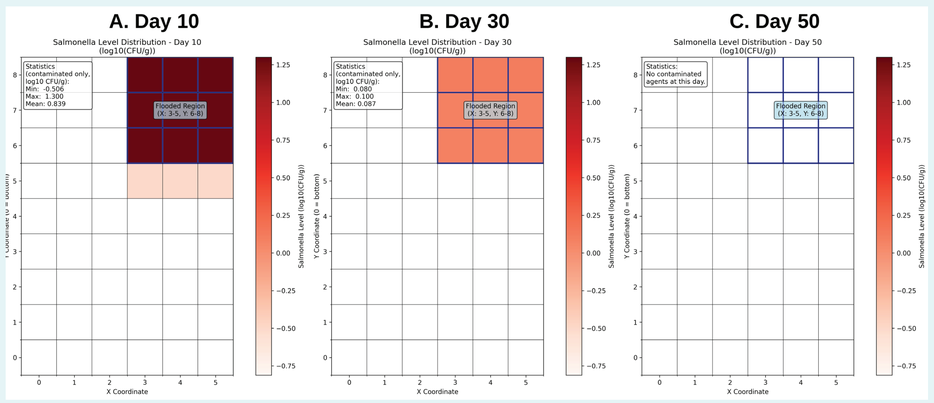

Figure 1:
Spatial distribution of *Salmonella* contamination across the produce field on days (A) 10, (B) 30, and (C) 50 of the flooding simulation from the model. The flooded source region (X: 3-5, Y: 6-8) is outlined in blue. Cells at or below the limit of detection (~0.81 log CFU/g) are shown in white. Each grid cell represents an agent corresponding to a 10 ft x 10 ft plot. Contamination and moisture were initialized only within the flooded source region; the simulation was run for 80 days total.

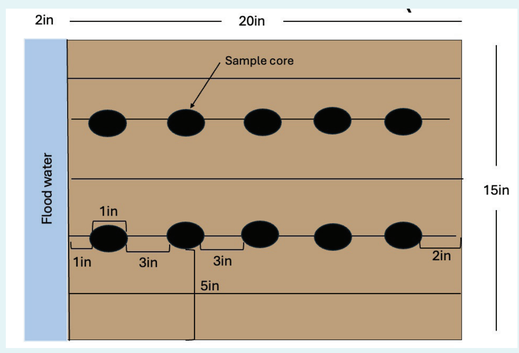

Figure 2:
Aerial-view diagram of the mesocosm showing the flood-water reservoir and sampling layout, with relevant length and width dimensions. Soil depth is approximately 8 inches (not shown). Black circles represent soil sample cores (1 inch in diameter) taken at five distances from the flood barrier. The closest sample is 1 inch from the flood barrier; adjacent cores are spaced 3 inches apart, with 2 inches between the farthest core and the far wall of the mesocosm. Samples are taken 5 inches in from the side wall to avoid soil with non-representative water flow along the walls of the mesocosm.

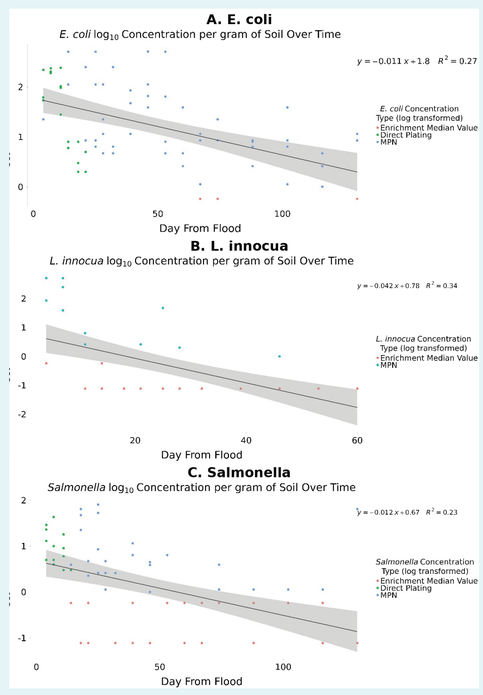

Figure 3:
Concentrations of *E. coli* (A), *L. innocua* (B), and *Salmonella* (C) in flooded areas of the simulated field-flooding experiment, based on four samples per day (2 locations x 2 soil depths). *E. coli* and *Salmonella* were tracked from day 0 through day 130; *L. innocua* was tracked through day 60 as its numbers decline more rapidly. Concentrations were measured by direct plating (green), Most Probable Number (MPN; blue), and enrichment (red); for each day only values above the detection limit are displayed, with priority given to direct plating, then MPN, then enrichment. Enrichment-positive samples are plotted at -0.2 log CFU/g soil; enrichment-negative samples are plotted at -1.1 log CFU/g soil (*L. innocua* direct-plating values were all below the detection limit). A linear decay model was fitted to each dataset, with the fitted equation shown in the top-right corner of each panel.

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