Florida Citrus Advanced Technology Program

QUARTERLY & FINAL REPORTS: Control of Citrus Greening, Canker & Emerging Diseases of Citrus

Instructions Complete the fields based on your project specs. When finished, save the form to your local disk using a unique name. Then, go to **http://research.fcprac.com**, and log in with your user name and password using Researcher Login in the lower left. Find this project title and click on **Submit a Report**. Update your profile information if needed, then upload this report as directed.

2009-2010 REPORT	CATEGORY (drop-down)	TODAY'S DATE (m/d/yr)
(●) *Quarterly Report* ( ) *Annual Report* ( ) *Final*	Management	9/30/09

WHAT IS THE "HEADLINE" FOR THIS REPORT (e.g. a one-sentence "newspaper headline" describing what you accomplished)

HLB control trials sho no difference between treatments and HLB model under development to test controls.

TITLE and CONTACT INFORMATION

Proposal Title Epidemiology and disease control of huanglongbing

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Phone 772-462-5883	*Project Duration (years)* 1 *Year of Project* 1
Organization USDA, ARS	*Total Direct Funds (current year)*

REPORT UPDATE (650 words; provide details about your headline)

Methods and models for the control of HLB disease of citrus. Citrus huanglongbing (HLB) is the most serious disease of citrus worldwide and presently for the very existence of citrus industry of Florida. The approach is two-fold:
First was the examination of the effect of various control strategies on HLB, in control plots, established in 2007. I this phase of the study, five treatments were examined: Minimal control, Insecticide vector control, Roguing, Roguing via PCR+, and Comprehensive. Results indicated that although treatments were significantly different, there was no benefit of any control treatment over another. Small differences were due to plot location, not treatment effects. The tests are being repeated, however, the results point to a need for regional control strategy and that small plantings that can't control neighbors cannot control the disease. Our estimates indicated that for each tree with visual symptoms, there were an average of 13 (range 2-52) that were infected but asymptomatic, i.e., infections that have occurred over the duration of the epidemic but that have not yet expressed symptoms. New plots have been established at the USDA, ARS , in Fort Pierce, Florida and the data collection is under way. Psyllids are also being trapped (in each plot) to estimate populations and correlate with disease progress in each plot.

The second approach is to develop epidemiological models of HLB disease dynamics which improve the understanding of vector-driven disease transmission and analyze disease control policies aimed at disrupting vector population dynamics. In previous and current work we have developed a model for citrus canker. This is the basis upon which we have built a preliminary model for HLB. The HLB simulation model is stochastic based on biological, epidemiological, and meteorological parameters using Markov Chain Monte-Carlo simulation methods and SIR modeling protocols. The model is fit to the HLB data collected in various observed epidemics from Florida and SE Asia by thousands of simulations. Linked-differential equations are used that describe the temporal increase in HLB infected trees and explicitly characterize the population dynamics of the vector. The effectiveness of different disease control measures such as intercropping with guava, roguing and insecticide use will be analyzed via this model and a suite of mathematical tools to identify the most effective strategies. HLB data sets will be correlated with various disease mitigation strategies/events from our epidemiology trials in Florida. The stochastic models allow testing of multiple disease management strategies in thousands of simulated epidemics to determine which will have the optimum effect and in what combination these methods can best be deployed for maximal disease control. The HLB model will continue to be augmented and improved over the next 1.5 years but are well near completion. Data continue to be generated for multiple test plots to parametrize the models. Models are being validated againse actual data to ensure correct estimation of disease dynamics.