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*	Genetics	10/19/09

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

Bioinformatic characterization of the Ca. Liberibacter asiaticus genome sequence for insights into niche adaptation

TITLE and CONTACT INFORMATION

Proposal Title Bioinformatic characterization and development of a central genome resources website for C. Liberibacter asiaticus

Principal Investigator Magdalen Lindeberg	*PI Last Name* Lindeberg
Email ML16@cornell.edu	*FDACS Contract Number* 123
Phone 607-254-7297	*Project Duration (years)* 3 *Year of Project* 1
Organization Cornell University	*Total Direct Funds (current year)* 140,084

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

Objective II: Website creation and development.
The Citrus Greening/HLB Genome Resources Website (http://www.citrusgreening.org/), brought online in the previous quarter, has been expanded to include a "News" column on the home page highlighting new genome analyses (discussed in more detail under Objective III), high interest genome-related publications with links to abstracts, and events relevant to genome researchers such as the upcoming HLB/Zebra Chip Meeting. In addition, a page listing a variety of citrus greening-related on-line resources has been created, linked to the home page under "Additional Information".
Objective III: Bioinformatic analysis of the Ca. Liberibacter genome.
A. A post-doctoral associate with training in biological systems and computational genome analysis has initiated bioinformatic characterization of extragenic sequence features in the recently published, closed genome sequence for Ca. Liberibacter asiaticus. To gain insight into co-regulated sets of genes that the bacterium may be using to exploit changing environmental niches as it moves from the psyllid vector to plant phloem and establishment in the phloem, candidate promoter sequences are being mapped genome-wide using (i) models derived from characterized promoters in related bacterial species and (ii) novel sequence motifs found present in Ca. Liberibacter. Repetitive sequences and variation in sequence composition are also being characterized.
B. To better assess its metabolic capabilities and limitations, unannotated regions in the published Ca. L. asiaticus genome sequence have been carefully analyzed, revealing the presence of numerous disrupted genes. Some disruptions are consistent with adaptation to a restricted environment while others are found in genes generally believed to be essential, suggesting possible errors in the published sequence. A listing of newly annotated pseudogenes can be found in in the "Access Data" section of the Citrus Greening/HLB Genome Resources Website in both table and Genbank format, the latter suitable for viewing with the Artemis genome viewer.
Objective I: Assess community needs.
The PI attended a special session on citrus greening at the 2009 Annual Meeting of the American Phytopathological Society (August 1-5) and engaged in fruitful discussions with interested researchers. The PI will be presenting a poster at the upcoming Joint Research Conference on HLB and Zebra Chip with the goal of promoting genome analysis tools available through the Citrus Greening/HLB Genome Resources Website, and establishing greater connections with researchers engaged in genome sequencing and genome scale analyses of additional strains and species of Ca. Liberibacter. Sequence comparison among isolates and species is predicted to yield important insights into the adaptation of this organism to different environmental niches.