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	1/11/10

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

Analysis of Liberibacter asiaticus regulatory gene products and binding sites indicates a highly simplified regulatory network

TITLE and CONTACT INFORMATION

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

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Phone 60-254-72977	*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 I: Assess community needs
The PI presented a poster entitled "Analysis of Ca. Liberibacter asiaticus Psy62 (Las) genome sequence data and creation of the CG-HLB genome resources web site" at the Joint Research Conference on HLB and Zebra Chip, November 2009 for the purpose of publicizing the available resources, and engaging with other researchers involved in genome analysis of Liberibacter.

Objective II: Website creation and development.
The Citrus Greening/HLB Genome Resources Website (http://www.citrusgreening.org/) has continued to expand. To assist CG/HLB researchers in navigating the growing number of Liberibacter-related datasets generated by 3rd party sites, links to these resources have been added to the Citrus Greening/HLB Genome Resources Website. Examples include pathway maps of Liberibacter metabolism generated by the Kyoto Encyclopedia of Genes and Genomes, and lists of genome structural features at the Genome Atlas Database. Links to other CG/HLB relevant sites including the Citrus Greening and Citrus canker publication list and web site for the International Psyllid Genome Consortium are also provided.

Objective III: Bioinformatic analyses of Ca. L. asiaticus sequence data.
Understanding Las biology and pathogenicity depends not only on knowing its raw genetic capability but also how and when individual genes are expressed. A list of predicted regulatory proteins encoded by the Las genome has been compiled. To initiate characterization of sites in the genome where these proteins bind (with implications for expression of downstream genes), sequences of experimentally characterized binding sites in related bacteria (e.g. Sinorhizobium, Rhizobium, and Agrobacterium) were assembled and used to create binding site models for computational analysis. These models are being applied to the Las genome sequence in order to identify candidate binding sites for three regulatory proteins: (RpoH (heat shock response), RpoD (constitutive expression), and RirA (response to iron availability). The models continue to be refined, but preliminary analyses suggest that in contrast to free-living bacteria which have distinct sets of co-regulated genes, Las has a much simpler regulatory profile. First, Las has many fewer regulatory proteins than do related free-living bacteria. Secondly, locations of predicted binding sites suggest that many genes that in free-living bacteria are tightly regulated in response to specific environmental conditions may be constitutively expressed in Las. Repetitive AT-rich sequences are also found in the promoter regions of several candidate virulence genes. It is hypothesized that their presence may enhance gene expression by allowing for easier separation of the DNA strands. The models described here can be readily applied to other Liberibacter strains and species as their genome sequences become available, with the potential to reveal sources of heat tolerance and other differences in environmental adaptation observed among isolates.