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	6/8/09

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

Citrus Greening-HLB Genome Resources Website established for deposition of genome sequence data and analysis

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 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. A Citrus Greening/HLB Genome Resources Website has been created and can be accessed at http://www.citrusgreening.org/.
Significant aspects of this objective achieved during this quarter include the following:
A. Development of a policy for data sharing. Concerns about publication priority, reluctance to release data that might be in error, and the slow pace at which sequence is generated have all contributed to a scarcity of publicly available genome data. In collaboration with the program manager, a policy was developed whereby the genome resources website would provide a venue where preliminary data and analyses generated from these data could be deposited, with access restricted to registered users. Prior to viewing the restricted data, users would be required to acknowledge the preliminary nature of the data and agree not to publish analyses based on these data without contacting the depositors.
B. Website organization. The http://www.citrusgreening.org/ website has been designed to accommodate both information with unrestricted access and data limited to registered users. Web pages with unrestricted access include those containing general information and links on the disease, pages providing guidelines and links for commonly used analytical tools such as BLAST analysis and genome viewing with the Artemis genome viewer, and pages summarizing the range of Ca. Liberibacter sequences that have been deposited at NCBI. With the exception of a 1.2 Mb draft genome sequence for Ca. L. asiaticus, all of the Ca. Liberibacter sequences currently available at NCBI fall into one of three gene clusters, diagrams of which have been posted on the website together with hyperlinks to their component accession records at NCBI.
In order to restrict access to pages containing preliminary data, a registration page has been set up requiring users, pending acceptance of the data sharing policy, to enter contact information and choose a user name and password. Once reviewed by the PI, the registrants are granted access to the restricted pages and their contact information added to the list of registered users. Information on data submission is included on the pages with unrestricted access.
While it is expected that the site will grow significantly as more data and analyses become available, the basic website structure has been designed to accommodate future growth.
Objective III: Bioinformatic analysis. Using the draft genome sequence for Ca. L. asiaticus deposited at NCBI, a single pseudomolecule has been generated from the deposited contigs to aid users in viewing the 34 contigs in their totality (draft sequences are deposited at NCBI as independently numbered and annotated contigs). Various feature files have been produced for the pseudomolecule, so that users can view annotations generated by the MG-RAST server as well as BLAST hits independent of gene calls. Functional roles predicted by the MG-RAST server have been mapped to KEGG metabolic maps and the results compared to maps generated for two fastidious plant pathogenic bacteria and four insect endosymbiotic bacteria. Comparison reveals that the deposited Ca. L. asiaticus sequence encodes only a small percentage of enzymes involved in amino acid, carbohydrate, energy, glycan, lipid, and nucleotide metabolism relative to these other organisms. This limited metabolic capability suggests that the deposited sequence may not represent a complete genome.
Objective I: Assess community needs. Various members of the citrus greening community have provided input during website development. Further conversations between the PI and community members about data deposition and desired analyses are expected at the special session on citrus greening to be held at the meeting of the American Phytopathological Society (August 1-5).