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	8/4/09

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

International consortium is moving ahead with sequencing a citrus genome, to provide tools in the fight against HLB

TITLE and CONTACT INFORMATION

Proposal Title International citrus genome consortium (ICGC): Providing tools to address HLB and other challenges

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Phone 8639561151	*Project Duration (years)* 3 *Year of Project* 1
Organization UF-CREC	*Total Direct Funds (current year)* $1,300,000

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

Funding is now in place among all the partners of the International Citrus Genome Consortium (US, Brazil, Spain, France, and Italy) to move forward with the project to sequence a haploid citrus genome. DNA samples for sequencing have been prepared, and the strict quality control standards required by the sequencing centers (JGI in the US, Genoscope in France, and IGA in Italy) have been met. DNA samples have been shipped only to Genoscope and IGA at this point. The University of Florida and Brazilian interests remain in negotiations with JGI over contract language, before JGI can proceed with their portion of the sequencing project. Meanwhile, work has proceeded at the UF-CREC to produce sample materials needed for the microarray experiments planned, using Affymetrix GeneChips, a new array platform developed by the co-PIs at UF using Agilent technology, and for the cDNA platform available through our co-PI in Spain. To this end, two sets of plants of sweet orange, rough lemon, and Volkamer lemon, representing the more susceptible and more tolerant types respectively, have been inoculated with budwood from HLB-infected Carrizo citrange (Carrizo is resistant to CTV, so viral interaction complications will be avoided) in an environmentally controlled greenhouse. Samples of RNA have been prepared from all of the plants at regular intervals, to be used in microarray experiments. Plants have been observed for symptoms, and qPCR has identified some that were successfully infected. The HarvEST Citrus EST database is in process of being updated, to provide an improved database for gene expressions studies. The EST sequences from our colleagues in Brazil and Japan have all been downloaded and reassembled, increasing the number of publicly available citrus ESTs to more than 465,000. The plans to exploit genome sequence information for a better understanding of the interactions of citrus plants with the pathogen causing HLB are ultimately most dependent on having the genome assembled and annotated; for this reason, our main focus will be on accomplishing that goal, while continuing to establish the experiments and collecting the samples that will be used for subsequent microarray analyses and deep transcriptome sequencing.