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	11/19/09

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

Sweet Orange Genome Sequencing Project Nears Completion

TITLE and CONTACT INFORMATION

Proposal Title Proposal for Supplemental Support to the Proposal Titled: Revision to the International Citrus Genome Consortium (ICGC) Sequencing Project: Part 1, Sequencing (March 2008)

Principal Investigator Fred G. Gmitter Jr.	*PI Last Name* Gmitter
Email fgg@crec.ifas.ufl.edu	*FDACS Contract Number*
Phone 8639561151	*Project Duration (years)* 1 *Year of Project* 1
Organization UF-CREC	*Total Direct Funds (current year)* $100000

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

This project was an extension in time and financial resources to the previously funded project titled "The International Citrus Genome Consortium (ICGC) sequencing project; Part 1, Sequencing" which was intended first to initiate the ICGC haploid genome sequencing project using Sanger sequencing. Those funds were allocated as a first investment intended to demonstrate good faith commitment on behalf of the Florida citrus industry. That goal was achieved, as evidenced by current funding in place for 4x coverage by our French collaborators through Genoscope, 2x coverage by our Italian colleagues through the Istituto di Genomica Applicata (IGA), 2x coverage through EMBRAPA funding of colleagues in Brazil plus 2x coverage through FCPRAC from the US together with the USDOE Joint Genome Institute (JGI). Because the timing to use the allocation first made by FCPRAC through this grant did not allow for our investment in Sanger sequencing through JGI (they require the project to be conducted at one time, not in pieces), I requested and was granted a revision to the objectives, to begin a sweet orange genome "re-sequencing project", using next-gen sequencing (454 of Roche Diagnostics). This is a collaborative effort between my lab, Dr. W Farmerie (UF-ICBR), Dr. D. Rokhsar (JGI), and Dr. T. Harkins (Roche Diagnostics/454). This project is in concert with the ICGC sequencing initiative plans to use next-generation sequencing technologies on several diploid genomes, as an added resource to the Sanger haploid sequencing project currently underway. Currently, all sequencing runs of the sweet orange genome have been completed, including 8x coverage of 454/FLX WGS, 6x coverage 454/Titanium WGS, 9x coverage of 3 kb insert libraries paired-end sequences (PE), and 6.7x coverage of 8 kb insert libraries (PE). Combined with a 1.2x Sanger sequencing effort by JGI several years ago, we now have >30x sweet orange genome coverage. In addition, 1.2 million ESTs have been produced by one Titanium run on an RNA library from leaf tissue, to aid in subsequent assembly, gene prediction, and annotation. Six preliminary assemblies of the genome sequence have been attempted by 454 scientists, using various versions of their in-house assembly program, Newbler, and two more assembly efforts will be made using modified parameters. To this point, this work has yielded fragmented assemblies upon which gene prediction models had a difficult time to work. Roche/454 is continuing their efforts at assembly. When the challenges of assembly can be overcome, it is likely that the sweet orange genome sequence will be made available to the research community sometime in the first half of 2010, following gene prediction and annotation procedures, to make it a useful resource for subsequent research. The sequence will be housed in a new database, Tree Fruit GDR, which was funded by a recent SCRI grant to include citrus. Further, the sequence will be available also through the JGI plant genome portal, and will also be deposited with NCBI. Though funding for this project was terminated in September 2009, the work will continue to completion. This will be a valuable tool for all research projects aimed at understanding HLB infection and disease, as well as empowering for the full scope of citrus genetic improvement objectives addressed by breeding and genetics research programs.