# 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 | 7/12/10 |

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

Genome browser for Ca. L. asiaticus implemented for easy visualization of genome properties

**TITLE and CONTACT INFORMATION**

*Proposal Title* Development of a central genome resources website for C. Liberibacter asiaticus


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|---|---|
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| *Phone* 607-280-9058 | *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)**

Note that this report corresponds to the first of the two additional quarterly updates mandated in amendment #1 of the no-cost extension for the first year of grant #123.

Objective III: Bioinformatic analysis of Ca. L. asiaticus sequence data
Bacterial proteins mediating interactions with the environment and with host organisms are commonly found in the periplasm and bacterial outer membrane. To identify the likely set of Las-encoded proteins targeted to regions of the cell outside the cytoplasm, all predicted Las proteins were evaluated for the presence of predicted signal peptides and lipoprotein signals using the SignalP and LipoP programs. Resulting predictions are posted on the CG-HLB Genome Resources website together with the repetitive sequences, transcription factor binding sites, and horizontally transferred regions predicted previously.

Objective II: Website creation and development
To better display the accumulated data on bioinformatic characterization of Ca. L. asiaticus, a new genome viewing utility is being added to the CG-HLB Genome Resources website for presentation at the upcoming Annual Meeting of the American Phytopathological Society (APS) Meeting (August 7-11). Guidelines and materials for use of the Artemis Genome Viewer will remain on the site; however, the GBrowse based viewer (see http://gmod.org/wiki/Ggb/ for typical display) is more easily accessed by a wider audience and can be readily expanded to include a broad range of bioinformatic data and comparative analyses. Data presented in the GBrowse viewer is organized as a linear display of genes as they are found in the Las genome, and through which the user can scroll or zoom. Tracks corresponding to different aspects of genome characterization are graphically displayed below the main genome entry with hyperlinks to other databases included as appropriate. Tracks have been installed for all predicted proteins with links to records at NCBI, all predicted proteins having links to the COG database (as a source of functional information), subcellular localization as predicted by Psortb, and operon predictions generated using DOOR. Transcription factor binding sites, repetitive regions (of particular interest for diagnostic purposes), and signal peptide predictions will also be incorporated. In addition to functioning as a central data clearinghouse for analyses performed by my group as well as by other genome-related databases, this type of display can also accommodate analyses such as the 3D protein structural predictions currently being generated by the Grishin group and orthology between the published Las genome sequence and those of other strains and species of Liberibacter.

The new genome viewer is expected to go live during the next couple weeks. At that time, all registered users of the CG-HLB Genome Resources Website will be invited to try out this new feature, and feedback and additional data will be solicited. Different features of the viewer as well as the component analyses will be discussed at the "Candidatus Liberbacter/ Epidemiology & Ecology" technical session at the upcoming APS meeting.