CITRUS ADVANCED TECHNOLOGY PROGRAM

QUARTERLY & FINAL REPORTS: Control of Citrus Greening, Canker & Emerging Diseases of Citrus

▶ INSTRUCTIONS

(●) *Quarterly Report* ( ) *Annual Report* ( ) *Final*

Required: What is the "headline" for this report (e.g. a one-sentence "newspaper headline" describing what you accomplished)

New sequences added to the Liberibacter genome viewer

Proposal Title

Development of a central genome resources website for Ca. Liberibacter asiaticus

Today's Date	Sponsoring Organization (drop-down)	Category (drop down)
4/6/11	Citrus Research and Development Foundation	Unclassified

REPORT UPDATE (500 words; summarize your accomplishments)

Website Creation and Development

As previously described, the CG-HLB Genome Resources website hosts a genome viewer for the purpose of providing a convenient interface for accessing Ca. Liberibacter genome features and analysis of predicted proteins (http://www.citrusgreening.org/HLB-GBrowse.html). The genome viewer is composed of 10+ "tracks" specifying various predicted features of the genome sequence. Public release of the genome sequence of Ca. Liberibacter solanacearum CLso-CZ1 and a sizable phage-associated region for Ca. Liberibacter asiaticus UF506 has led to incorporation of these additional sequences into the genome viewer along with predictions for the genome features found therein. Addition of new tracks and links to the genome viewer is ongoing as more bioinformatic analyses are performed. In addition, a continuously updated list of research publications on Liberibacter has been added as one of the additional resources provided by the CG-HLB website.

Bioinformatic Analyses

In conjunction with incorporation of the Lso CLso-CZ1 and Las UF506 phage sequences into the Liberibacter genome browser, more attention is being given to how sequence variation among strains and species might best be represented and used in design of diagnostic primers. Currently, regions of the Las genome determined to be unique relative to the Lso genome (E value cutoff of 1e-5) are shown in a track on the genome viewer. However, we are working on different approaches for displaying variation on a finer scale. This viewer is extendable to displaying variation among multiple strains as they become available.

Outreach

Information on the CG-HLB Genome Resources web site and associated genome viewer was presented at the 2nd IRCHLB research conference in Orlando Florida and contacts made with researchers sequencing additional Ca. Liberibacter strains. We are also assisting Dr. Wayne Hunter (ARS, Fort Pierce) with metagenome analysis of the Asian citrus psyllid with a particular focus on Wolbachia, the other alpha-proteobacteria associated with this insect. Regions of high similarity between Liberibacter and Wolbachia will be documented in the genome viewer and predicted metabolic capabilities compared between the two bacteria to evaluate the likelihood of complementary metabolism.

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Organization Cornell University

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SUBMIT REPORT

CITRUS RESEARCH AND DEVELOPMENT FOUNDATION, INC.