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*	HLB Pathology	6/27/09

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

Understand the virulence mechanism of HLB pathogen by genome sequencing and functional genomics approaches

TITLE and CONTACT INFORMATION

Proposal Title Original: Genome sequencing of Candidatus Liberibacter asiaticus. Revised: Understand the virulence mechanism of Ca. Liberibacter asiaticus by genome sequencing and functional genomics approaches

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Organization Citrus Research and Education Center, UF	*Total Direct Funds (current year)* 160916

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

Citrus Huanglongbing (HLB) is the biggest threat to the Florida citrus industry. Florida accounted for 70% of the total U.S. production in 2006-07. HLB, known as citrus greening, can debilitate the productive capacity of citrus trees with losses of 30-100% reported. HLB was found in Florida in 2005 and has spread throughout thirty of the citrus producing counties in Florida by January 2008.

The overall goal of this proposed work is to characterize the virulence mechanisms of Candidatus Liberibacter asiaticus (Las), the citrus Huanglongbing (HLB) pathogen, thus to come up with new management strategies by genome sequencing and functional genomics approaches. The original goal of the proposed research is to further complete the genome sequencing of Candidatus Liberibacter asiaticus, for which a draft sequence is available. The goal was modified to meet the current progress in genome sequencing of Candidatus Liberibacter asiaticus with the advice and permission from program manager of FCPRAC. The tile has been changed to the following to better suit the goal: Understand the virulence mechanism of Candidatus Liberibacter asiaticus by genome sequencing and functional genomics approaches.

Bioinformatics analysis was performed to identify potential virulence factors. The SignalP v3.0 program was used to predict the presence of signal peptide within the proteins. The secretomeP 2.0 program was used to predict the non-classical secretion proteins without signal peptide. ORF containing transmembrane domains was predicted by TMHMM2.0 program. Smart and other programs were used to further mine the genome sequence of Candidatus Liberibacter asiaticus.

Progress was made on characterization of the virulence mechanism of Candidatus Liberibacter asiaticus. Both microarray and real time PCR approaches were used to compare the gene expression profile of Candidatus Liberibacter in planta and in psyllids. The microarray covers all the genes of Candidatus Liberibacter asiaticus. Genome of the HLB pathogen was analyzed for homologs of known virulence genes, genes containing domains and motifs which may play roles in virulence and pathogenicity. Totally, 560 genes were included in quantitative revere transcriptional PCR analysis. It is expected that genes which are critical for survival and growth in planta and psyllids, virulence in citrus, transmission in psyllids will be differentially expressed in planta and in psyllids. Totally, more than 260 genes were identified which are differentially expressed in planta and in psyllids. Among them, some genes were shown to be potential virulence factors. Our preliminary results suggest that Candidatus Liberibacter asiaticus affecting gene expression of the host by secreting some putative virulence factors into the phloem of citrus. Further functional analysis is of those potential virulence factors is being performed in the Wang lab and collaborators lab. For example, both gene ontology and KEGG pathway analyses are being performed to further understand the transcriptional profiling of the HLB pathogen in different environments. Analysis of the genome of the HLB pathogen also revealed multiple potential target of developing bactericides and other approaches of controlling HLB. The potential of utilizing those approaches are being tested.